

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 7, 2004, 07:35:55 ; Search time 131 Seconds  
(without alignments)  
2122.369 Million cell updates/sec

Title: US-10-014-101-4  
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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 682709 seqs, 277475446 residues  
Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-DB=Issued Patents NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0  
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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	1141	44.0	1605	3	US-09-124-541-3	Sequence 3, Appli
2	1141	44.0	1605	4	US-09-663-326-3	Sequence 3, Appli
3	1014	39.1	6733	3	US-09-124-541-2	Sequence 2, Appli
4	1014	39.1	6733	4	US-09-663-326-2	Sequence 2, Appli
5	835	32.2	1602	3	US-09-124-541-10	Sequence 10, Appli
6	835	32.2	1602	4	US-09-663-326-10	Sequence 10, Appli
7	198.5	7.6	4403785	3	US-09-103-840A-2	Sequence 2, Appli
8	196.5	7.6	4411529	3	US-09-103-840A-1	Sequence 1, Appli
9	183.5	7.1	37769	4	US-08-311-731A-23	Sequence 23, Appli
10	178	6.9	1419	4	US-08-266-965-61	Sequence 61, Appli
11	178	6.9	53500	4	US-09-266-965-76	Sequence 76, Appli
12	177.5	6.8	1833	4	US-09-630-983A-2	Sequence 2, Appli

13	175.5	6.8	2034	4	US-09-423-468A-12	Sequence 12, Appli
14	175.5	6.8	2064	4	US-09-630-983A-4	Sequence 4, Appli
15	174	6.7	1407	4	US-09-328-352-1897	Sequence 1897, Ap
16	171.5	6.6	1553	3	US-09-217-490-1	Sequence 1, Appli
17	169	6.5	2120	4	US-08-630-983A-10	Sequence 10, Appli
18	168.5	6.5	1981	4	US-09-647-390-17	Sequence 17, Appli
19	166	6.4	3111	4	US-09-489-039A-3095	Sequence 3095, Ap
20	160	6.2	3060	4	US-09-543-681A-275	Sequence 275, Ap
21	155.5	6.0	3680	4	US-09-647-390-15	Sequence 15, Appli
22	153.5	5.9	1474	4	US-08-624-447-1	Sequence 1, Appli
23	150.5	5.8	1365	4	US-09-894-844-73	Sequence 73, Appli
24	150.5	5.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
25	150.5	5.8	4411529	3	US-09-103-840A-1	Sequence 1, Appli
26	146.5	5.6	1545	4	US-09-266-965-31	Sequence 31, Appli
27	146.5	5.6	18331	4	US-09-266-965-96	Sequence 96, Appli
28	146.5	5.6	53500	4	US-09-266-965-76	Sequence 76, Appli
29	142.5	5.5	1809	4	US-09-589-733C-5	Sequence 5, Appli
30	138.5	5.3	1830121	4	US-09-557-884-1	Sequence 1, Appli
31	138.5	5.3	1830121	4	US-09-643-990A-1	Sequence 1, Appli
32	133	5.1	2169	5	PCT-US96-05320A-264	Sequence 264, App
33	133	5.1	1830121	4	US-09-557-884-1	Sequence 1, Appli
34	133	5.1	1830121	4	US-09-643-990A-1	Sequence 1, Appli
35	132	5.1	1284	4	US-09-894-844-106	Sequence 106, App
36	129.5	5.0	1581	4	US-09-630-983A-6	Sequence 6, Appli
37	129.5	5.0	2138	4	US-09-630-983A-8	Sequence 8, Appli
38	127	4.9	99629	4	US-09-596-002-37	Sequence 37, Appli
39	126.5	4.9	1392	4	US-09-252-991A-7430	Sequence 7430, Ap
40	126.5	4.9	1932	4	US-09-252-991A-7271	Sequence 7271, Ap
41	126	4.9	1422	4	US-09-540-236-1736	Sequence 1736, Ap
42	116	4.5	1509	4	US-09-252-991A-11048	Sequence 11048, A
43	116	4.5	1590	4	US-09-252-991A-11206	Sequence 11206, A
44	116	4.5	4061	3	US-08-425-843-1	Sequence 1, Appli
45	115	4.4	1467	4	US-09-540-236-761	Sequence 761, App

ALIGNMENTS

RESULT 1  
US-09-124-541-3  
; Sequence 3, Application US/09124541A  
; Patent No. 6229066  
; GENERAL INFORMATION:  
; APPLICANT: Morris Ph.D., Roy O.  
; TITLE OF INVENTION: A CYTOKININ OXIDASE  
; FILE REFERENCE: UMO1490  
; CURRENT APPLICATION NUMBER: US/09/124.541A  
; EARLIER FILING DATE: 1998-07-29  
; EARLIER FILING DATE: 1997-07-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 1605  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1605)  
US-09-124-541-3

Alignment Scores:	6.23e-132	Length:	1605
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Score:	63.71%	Conservative:	83
Best Local Similarity:	46.98%	Mismatches:	152
Query Match:	43.95%	Indels:	28
DB:	3	Gaps:	11

US-10-014-101-4 (1-501) x US-09-124-541-3 (1-1605)

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QY 50 GlyAsnIleThrThrValThrProGlyGlyValIleCysProSerSerThrAlaAspIle 69  
Db 184 GGCALCATCATCGTGGCGCTCCCGCGCGGTCTCGTACCGTCTGTCACCGCGGACCTG 243  
QY 70 SerArgLeuLeuGlnTyrAlaAlaGlnGlyLysSer-----ThrPheGlnValAlaAla 87  
Db 244 GTGGCGCTGCTCAGC---CGGCCCAACTCCACCCCGGGTGGCCCTACACCATCGCGTTC 300  
QY 88 ArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsn 107  
Db 301 CGCGCGCGCGGACATCCCTCATGGCCAGGCTTCGCCCGCGCGGTGCTGCTCAGC 360  
QY 108 MetThrCysIleThrAsp-----ValValSerLysAspLysLys 121  
Db 361 ATGGGCTCCCTGGCGGACCGCGCGCGCGCGCATCAACGTTCTCGCGGACCGCGCGC 420  
QY 122 TyrAlaAspValAlaAlaGlyThrLeuTyrValAspValLeuLysLysThrAlaGluLys 141  
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QY 142 GlyValSerProValSerThrThrAspTyrLeuHisIleThrValGlyGlyThrLeuSer 161  
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QY 162 AsnGlyGlyIleGlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGlu 181  
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QY 182 LeuAspValIleThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGlu 201  
Db 601 ATGACGTTATACCG 660  
QY 202 LeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleThrArgAlaGlyIle 221  
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QY 222 ValLeuAspHisAlaProLysArgAlaLysTyrPheArgMetLeuTyrSerAspPheThr 241  
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QY 242 ThrPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGly----- 258  
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QY 272 ValValAspThrSerPheProSerAspGlnSerLysValAlaAspLeuValLys 291  
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QY 292 GlnHisGly-----IleIleTyrValLeuGluValAlaLysTyrTyrAspAspProAsn 309  
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QY 428 Leu---GlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGluLysIle 446  
Db 1372 CTCTTCGTCG 1431  
QY 447 IleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyrThrSer 466  
Db 1432 CTGCGCTTCTGCGACCTCGCGCGATCCAGTACAGACCTACCTGGCGCGCGCACGGAC 1491  
QY 467 LysGluAspTrpIleGluHisPheGly---SerLysTyrAspAspPheSerLysArgLys 485  
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RESULT 2  
US-09-663-326-3  
; Sequence 3, Application US/09663326  
; Patent No. 6617497  
; GENERAL INFORMATION:  
; APPLICANT: Morris Ph.D., Roy O.  
; TITLE OF INVENTION: A CYTOKININ OXIDASE  
; FILE REFERENCE: UMO1490  
; CURRENT APPLICATION NUMBER: US/09/663,326  
; CURRENT FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: 60/054,268  
; PRIOR FILING DATE: 1997-07-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 1605  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1605)  
US-09-663-326-3

Alignment Scores:  
Prod. No.: 6 23e-132 Length: 1605  
Score: 1141.00 Matches: 233  
Percent Similarity: 63.71% Conservative: 83  
Best Local Similarity: 46.98% Mismatches: 152  
Query Match: 43.95% Indels: 28  
DB: 4 Gaps: 11

US-10-014-101-4 (1-501) x US-09-663-326-3 (1-1605)

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QY 70 SerArgLeuLeuGlnTyrAlaAlaGlnGlyLysSer-----ThrPheGlnValAlaAla 87  
Db 244 GTGGCGCTGCTCAGC---CGGCCCAACTCCACCCCGGGTGGCCCTACACCATCGCGTTC 300  
QY 88 ArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsn 107  
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QY 108 MetThrCysIleThrAsp-----ValValValSerLysAspLysLys 121  
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QY 162 AsnGlyGlyIleGlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGlu 181  
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QY 259 -----ValAspTyrLeuGluGlyGlnIlePhe-----LeuSerAsnGly 271  
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QY 272 ValValAspThrSerPhePheProSerAspGlnSerLysValAlaAspLeuValLys 291  
Db 901 CTGGCGAACACGGGTTCTTACCCGACCGCGAGCTCGCCGCGATCGTCGCGCTCGCGCGG 960  
QY 292 GlnHisGly-----IleIleTyrValLeuGluValAlaLysTyrTyrAspAspProAsn 309  
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QY 310 -----LeuProIleLeuSerLysValIleAspThrLeuThrLysThrLeuSerTyrLeu 327  
Db 1021 GC 1080  
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Db 1081 GAGGGGTTCCGCTCCAGC 1140  
QY 348 GluGluAsnLysLeuArgSerLeuGlyLeuTyrGluLeuProHisProTrpLeuAsnLeu 367  
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Db 1201 TTCGTGCGCGCTCGC 1257  
QY 388 LysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAsp 407  
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QY 408 AsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIleGlyLeu 427  
Db 1318 GACGGCATGTGCGCGCGCGCGCGCG-----TCTGAGGACGTGTCTACGCGGTGCGGTG 1371  
QY 428 Leu-----GlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGluLysIle 446  
Db 1372 CTCTTCTCGTGGTGGC 1431  
QY 447 IleArgPheCysLysAspSerGlyIleLysIleLysLeuThrMetHisTyrThrSer 466

Db 1432 CTGCGCTTCTGGACCTCGCGCGGATCCAGTACAAGACCTACCTGCGCGGCACACGGAC 1491  
QY 467 LysGluAspTrpIleGluHisPheGly---SerLysTrpAspAspPheSerLysArgLys 485  
Db 1492 CGAGTGACTGGTCCGCCACTTCGGCGCGCGCAAGTGAATCGCTTCTGGAGATGAAG 1551  
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Db 1552 AACCAAGTACGAGCCCAAGAGGCTGCTCTCCCGCGCGCAGGACATCTTC 1599

RESULT 3  
US-09-124-541-2  
; Sequence 2, Application US/09124541A  
; Patent No. 6229066  
; GENERAL INFORMATION:  
; APPLICANT: Morris Ph.D., Roy O.  
; TITLE OF INVENTION: A CYTOKININ OXIDASE  
; FILE REFERENCE: UMO1490  
; CURRENT APPLICATION NUMBER: US/09/124,541A  
; EARLIER FILING DATE: 1998-07-29  
; EARLIER APPLICATION NUMBER: 60/054,268  
; EARLIER FILING DATE: 1997-07-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 6733  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1)..(6733)  
; OTHER INFORMATION: genomic sequence for a cytokinin oxidase from Zea  
; OTHER INFORMATION: mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1497)..(2111)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2524)..(3216)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (3311)..(3607)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (5697)  
US-09-124-541-2

Alignment Scores:  
Pred. No.: 5,5e-115 Length: 6733  
Matches: 233  
Conservative: 84  
Best Local Similarity: 47.60%  
Query Match: 34.98%  
Indels: 151  
Gaps: 198  
DB: 13

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Db 1680 GGCAACATCATCGTGGCGCGCTCCCGCGCGCGCTGTGTACCCGCTGTCCACGGCGACCTG 1739  
QY 70 SerArgLeuLeuGlnTyrAlaAlaAsnGlyLysSer-----ThrPheGlnValAlaAla 87  
Db 1740 GTGGCGCTGCTGAC---GGGGCAACTCCACCGCGGGGTGGCGCTACACCATCGCGTTC 1796  
QY 88 ArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsn 107  
Db 1797 GCGGCGCGCGCGCACTCCCTCATGGCGCAGGCGCTTCGCCCCCGCGCGCGCTGCTGCTCAAC 1856

QY 108 MetThrCysIleThrAsp-----ValValValSerIysAspIysLys 121  
Db 1857 ATGGCTCCCTGGGCGACGCGCGCGCGCGCGCGCATCAACGTGTTCGCGGACGCGCGC 1916  
QY 122 TyrAlaAspValAlaAlaGlyThrLeuTrpValAspValLeuLysThrAlaGluLys 141  
Db 1917 TAGCTGGAGCGCGCGCGCGAGCGAGGTGTGTGATCGAGCTTTCGCGCGCTGGCGGCGC 1976  
QY 142 GlyValSerProValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSer 161  
Db 1977 GCGGTGGCGCGCGCTCCTGGAAACGACTACCTCTACCTCACCGTGGCGGCGACGTGCC 2036  
QY 162 AsnGlyGlyIleGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGlu 181  
Db 2037 AACGCGAGGATCAGCGCGCGAGCGGTTCGCGCACGCGCGCCACAGATATCTAACGTGCTGGAG 2096  
QY 182 LeuAspValIleThrGlyLys----- 188  
Db 2097 ATGACGTTATCACCGGTGACGTGTGCACCTACTACTACTATTTTCCCTCCCTTGCACAGT 2156  
QY 188 ----- 188  
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Db 2637 GCGCGCGCGCGCGCGGGCGGGTGGTGGTTCGTGTCACCGACTTCGCGCGCTTCAG 2696  
QY 244 rLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGly----- 258  
Db 2697 CGCGCGACGAGCGGCTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCG 2756  
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Db 2937 GCGCGCGTGGACGAGAGCTCGCTCGCTGGGCGACGCTGAGCTACGTGAGGGGTT 2996  
QY 330 eIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArgValHisValGluGluAs 350  
Db 2997 CGCTTCCAGCGCGAGCTGCTACCGCGGCTTCTTGACCGGCTGCACGCGGAGGT 3056  
QY 350 nLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeuAsnLeuTyrValPr 370  
Db 3057 GCGCTCAACAAGCTGGGCGTGTGGCGGTCGCGCACCGCTGGCTCAACATGCTGTCGCC 3116  
QY 370 oLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLeuLysGlnLy 390  
Db 3117 GCGCTCGCGATCGCGACTTCGACCGCGGCTGTTCAGGGCATC---CTGACGGGCAC 3173  
QY 390 sSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsn----- 404  
Db 3174 CGACATCGTGGCGCGCTCATCGTCTACCGCTCAACAAATCCATGCTGTTGTAATCG 3233  
QY 404 ----- 404  
Db 3234 ATCGGCTAGTAGTAGTAGGACGCGCGCGCGCTCTGACGACTCGACCGGTCTTT 3293  
QY 405 -----LysTrpAspAsnArgMetSerAlaMetIleProGluIleAspG 419  
Db 3294 CTGGGCTTGTGTTTTTTCATGTGGGACGACGGCATGTGCGCGCGACGCCG---TCTG 3347  
QY 419 luAspValIleTyrIleIleGlyLeuLeu---GlnSerAlaThrProLysAspLeuProG 438  
Db 3348 AGGACGTGTTCTACCGGCTGCTGCTCTCTCTCGTGGTGGCGCCCAACGACCTGCGCA 3407  
QY 438 luValGluSerValAsnGluLysIleIleArgPheCysLysAspSerGlyIleLysIleL 458  
Db 3408 GGCTGCAGGACAGACAGGAGGATCTCGCTTCTCGACCTCGCGCGGATCCAGTACA 3467  
QY 458 ysGlnTyrLeuMetHisTyrThrSerLysGluAspTrpIleGluHisPheGly---SerL 477  
Db 3468 AGACCTACCTGGCGCGCACACGACCGCAGTACTGGGTCCGCGACTTCGCGCGCGCCA 3527  
QY 477 ystTpAspPheSerLysArgLysAspLeuPheAspProLysLeuLeuSerProG 497  
Db 3528 AGTGAATCGTTCTGAGAGATGAAGAACAGTACGACCCCAAGAGGCTGCTCTCCCCC 3587  
QY 497 lyGlnAspIlePhe 501  
Db 3588 GCCAGGACATCTTC 3601  
RESULT 4  
US-09-663-326-2  
; Sequence 2, Application US/09663326  
; Patent No. 6617497  
; GENERAL INFORMATION:  
; APPLICANT: Morris Ph.D., Roy O.  
; TITLE OF INVENTION: A CYTOKININ OXIDASE  
; FILE REFERENCE: UMO1490  
; CURRENT APPLICATION NUMBER: US/09/663,326  
; CURRENT FILING DATE: 2000-09-15  
; PRIOR APPLICATION NUMBER: 60/054,268  
; PRIOR FILING DATE: 1997-07-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO: 2  
; LENGTH: 6733  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1)..(6733)  
; OTHER INFORMATION: Genomic sequence for a cytokinin oxidase from Zea  
; NAME/KEY: CDS  
; LOCATION: (1497)..(2111)



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; NAME/KEY: CDS
; LOCATION: (2524)..(3216)
; NAME/KEY: CDS
; LOCATION: (3311)..(3607)
; NAME/KEY: unsure
; LOCATION: (5697)
US-09-663-326-2

Alignment Scores:
Pred. No.: 5,5e-115 Length: 6733
Score: 1014.00 Matches: 233
Percent Similarity: 47.60% Conservative: 84
Best Local Similarity: 34.98% Mismatches: 151
Query Match: 39.06% Indels: 198
DB: 4 Gaps: 13

US-10-014-101-4 (1-501) x US-09-663-326-2 (1-6733)

QY 30 SerLeuAsnLeuThrLeuSerThrAspProSerIleLeuSerAlaAlaSerHisAspPhe 49
Db 1620 GCCTTGGACGGCAAGCTCCGACCGACAGCAACAGCGACGGCGGGCGCTCGACGGACTTC 1679
QY 50 GlyAsnIleThrThrValThrProGlyGlyValIleCysProSerSerThrAlaAspIle 69
Db 1680 GGCAACATCACGTGGCGCTCCCGCGCGCGTCTGTGTACCGTGTGTCCACGGCGACCTG 1739
QY 70 SerArgLeuLeuGlnThrAlaAlaAsnGlyLysSer-----ThrPheGlnValAlaAla 87
Db 1740 GTGGCGCTGCTGAGC---CGCGCAACTCCACCCCGGGGTGGCCCTCACACATCGCGTTC 1796
QY 88 ArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsn 107
Db 1797 CGCGCGCGGGCCATCTCTCTATGCGCCAGGCTTCGCGCCCGCGCGGTGTGTGTCAAC 1856
QY 108 MetThrCysIleThrAsp-----ValValValSerLysAspLysLys 121
Db 1857 ATGGCGTCCCTGGCGAGCGCGCGCGCGCGCATCAACAGTGTCCGCGAGCGCGCGC 1916
QY 122 TyrAlaAspValAlaAlaGlyThrLeuTrpValAspValIleLysLysThrAlaGlnLys 141
Db 1917 TACGTGGACGCGCGGGGAGGAGGTGTGTGATGACAGTGTTCGCGCGTCTCGTGGCGGC 1976
QY 142 GlyValSerProValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSer 161
Db 1977 GCGGTGGCGCGCGCTCTCTGGAACAGCTACTCTACTCTACCTCAGCTCGCGGCGACGTGTC 2036
QY 162 AsnGlyGlyIleGlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGlu 181
Db 2037 AACGAGGAGATCAGCGCGCGCGGTTCGCCACGCGCCACAGATATCTAACGTGTGGAG 2096
QY 182 LeuAspValIleThrGly-Lys----- 188
Db 2097 ATGGACGTTATCACCGGTACGTGTGCACCTACTACTACTTTTTTCCCTCCCTTGCACAGT 2156
QY 188 ----- 188
Db 2157 GCACAACCACACACAGCAAGCAAGAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2216
QY 188 ----- 188
Db 2217 TGCATCGACTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2276
QY 188 ----- 188
Db 2277 TCGTTTACCTACATTGGAATCATATATTATTTTATTTTATTTTATTTTATTTTATTTTAT 2336
QY 188 ----- 188
Db 2337 GTTAATGTCGCGCTGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 2396
QY 188 ----- 188
Db 2397 TTAATAACTAGTCAATAAATACGATGCATGTGGCTCTCGAGCTGGTGGTGGTGGTGGTGGT 2456
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QY 188 ----- 188
Db 2457 TGCCTTTGTTGTTTTCGGCTAATAGAAATTATATTGTTGGGGTGTGACTTTTGTGTGATC 2516
QY 189 -----GlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTy 204
Db 2517 GAACGCGAGCCATGGGGAGATGTTGACGTGCTCCAAGCAGCTGAACGCGGACTGTGTGCA 2576
QY 204 rGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAs 224
Db 2577 CGCCGTCTTGGCGGGCTGGGGCAGTTCGGAGTGTATCACCCGGGGCCGATCGCGGTGGA 2636
QY 224 pHisAlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheTh 244
Db 2637 GCGGCGCGCGCGCGCGCGTGGTGTGCTGTACACCGACTTCGCGCGCTGAC 2696
QY 244 rLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGly----- 258
Db 2697 CGCCGACAGGAGCGCTACCGCCCGCGCGCGCGCGCGCGCGCGCTGCTTCGGGCC 2756
QY 259 -ValAspTyrLeuGluGlyGlnIlePhe-----LeuSerAsnGlyValValAs 274
Db 2757 GATGAGCTACGTGGAAGGTGCTGTTCTGTGAACACGAGCTTGGGACCGACTGCGGAA 2816
QY 274 pThrSerPheProSerAspGlnSerLysValAlaAspLeuValLysGlnHisGln 294
Db 2817 CACGGGTCTTTCACGACGCGGACGTCGCCGATGCTGCGCTCGCGCGGGAGCGGAA 2876
QY 294 y-----IleIleTyrValLeuGluValAlaLysTyrTyrAspAspProAsn-----Le 310
Db 2877 CGCCACACCGTGTACAGCATCGAGCCACGCTCAACTACGACACGCGCGCGCGCGC 2936
QY 310 uProIleIleSerLysValIleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPh 330
Db 2937 GCGCGCGGTGGACGAGCTCGCTCGTGTGGCGACGCTGAGCTAGCTGAGGGGT 2996
QY 330 eIleSerMetHisAspValAlaLysPheAspPheLeuAsnArgValHisValGluLys 350
Db 2997 CGCGTTCACGCGCGAGCTGCGCTACCGCGGTTCCTTACCGGGTGCACGGGAGGT 3056
QY 350 nLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeuAsnLeuTyrValPr 370
Db 3057 GCGGCTCAACAAAGCTGGGTGTGGCGGTGGCGCGCGCGCGCTCAAGTGTGTGTC 3116
QY 370 oLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLysGlnLy 390
Db 3117 GCCTCGCGATCGCGACTTCGACCGCGGTGTTCAGGGCATC---CTGAGGGCAC 3173
QY 390 sSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsn----- 404
Db 3174 CGACATCGTCGGCGCGCTCATGCTTACCCCTCAACAAATCCATGCTAGCTGTGAATCG 3233
QY 404 ----- 404
Db 3234 ATCGGTAGCTAGTAGTAGGACCGCGCGCGCTCTGACGACTCGACGGTCTTT 3293
QY 405 -----LysTrpAspAsnArgMetSerAlaMetIleProGluIleAspG 419
Db 3294 CTGGGTTTGGTTTTTTCATGTGGACGACGGCATGTGCGCGCGCGCGCGCG---TCTG 3347
QY 419 luAspValIleTyrIleIleGlyLeuLeu---GlnSerAlaThrProLysAspLeuProG 438
Db 3348 AGGACGTTTCTACGCGGTGCTGCTCTTCTGCTGCGTGGCGCCCAACGACTCGCGA 3407
QY 438 luValGluSerValAsnGluLysIleArgPheCysLysAspSerGlyIleLysIleL 458
Db 3408 GGCTGCAGGAGCAGACAGGAGGATCTGCGCTTCTGCGACTTCGCGCGGATCCAGTACA 3467
QY 458 yGlnTyrLeuMetHisTyrThrSerLysGluAspTrpIleGluHisPheGly---SerL 477
Db 3468 AGACCTACTGTCGGCGCGCACACGACCGAGTGTGCTGCGCTCGCGCGCGCGCGCG 3527
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US-10-014-101-4 (1-501) x US-09-124-541-10 (1-1602)	
Qy	37 ThrAspProSerIleIleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThr 56
Db	145 ACNGAYWSNAAYCNCACGCGCNCWNCACNGAYTTTGGNAAYATHACNCWSGNCYTN 204
Qy	57 ProGlyGlyValIleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAla 76
Db	205 CCNGCNGCGTNTYTNTAYCCNSNWSNACNCGNGAY---YTNGTNCNTNTYTNWSGNCN 261
Qy	77 AlaAsnGlyLysSer-----ThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeu 94
Db	262 GCNAAYWSNACNCCNGTGGCCNTAYACNATHGCTTYMGNGGNGCNCAYWSNYTN 321
Qy	95 AsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIleThrAsp--- 113
Db	322 ATGGCNCARGCNTTYGCNCGGCGGTGTGTNAAYATGCGNWSNTNGCNGAYGCN 381
Qy	114 -----ValValValSerLysAspLysLysTyrAlaAspValAlaAlaGly 128
Db	382 GCNGCNCNCCNMGNAATHAAYGTNWSGNCNGAYGCGNMGNTAYGTNGAYCNGGNGGAR 441
Qy	129 ThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerProValSerTrp 148
Db	442 CARGTNTGGATHGAYGTNTNMGNCNWSNYTNGCNGGCGGTGTNGCNCNMGNWSNTG 501
Qy	149 ThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIleGlyGln 168
Db	502 AAYGAYTAYTNTAYTNTACNGTNGGNGNACNYTNWSNAAYCNCNATHWSNCGNCAR 561
Qy	169 ValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThrGlyLys 188
Db	562 GCNTTYMGNCAYCGCNCNCARATHWSNAAYGTNTNGARATGGAYGTNATHACNGNCAY 621
Qy	189 GlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGlyValLeuGly 208
Db	622 GCGARATGGTACNTGTGYSNAARCARYTNAAYGCGNGAYTTNTTYGCGNGTNTYNGN 681
Qy	209 GlyLeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHisAlaProLys 228
Db	682 GGYTNGCNCARTTYGGNGTNAATHACNMGNCNMGNAHGCNGTNGARCCNGCNCNGCN 741
Qy	229 ArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGlnGlu 248
Db	742 MNGCNCNMGNTGGTNGTNTYTNTAYACNGAYTTTYGCGNCNTTYWSNCGNCAYCARGAR 801
Qy	249 ArgLeuIleSerMetAlaAsnAspIleGly-----ValAspTyrLeu 262
Db	802 MGYTNACNCCNMGNCNCGGNGGNGGNGCNCWSNTTYGNCNCNATGWSNTAYGTN 861
Qy	263 GluGlyGlnIlePheLeu-----SerAsnGlyValValAspThrSerPhePhe 278
Db	862 GARGNWSNGTNTTYGTNAAYCARWSNYTNGCNCACNGAYTNGCNAAYACNGGNTTTTY 921
Qy	279 ProProSerAspGlnSerLysValAlaAspLeuValLysGlnHisGly----- 294
Db	922 ACNGAYCNCAY-----GTCNMGNTATGTGTCNCGNGGNGARMGNAAYGCN 972
Qy	295 ---IleIleTyrValLeuGluValAlaLysTyrAspAspProAsnLeuProIleIle 313
Db	973 ACNACNGTNTAYWSNATHGARGCNCACNYTNAAYTAYGAY-----AAYGCNACGNCN 1026
Qy	314 SerLysValIleAsp-----ThrLeuThrLysThrLeuSerTyrLeuProGly 329
Db	1027 GCNGCNCNGTNGAYCARGARYTNGCNCWSNGTNTYTGNCNACNTNWSNTAYGTNGARGGN 1086
Qy	330 PheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArgValHisValGluGlu 349
Db	1087 TTYGCTTYTCARMGNGAYGTGTCNAYGCGNCNTTYTNGAYMGNTCAYGCGARGAR 1146
Qy	350 AsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeuAsnLeuTyrVal 369
Db	1147 GTNGCNYTNAAYARYTNGGNTNTGTGNGTNCNCAYCCNTGGYTNAAYATGTTYGTN 1206

Alignment Scores:  
Pred. No.: 9,87e-94  
Score: 835.00  
Percent Similarity: 48.99%  
Best Local Similarity: 37.65%  
Query Match: 32.16%  
DB: 3  
Length: 1602  
Matches: 186  
Conservative: 56  
Mismatch: 214  
Indels: 38  
Gaps: 13





Db 862 GARGNWSNGNTTYGTNAAYCARWSNTYNGNACNGAYTYNGCNAAVACNGGNTTYTY 921  
Qy 279 ProProSerAspGlnSerLysValAlaAspLeuValLysGlnHisGly----- 294  
Db 922 ACNGAYGCGNGAY-----GTNGCNMGNAHTGTNGCNNTYNGCNNGGARMGNAAYGCN 972  
Qy 295 ---llelleTyrValLeuGluValAlaLysTyrTyrAspAspProAsnLeuProIleile 313  
Db 973 ACNACNGNTNAYWSNATHGARGCNACNTNAYAYTAYGAY-----AAYGCVACNGGNGCN 1026  
Qy 314 SerLysValIleAsp-----ThrLeuThrLysThrLeuSerTyrLeuProGly 329  
Db 1027 GCGNGCGNGGNTNGAYCARGARYTYNGCNWSNGNTYNGGNACNTNWSNTAYGTNGARGGN 1086  
Qy 330 PheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArgValHisValGluGlu 349  
Db 1087 TTYGNTTYCARMGNGAYTYNGCNTAYCGNGNTTYTYNGAYMNGNTNCAVGGNGARGAR 1146  
Qy 350 AsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeuAsnLeuTyrVal 369  
Db 1147 GTNGCNNTNAAVARYTYNGGNTYNGMNGNTGCCNCAVCCNTGGYTNAAYATGTYGTN 1206  
Qy 370 ProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLysGln 389  
Db 1207 CCNMGNSWNGNATHGCGAYTYTYGAYMNGGNGNTTYAARGGNATH---YTNCARGGN 1263  
Qy 390 LysSerAlaSerGlyLeuAlaLeuTyrProThrAsnArgAsnLysTrpAspAsnArg 409  
Db 1264 ACNGAYATHGTNGGNCNTNATHGTNTAYCNYTNAAYARWSNATGTGGGAYGAYGNGN 1323  
Qy 410 MetSerAlaMetIleProGluLeuAspGluAspValIleTyr---IleIleGlyLeuLeu 428  
Db 1324 ATGWSNGCGNCACNCCN-----WSNGARGAYGNTTYTYGCGNTGWSNTYNTNTTY 1377  
Qy 429 GlnSerAlaThrProLysAspLeuProGluValGlnSerValAsnGluLysIleIleArg 448  
Db 1378 WSNWSNGTNGCCNAAAYGAYTYNGCMNGNTNARGARCARAAVYMGNGNATHYTNMGN 1437  
Qy 449 PheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyrThrSerLysGlu 468  
Db 1438 TTYTGAYTYTYNGGNGNATHCARTAYAAACNTAYTYNGCMNGNCAVACNGAYMNGWSN 1497  
Qy 469 AspTrpIleGluHisPheGly---SerLysTrpAspAspPheSerLysArgLysAspLeu 487  
Db 1498 GAYTGGTNGMNCAYTYTYGGNGCGNCAARTGGAAVYMGNTTYGTNGARATGAABAAYAR 1557  
Qy 488 PheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501  
Db 1558 TAYGAYCCNAAARMGNTYNTYTNWSNCCNGGNCARGAYATHTY 1599

## RESULT 7

US-09-103-840A-2  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; TITLE OF INVENTION: TUBERCULOSIS  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; OTHER INFORMATION: CDC 1551  
; OTHER INFORMATION: "n" bases at various positions throughout the sequence

OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2  
Alignment Scores: 3,04e-08 Length: 4403765  
Score: 198.50 Matches: 71  
Percent Similarity: 40.67% Conservative: 38  
Best Local Similarity: 26.49% Mismatches: 124  
Query Match: 7.65% Indels: 35  
DB: 6  
US-10-014-101-4 (1-501) x US-09-103-840A-2 (1-4403765)  
Qy 57 ProGlyGlyValIleCysProSerSerThrAla-----AspIleSer 70  
Db 4154512 CCGGACTCCTTGGTGGTATTCGACCCGCGCACCCGGATCGAGGGGAGTTGTCG 4154571  
Qy 71 ArgLeuLeuGlnTyrAlaAlaAsnGlyLysSerThrPheGlnValAla---AlaArgGly 89  
Db 4154572 AGGACTAGGATATATCGGTGCTGCTCCCTGGATCTGCACATCGCTTACGCTCGGCG 4154631  
Qy 90 GlnGlyHisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMet--- 108  
Db 4154632 GTCGAGCGGTGCTGCGGAGCTATCGATCCATCCCGCGACTGCATCCATCCGCTTGC 4154691  
Qy 108 ----- 108  
Db 4154692 AAGCCACCTCAATCTGTTCCGCGCCCGCTCAACACATGCACGCGCGCTGGACGCA 4154751  
Qy 109 ThrCysIleThrAspValVal---ValSerLysAspLysLysTyrAlaAspValAlaAla 127  
Db 4154752 TCGGAGTACCGGTGTCTATCGGTATCGATCCGAGCGCGCACCCGCGCGCGCG 4154811  
Qy 128 GlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerProValSer 147  
Db 4154812 ATGTGCACATCAGAGCACTAATCGCGCGGACACTGCATCTACGCTCTGCACCTTGGT 4154871  
Qy 148 TrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIleGlyGly 167  
Db 4154872 GTTCCGCGAGCTGAGGACGATCACATTTGGCGGAGCGGTACCGGCTTGGGTATCGAGTCG 4154931  
Qy 168 GlnValPheArgAsnGlyProLeuValSerAsnValLeuLeuAspValIleThrGly 187  
Db 4154932 GCGTCGTTCGCGAACCGCTCGCCCGACGATCGGTGCTGGAGATGGATATCTCACCAGCG 4154991  
Qy 188 LysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGlyValLeu 207  
Db 4154992 GCAGAGAACTTCTCACCGTCTGCGCGGACAGCACTCCGACTTGTACGCTGATTCCT 4155051  
Qy 208 GlyGlyLeuGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHisAlaPro 227  
Db 4155052 AACTCGTATGGACACTGGGCTATTCAACCGCGCTTCGAATCCAGCTGGAGCGGCTCCG 4155111  
Qy 228 LysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGln 247  
Db 4155112 CCGTTTGTGCGGCTGGCGACATCCCGATTAGCTGTTGACGCGGATGTTGGCGGCAATG 4155171  
Qy 248 GluArgLeuIleSerMetAlaAsnAspIleGly-----ValAspTyrLeuGluGlyGln 265  
Db 4155172 GAGCGCATCTCGACACCGCGGACTGGACGCGGAATCGGTGGACTATCTCGAGCGGGTG 4155231  
Qy 266 IlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLys 285  
Db 4155232 GTTTTCAGCGCT-----GACGAAGTACTCTGTGTCATCGCATCGCAGACGAGC 4155279  
Qy 286 ValAlaAspLeuValLysGlnHis 293  
Db 4155280 GTACCGGCGCGGTTCAGCGACTAC 4155303

## RESULT 8

US-09-103-840A-1  
; Sequence 1, Application US/09103840A  
; Patent No. 6294328

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; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
; US-09-103-840A-1

Alignment Scores:
Pred. No.: 5,42e-08 Length: 4411529
Score: 196 50 Matches: 57
Percent Similarity: 47.31% Conservative: 31
Best Local Similarity: 30.65% Mismatches: 91
Query Match: 7.57% Indels: 7
DB: 3 Gaps: 3

US-10-014-101-4 (1-501) x US-09-103-840A-1 (1-4411529)
Qy 111 IleThrAspValVal--ValSerLysAspLysLysValAlaAspValAlaAlaGlyThr 129
Db 4162507 CTGACCGGTGTCATCGGTATGATCCCGAGCCGCGACCGCGGCGGCGGATGTC 4162566
Qy 130 LeuTrpValAspValLeuLysThrAlaGluLysGlyValSerProValSerTrpThr 149
Db 4162567 ACATACGAGGACCTAATCGCGCGACACTGCACCTACGGTCTGTCCACCATGGTGGTTCG 4162626
Qy 150 AspTyrLeuHisIleThrValGlyThrLeuSerAsnGlyGlyIleGlyGlyGlnVal 169
Db 4162627 CAGCTGAGGAGCATCACATGGCGGCGGCGGTACCGGCTTGGGTATCGATCGGCGTCG 4162686
Qy 170 PheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThrGlyLysGly 189
Db 4162687 TTCCGCAACGGCTCCCGACGAGTCGGTGTGGAGATGGATATCCTCACCGCGCGAGGA 4162746
Qy 190 GluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGlyValLeuGlyGly 209
Db 4162747 GAACTTCTCACCGTCTCGCGCGACGACACTCCGACTGTACCGGTGCATCCCTAACTCG 4162806
Qy 210 LeuGlyGlnPheGlyIleThrArgAlaArgIleValLeuAspHisAlaProLysArg 229
Db 4162807 TATGGACACTGGGTATTCACCCGGCTTGAATCCAGCTGGAGCCGTCGGCGCGTTT 4162866
Qy 230 AlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGlnGluArg 249
Db 4162867 GTCGCGCTCGGCACATCCGATTAGCTTGTAGCTGGTGGCGGATGGTGGCGGCAATGAGCGC 4162926
Qy 250 LeuIleSerMetAlaAsnAspIleGly-----ValAspTyrLeuGluGlyGlnIlePhe 267
Db 4162927 ATCATCGACACCGCGGAGTACGACCGGATCGGTGGATATCTCCAGCGGTGTTTC 4162986
Qy 268 LeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLysValAla 287
Db 4162987 AGCGCT-----GACGAAAGCTACCTGTGATCGCATCGCATCGACGAGCGTACCG 4163034
Qy 288 AspLeuValLysGlnHis 293
Db 4163035 GCGCCCGTTCGCGACTAC 4163052

RESULT 9
US-08-311-731A-23
; Sequence 23, Application US/08311731A
; Patent No. 6593266

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; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF INVENTION: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37769 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIUM LAPRAE
; US-08-311-731A-23

Alignment Scores:
Pred. No.: 5,42e-10 Length: 37769
Score: 183 50 Matches: 55
Percent Similarity: 46.41% Conservative: 29
Best Local Similarity: 30.39% Mismatches: 88
Query Match: 7.07% Indels: 9
DB: 4 Gaps: 3

US-10-014-101-4 (1-501) x US-08-311-731A-23 (1-37769)
Qy 111 IleThrAspValVal--ValSerLysAspLysLysValAlaAspValAlaAlaGlyThr 129
Db 34022 CTGACCGGTGTCATAGTATCGACACCGAGAGTCGACCGCGGCGGCGGATGTCG 34081
Qy 130 LeuTrpValAspValLeuLysThrAlaGluLysGlyValSerProValSerTrpThr 149
Db 34082 ACCTACGAGGACCTGGTAGCGCGCAACCTTGCCTTACGGTCTTTTGGCACTGGTGGTTCG 34141
Qy 150 AspTyrLeuHisIleThrValGlyThrLeuSerAsnGlyGlyIleGlyGlyGlnVal 169
Db 34142 CAATCAAGACTATCACCTCGCGGCGTGCAGTACCGGCGGCGGATCGAATCGGCGCTCG 34201
Qy 170 PheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThrGlyLysGly 189
Db 34202 TTTCGCAATGGCTTACCCACAGATCGGTCTCGAATGGATATCTCTACCGCGGCTGGA 34261
Qy 190 GluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGlyValLeuGlyGly 209
Db 34262 GAATTGCTCAGTATCTGCAAAACGACGCGGCGGCGTACCGTGCCTTCCCAATTC 34321

```

QY 210 LeuGlyGlnPheGlyIleThrArgAlaArgIleValLeuAspHisAlaProLysArg 229  
 Db 34322 TATGGTAGTTAGGATATTCACACGGTTTCGGATCTCCCTGGAACTGTGAACCCCTTT 34381  
 QY 230 AlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGlnGluArg 249  
 Db 34382 GTAGCACTGCGACACATCCGATTTCACTTGTGTGACCGAGATGGTCCAGCGCATGGAAC 34441  
 QY 250 LeuIleSerMetAlaAsnAspIleGly-----ValAspTyrLeuGluGlyGlnIlePhe 267  
 Db 34442 ATCATCGACACCGCGGACACGATGCGTCCCGATGATATTCGACGGTGTGGTTC 34501  
 QY 268 LeuSerAsn-----GlyValValAspThrSerPhePhePheProSer 281  
 Db 34502 AGTGTACGAAAGCTACCTATGCTATCGTAAACGACCAACACCGCGGACCTGTGACG 34561  
 QY 282 Asp 282  
 Db 34562 GAC 34564

RESULT 10  
 US-09-266-965-61  
 ; Sequence 61, Application US/09266965  
 ; Patent No. 6495348  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sherman, D  
 ; APPLICANT: Mao, Y  
 ; APPLICANT: Varoglu, M  
 ; APPLICANT: He, M  
 ; APPLICANT: Sheldon, P  
 ; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster  
 ; FILE REFERENCE: 600.456US1  
 ; CURRENT APPLICATION NUMBER: US/09/266,965  
 ; EARLIER FILING DATE: 1999-03-12  
 ; EARLIER APPLICATION NUMBER: US 08/624,447  
 ; EARLIER FILING DATE: 1996-08-19  
 ; EARLIER APPLICATION NUMBER: PCT/US94/11279  
 ; EARLIER FILING DATE: 1994-10-06  
 ; EARLIER APPLICATION NUMBER: US 08/133,963  
 ; EARLIER FILING DATE: 1993-10-07  
 ; NUMBER OF SEQ ID NOS: 145  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 61  
 ; LENGTH: 1419  
 ; TYPE: DNA  
 ; ORGANISM: Streptomyces lavendulae  
 US-09-266-965-61

Alignment Scores:  
 Pred. No.: 8.37e-12 Length: 1419  
 Score: 178.00 Matches: 50  
 Percent Similarity: 50.00% Conservative: 35  
 Best Local Similarity: 29.41% Mismatches: 73  
 Query Match: 6.86% Indels: 12  
 DB: 4 Gaps: 5

US-10-014-101-4 (1-501) x US-09-266-965-61 (1-1419)

QY 57 ProGlyGlyValIleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAla 76  
 Db 160 CCGCCCTCGTGTGTCGCGCACCGTGGCGGATGTATCCCGCGGCTTCGCC 219  
 QY 77 ---AlaAsnGlyLysSerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsn 95  
 Db 220 AGGCGCCGGGCGC-----CTTGGATCGCGTCCAGCCACCGGTAC----- 261  
 QY 96 GlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIleThrAspValVal 115  
 Db 262 GGGAAAGTCTTCGGCGGACCGAGCTCTCATGACACCGCGGATGACCGCGGTACG 321  
 QY 116 ValSerLysAspLysLysTyrAlaAspValAlaAlaGlyThrLeuTrpValAspValLeu 135  
 Db 322 GTCACCGCGGCGCGCGCGGATCGAGCGCGGCGTGGCGGTGGAGCAGGTATC 381

QY 136 LysLysThrAlaGluLysGlyValSerProValSerTrpThrAspTyrLeuHisIleThr 155  
 Db 382 CACGAGCGCGCGCGCACGGTCTTGACCGCTGAGCGGCTCGCGCGCTTC----- 432  
 QY 156 ValGlyGlyThr-----LeuSerAsnGlyGlyIleGlyGlyGlnValPheArgAsnGly 173  
 Db 433 GTCGGCGCGGTCTCTACCTCTCTCGCGCGGCTCGGCTCTCTCGCGGAGTACGGG 492  
 QY 174 ProLeuValSerAsnValLeuGluLeuAspValIleThrGlyLysGlyGluMetLeuThr 193  
 Db 493 TTCCGCGCGGACCATGTCTCTCGCTCGACCTGTGTGACGCGCGACGCGCGGTCTCTCCAG 552  
 QY 194 CysSerArgGlnLeuAsnProGluLeuPheTyrGlyValLeuGlyGlyLeuGlnPhe 213  
 Db 553 GTCTCCGCGGAGAACACCCCGGATCTCTCTCGGCGGTGCGGCGGACGAGGGAACCTC 612  
 QY 214 GlyIleIleThrArgAlaArgIleValLeu 223  
 Db 613 GGCATGTCACCTCCGTCGAGGTGCGGCTG 642

RESULT 11  
 US-09-266-965-76/c  
 ; Sequence 76, Application US/09266965  
 ; Patent No. 6495348  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sherman, D  
 ; APPLICANT: Mao, Y  
 ; APPLICANT: Varoglu, M  
 ; APPLICANT: He, M  
 ; APPLICANT: Sheldon, P  
 ; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster  
 ; FILE REFERENCE: 600.456US1  
 ; CURRENT APPLICATION NUMBER: US/09/266,965  
 ; EARLIER FILING DATE: 1999-03-12  
 ; EARLIER APPLICATION NUMBER: US 08/624,447  
 ; EARLIER FILING DATE: 1996-08-19  
 ; EARLIER APPLICATION NUMBER: PCT/US94/11279  
 ; EARLIER FILING DATE: 1994-10-06  
 ; EARLIER APPLICATION NUMBER: US 08/133,963  
 ; EARLIER FILING DATE: 1993-10-07  
 ; NUMBER OF SEQ ID NOS: 145  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 76  
 ; LENGTH: 5350  
 ; TYPE: DNA  
 ; ORGANISM: Streptomyces lavendulae  
 US-09-266-965-76

Alignment Scores:  
 Pred. No.: 4.84e-09 Length: 5350  
 Score: 178.00 Matches: 50  
 Percent Similarity: 50.00% Conservative: 35  
 Best Local Similarity: 29.41% Mismatches: 73  
 Query Match: 6.86% Indels: 12  
 DB: 4 Gaps: 5

US-10-014-101-4 (1-501) x US-09-266-965-76 (1-5350)

QY 57 ProGlyGlyValIleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAla 76  
 Db 36540 CCGCCCTCGTGTGTCGCGCACCGTGGCGGATGTATCCCGCGGCTTCGCC 36481  
 QY 77 ---AlaAsnGlyLysSerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsn 95  
 Db 36480 AGGCGCCGGGCGC-----CTTGGATCGCGTCCAGCCACCGGTAC----- 36439  
 QY 96 GlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIleThrAspValVal 115  
 Db 36438 GGGAAAGTCTTCGGCGGACCGAGCTCTCATGACACCGCGGATGACCGCGGTACG 36379  
 QY 116 ValSerLysAspLysLysTyrAlaAspValAlaAlaGlyThrLeuTrpValAspValLeu 135  
 Db 36379 GTCACCGCGGCGCGCGCGGATCGAGCGCGGCGTGGCGGTGGAGCAGGTATC 381





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Db 1654 GAACATTGGCTAAATTGAGATACCAAAAGACAAAGAACTTGAAGCCTTACAGCA 1713
Qy 477 -----LysTrpAspAspPheSerLysArgLysAspLeuPheAspPro 490
Db 1714 AGAATAAGAAACGTTTCCAGTGTGATGATACAAACAAAGACAGTAGGAGGCTGGACCCA 1773
Qy 491 LysLysLeuLeuSer 495
Db 1774 AATAGAATCTCTCC 1788

```

## RESULT 13

```

US-09-423-468A-12
; Sequence 12, Application US/09423468A
; Patent No. 6469149
; GENERAL INFORMATION:
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol
; APPLICANT: Guy Jerome Corneel Bauw
; APPLICANT: Mark William Davey
; APPLICANT: Jens Ostergaard
; APPLICANT: Marc Charles Ernest Van Montagu
; TITLE OF INVENTION: PRODUCTION OF ASCORBIC ACID IN PLANTS
; FILE REFERENCE: DECLES.001APC
; CURRENT APPLICATION NUMBER: US/09/423,468A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: NL 1006000
; PRIOR FILING DATE: 1997-05-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 2034
; TYPE: DNA
; ORGANISM: Brassica oleracea
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (44)...(1846)
US-09-423-468A-12

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## Alignment Scores:

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Pred. No.: 3 23e-11 Length: 2034
Score: 175.50 Matches: 106
Percent Similarity: 38.07% Conservative: 95
Best Local Similarity: 20.08% Mismatches: 229
Query Match: 6.76% Indels: 99
DB: 4 Gaps: 20

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US-10-014-101-4 (1-501) x US-09-423-468A-12 (1-2034)

```

Qy 31 LeuAsnLeuThrLeuSerThrAspProSerIleIleSerAlaAlaSerHisaspPheGly 50
Db 324 CTCCTCCCGAAGATCTCCACA--CCGTCTCTAACTGGAGTGGTA----- 365
Qy 51 AsnIleThrValThrProGlyGlyValIleCysProSerSerThrAlaAspIleSer 70
Db 366 ---CTCAGAGGTCGACAGCAGGACTTTAACAG-CCGAGACTCTGCCGATCTCGAA 421
Qy 71 ArgLeuLeuGlnTyrAlaAlaAsnGlyLysSerThrPheGlnValAlaAlaArgGlyGln 90
Db 422 GCTCTCTCAAGAGAGCTCATGAGAAGAAGAAC-----AGGATCCGACCCGTTGGATCC 475
Qy 91 GlyHisSerLeuAsnGlyGlnAlaSerValSerGlyValIleValAsnMetThrCys 110
Db 476 GGTCTTTCCTCCCAATGGG---ATCGGTTTGTCTCGCTCGGGATGGTGAATTCGGCTC 532
Qy 111 IleThrAspValVal---ValSerLysAspLysLysTyrAlaAspValAlaAlaGlyThr 129
Db 533 ATGGACAAGTCTCTCGAGGTGGATTAAGAGAAGAGAGATCCGTTGTGAGCTGGATT 592
Qy 130 LeuTrpValAspValLeuLysThrAlaGluLysGlyValSerProValSerTrpThr 149
Db 593 AGGGTTACAGAGCTTGTGAGCCATTCAGAGATATGGTCTCACTCTCCAGAACATTTGCT 652
Qy 150 AspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIleGlyGlyGlnVal 169

```

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Db 653 TCCATTAGAGAGCAGCAGATTGGTGGCATCATTCAGGTTGGGGCACATGGGACAGGTGCT 712
Qy 170 PheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThrGlyLysGly 189
Db 713 ---AGATTGCTCTCTATCATGAGCAAGTGGATGGCATGAAGCTTGCTACTCTCTGCTAAG 769
Qy 190 GluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGlyValLeuGlyGly 209
Db 770 GGAACATATTGAGCTTTCTAAGGATAATATGATCCGGAGCTCTTTCATCTGCTCGATGGGC 829
Qy 210 LeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHisAlaProLysArg 229
Db 830 CTGGGTGGAGCTTGGAGTTGTT---GCTGAGTCCACCTCCAGTCCGCTTGAAGACAG 883
Qy 230 AlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGlnGluArg 249
Db 884 GAGCTTTGGAGCACACTTACGCTCTCCACTTGGAAAGAGATCAAGAAAAAATCACAAAAAG 943
Qy 250 LeuIleSerMetAlaAsnAspIleGly-----ValAspTyrLeuGluGlyGlnIle 266
Db 944 TTGCTCTCTACAAAATAGCATGTCAAGTACCTGTATATATCCATATCTACACGGTCGTG 1003
Qy 267 PheLeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLys--- 285
Db 1004 GTTGTACATGCAACCTGTATCAAAATGGAGTGGGGCACCTAAGGACAAACCAAGTAC 1063
Qy 286 -----ValAlaAspLeuValLysGlnHisGlyIleIleTyr 297
Db 1064 ACTACAGAGAGGCTTTAAAGCATGTCCGTGACCTGTATAGAGAGAGCATTTGTAAGTAT 1123
Qy 298 ---ValLeuGluValAlaLysTyrTyrAspAspProAsnLeuProIleIleSerLysVal 316
Db 1124 AGGTCAGAGCTCTAGTAAAGACTCTCTGACGTAGGAGCCAGACATTAACGAGCTT 1183
Qy 317 IleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPheIleSerMetHisAsp--- 335
Db 1184 -----TCATTTACAGAGTTGAGAGATAAG 1207
Qy 336 ValAlaLysPheAspPheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeu 355
Db 1208 CTGATGGCTCCCTAGATCTCTCAATGAGCTTCAGTTGGAAAGTGAATCAAGCTGAGGCT 1267
Qy 356 GlyLeuTrp----- 358
Db 1268 GAGTTTTGGAAAAAATCAGAAGGATACAGATAGGTGGAGTGATGATAATCTCTGGGCTTT 1327
Qy 359 -----GluLeuProHisProTrpLeuAsnLeuTyrVal 369
Db 1328 GACTGTGGTGGTCAACAGTGGGTATCAGAAACTGTTTCTCTCTGGAATCTCTCGCTAAA 1387
Qy 370 ProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLysGln 389
Db 1388 CCTAGCATGAAGACCTTTGAGTACATAGAA--CAGCTGAAGAGAGTTGATACAAAAAGAA 1444
Qy 390 LysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsn---ArgAsnLysTrpAspAsn 408
Db 1445 -----GCATATCCAGCACCTTCTCCCATAGAGCAGCGGTGGACAGGC 1486
Qy 409 Arg-----MetSerAlaMetIleProGluIleAspGluAspValIleTyrIle 424
Db 1487 CGAAGTAAGAGCCCTATGAGTCTCGCATTCAGACTCGAGAGGAGGACATTTCTCATGG 1546
Qy 425 IleGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGlu 444
Db 1547 GTTGGTATAATCATGTATCTCCCGACAGCAGACCCCTCGCCAGAGAAAGACATCCGGAT 1606
Qy 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr 464
Db 1607 GAATTTTCCATATAGACATTTGACACAGGCAAAATTTGGGAC-----CAGTAT 1657
Qy 465 ThrSerLysGluAspTrpIle----- 471

```

Db 1658 TCTGGTATGAACATTGGGCTAAATTCAGATACCAAGGATTAAGAGGAACTTGAAGCC 1717

Qy 472 -----GluHisPheGlySerLysTrp-----AspAspPheSerLysAspLeu 487

Db 1718 CTACAAGAAAGACTCAGAAAACGATTCCCGGTGATGATACACAAAGACGAAGGAG 1777

Qy 488 PheAspProLysLysLeuSer 495

Db 1778 CTGACCCCAACAGAAATCTCTCA 1801

RESULT 14

US-09-630-983A-4

; Sequence 4, Application US/09630983A

; Patent No. 6630330

; GENERAL INFORMATION:

; APPLICANT: Pozzo, Danilo

; APPLICANT: Sauer, Michael

; TITLE OF INVENTION: Ascorbic Acid Production from Yeast

; FILE REFERENCE: 2028.594000

; CURRENT APPLICATION NUMBER: US/09/630.983A

; CURRENT FILING DATE: 2000-08-02

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 2064

; TYPE: DNA

; ORGANISM: Brassica oleracea

US-09-630-983A-4

Alignment Scores:

Pred. No.: 3.31e-11 Length: 2064

Score: 175.50 Matches: 106

Percent Similarity: 38.07% Conservative: 95

Best Local Similarity: 20.08% Mismatches: 229

Query Match: 6.76% Indels: 99

DB: 4 Gaps: 20

US-10-014-101-4 (1-501) x US-09-630-983A-4 (1-2064)

Qy 31 LeuAsnLeuThrLeuSerThrAspProSerIleSerAlaAlaSerHisAspPheGly 50

Db 336 CTCCTCCCGAAGATCTCCACA--CCGCTCTAACTGAGTGGTA----- 377

Qy 51 AsnIleThrValThrProGlyGlyValIleCysProSerSerThrAlaAspIleSer 70

Db 378 ---CTCAGAGGTCCAGACCCAGGAACCTTAAACAG--CCGGAGACTCGCCGATCTCGAA 433

Qy 71 ArgLeuLeuGlnThrAlaAlaAsnGlyLysSerThrPheGlnValAlaAlaArgGlyGln 90

Db 434 GCTCTCGTCAAGGAAGCTCATGAGAGAGAAC-----AGGATCCGACCCGTTGGATCC 487

Qy 91 GlyHisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCys 110

Db 488 GGTCTTTCCCAATGGG---ATCGGTTTGTCTCGCTCGGGGATGGTGAATTTGGCGCTC 544

Qy 111 IleThrAspValVal---ValSerLysAspLysLysValAlaAspValAlaAlaGlyThr 129

Db 545 ATGGACAGAGTCTCGAGGTGATTAAGAGAGAGAGAGAGTCCGTGTGAGGCTGGGATT 604

Qy 130 LeuTrpValAspValLeuLysThrAlaGluLysGlyValSerProValSerTrpThr 149

Db 605 AGGGTTACAGCATTTGAGCCCATTCAGAGTATGCTCTCACTCCAGAACTTTGCT 664

Qy 150 AspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyIleGlyGlyGlnVal 169

Db 665 TCCATTAGAGAGCAGCATGGTGGCATCATTCAGTTGGGGCAGCATGGGACAGGTGCT 724

Qy 170 PheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThrGlyLysGly 189

Db 725 ---AGATTGCTCTTCATCGATGAGCAAGTGTGATGGCATGAGCTTGTCACTCTCTGAAG 781

Qy 190 GluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGlyValLeuGlyGly 209

Db 782 GGAACATTATTGACCTTTCTAAGGATTAATGATCCGAGACTCTTTTCATCTTGTCTGATGGC 841

Qy 210 LeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHisAlaProLysArg 229

Db 842 CTTGGTGGACTTGGAGTTGTT-----GCTGAGGTCACTCCCTCCAGTGGCTTGAAGACAG 895

Qy 230 AlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGlnGluArg 249

Db 896 GAGCTTTTGGAGCACACTTACGCTCTCCACCTTGGAGAGATCAAGAAAATCACAAGAG 955

Qy 250 LeuIleSerMetAlaAsnAspIleGly-----ValAspTyrLeuGluGlyGlnIle 266

Db 956 TTGCTCTCTACAAATAAGCATGTCAGTACCTGTATATTCCATATACACACGCTCGTG 1015

Qy 267 PheLeuSerAsnGlyValValAspThrSerPhePheProSerAspGlnSerLys--- 285

Db 1016 GTTGTTCATGCAACCTGTATCAAAATGGAGTGGGGCACCTTAAGCAACCAAGTAC 1075

Qy 286 -----ValAlaAspLeuValLysGlnHisGlyIleIleTyr 297

Db 1076 ACTACAGAGGAGCTTTAAAGCATGTCCTGACCTGTATAGAGAGCATTTGTAAGTAT 1135

Qy 298 ---ValLeuGluValAlaLysTyrTyrAspAspProAsnLeuProIleSerLysVal 316

Db 1136 AGGGTCCAGGACTCTAGTAAAGACTCTCTGACGTAGGAGCCAGACATTAACGAGCTT 1195

Qy 317 IleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPheIleSerMetHisAsp--- 335

Db 1196 -----TCATTTACAGAGTTGAGAGTAAG 1219

Qy 336 ValAlaTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeu 355

Db 1220 CTGATTGCCCTAGATCTCTCAATGACGTTCACGTGGAAAGTGAATCAAGCTGAGGCT 1279

Qy 356 GlyLeuTrp----- 358

Db 1280 GAGTTTGGAAAAATCAGAGGATACAGAGTAGGTGAGTGATGAATCTCGGCTTT 1339

Qy 359 -----GluLeuProHisProTyrPheAsnLeuTyrVal 369

Db 1340 GACTGTGGTGGTCAACAGTGGGTATCAGAAACTTGTCTTCTCGTGGAACTTCGCTAAA 1399

Qy 370 ProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLysGln 389

Db 1400 CCTAGCATGAAGACCTTGGTACATAGAA---CAGCTGAAGAGATTGATACAAAAGAA 1456

Qy 390 LysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsn---ArgAsnLysTrpAspAsn 408

Db 1457 -----GCAATACAGCACCTTCTCCCATAGAGCAGCGTTGGACAGGC 1498

Qy 409 Arg-----MetSerAlaMetIleProGluIleAspGluAspValIleTyrIle 424

Db 1499 CGAAGTAAGAGCCCTATGATCTCCGACAGCAGACCCCTCCGACAGAGAGACATCCAGAT 1558

Qy 425 IleGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGlu 444

Db 1559 GTTGGTATTAATCATGTATCTCCGACAGCAGACCTCCGACAGAGAGACATCCAGAT 1618

Qy 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr 464

Db 1619 GAATTTTCCACTATAGACATTTGACACAGGCAAAATTTGGGAC-----CAGTAT 1669

Qy 465 ThrSerLysGluAspTrpIle----- 471

Db 1670 TCTGCTATGAACATTTGGCTAAAATTGATACCAAGGATTAAGAGAACTTGAAGCC 1729

Qy 472 -----GluHisPheGlySerLysTrp-----AspAspPheSerLysArgLysAspLeu 487

Db 1730 CTACAAGAAAGACTCAGAAAACGATTCCCGGTGGATGATACACAAAGACCAAGAGGAG 1789

Qy 488 PheAspProLysLysLeuLeuSer 495

Db 1790 CTGGACCCCAACAGAAATCTCTCA 1813

Search completed: April 7, 2004, 11:48:47  
Job time : 4274 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 7, 2004, 05:49:35 ; Search time 629 Seconds  
(without alignments)

3383.700 Million cell updates/sec

Title: US-10-014-101-4

Perfect score: 2596

Sequence: 1 MANRLMTLITVLMITKSS.....SKRKDLFPKXLLSPGQDIF 501

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pfco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10014101@cgn1\_1\_470@runat\_05042004\_154153\_8568 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
-DEV\_TIMECUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_29Jan04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2003as:\*
- 8: Geneseqn2003bs:\*
- 9: Geneseqn2003cs:\*
- 10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2596	100.0	1506	6	ABK28625
2	2596	100.0	1506	8	ACC85294
3	2596	99.3	1548	3	ABK43214
4	2226.5	85.8	2391	8	ABK28607
5	2226.5	85.8	2391	8	ACC85276
6	1822	70.2	1575	3	AAC42983
7	1822	70.2	1575	6	AB214284
8	1822	70.2	1575	6	ABK28627

## ALIGNMENTS

RESULT 1

ABK28625

ID ABK28625 standard; cDNA; 1506 BP.

AC ABK28625;

DT 09-APR-2002 (first entry)

DE cDNA encoding A. thaliana cytokinin oxidase AtCKX2.

XX Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;  
XX root growth; lateral root; adventitious root; root geotropism; herbicide;  
XX root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ss.

OS Arabidopsis thaliana.

PN WO200196580-A2.

PD 20-DEC-2001.

PF 18-JUN-2001; 2001WO-EP006833.

PR 16-JUN-2000; 2000EP-00870132.

PR 27-DEC-2000; 2000US-0258415P.

PR 16-MAR-2001; 2001EP-00870053.

PA (SCHM/) SCHMULLING T.

PA (WERN/) WERNER T.

PI Schmullling T, Werner T;

DR WPI; 2002-130736/17.

9	1822	70.2	1575	7	ADA68648	ADA68648 Arabidops
10	1822	70.2	1575	8	ACC85296	ACC85296 Arabidops
11	1539.5	59.3	2782	8	ABK28609	ABK28609 DNA enco
12	1339.5	59.3	2782	8	ACC85278	ACC85278 Arabidops
13	1292	49.8	1572	8	ABK28626	ABK28626 cDNA enco
14	1292	49.8	1572	8	ACC85295	ACC85295 Arabidops
15	1184	45.6	1611	8	ABK28628	ABK28628 cDNA enco
16	1184	45.6	1611	8	ACC85297	ACC85297 Arabidops
17	1184	45.6	1620	8	ABK28632	ABK28632 cDNA enco
18	1184	45.6	1620	8	ACC85301	ACC85301 Arabidops
19	1141.5	44.0	1608	3	ACC86501	ACC86501 DNA enco
20	1141	44.0	1608	2	AAK02914	AAK02914 Z. mays c
21	1091	42.0	1566	7	ADAY7115	ADAY7115 Rice gene
22	1091	42.0	1593	7	ADA69430	ADA69430 Rice gene
23	1076	41.4	1677	7	ADA70177	ADA70177 Rice gene
24	1074	41.4	1587	7	ADA69574	ADA69574 Rice gene
25	1063.5	41.0	1590	7	ADA69773	ADA69773 Rice gene
26	1056.5	40.7	1728	8	ABK28624	ABK28624 cDNA enco
27	1056.5	40.7	1728	8	ACC85293	ACC85293 Arabidops
28	1014	39.1	6733	2	AAK02913	AAK02913 Z. mays c
29	993	38.3	1515	6	ABK28629	ABK28629 cDNA enco
30	993	38.3	1515	8	ACC85298	ACC85298 Arabidops
31	920.5	35.5	1936	6	ABK28611	ABK28611 DNA enco
32	920.5	35.5	1936	8	ACC85280	ACC85280 Arabidops
33	920.5	35.5	2805	6	ABK28610	ABK28610 DNA enco
34	920.5	35.5	2805	8	ACC85279	ACC85279 Arabidops
35	920.5	35.5	2814	6	ABK28631	ABK28631 DNA enco
36	920.5	35.5	2814	8	ACC85300	ACC85300 Arabidops
37	905.5	34.9	3302	6	ABK28608	ABK28608 DNA enco
38	905.5	34.9	3302	8	ACC85277	ACC85277 Arabidops
39	903.5	34.8	2236	6	ABK28606	ABK28606 DNA enco
40	903.5	34.8	2236	8	ACC85275	ACC85275 Arabidops
41	835	32.2	1602	2	AAK02912	AAK02912 Z. mays c
42	791	30.5	503	3	ACC36788	ACC36788 Arabidops
43	457	17.6	1464	7	ABT32136	ABT32136 Benzodiaz
44	457	17.6	32539	7	ABT32129	ABT32129 Benzodiaz
45	226.5	8.7	1545	5	AAH65600	AAH65600 C glutami

XX Polynucleotide encoding novel plant protein having cytokinin oxidase  
PT activity and the protein useful for stimulating root growth, enhancing  
PT the formation of lateral or adventitious roots, altering root geotropism.  
XX Claim 2; Page 146-147; 154pp; English.  
XX The invention relates to an isolated polynucleotide (I) encoding a novel  
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for  
CC production of transgenic plants, plant cells or tissues; for production  
CC of altered plants, plant cell or tissues; and for effecting the  
CC expression of (II) where (II) is operably linked to one or more control  
CC sequences. The methods further comprises regenerating a plant from the  
CC plant cell. (I) and (II) are useful for stimulating root growth;  
CC enhancing the formation of lateral or adventitious roots; altering root  
CC geotropism, leading to an increase in yield; and for screening growth  
CC promoting chemical of herbicides. (I) is useful for increasing the size of the  
CC of the root meristem; increasing root size; increasing the size of the  
CC shoot meristem; delaying leaf senescence and altering leaf senescence;  
CC increasing leaf thickness; reducing or increasing the vessel size;  
CC inducing parthenocary; improving standability of the seedlings;  
CC to (II) is useful for identifying and obtaining proteins interacting with  
CC (II) comprising a screening assay, preferably a two-hybrid screening  
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase  
CC coding sequences and PCR primers of the invention  
XX  
SQ Sequence 1506 BP; 431 A; 328 C; 324 G; 423 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 2,19e-265 Length: 1506  
Score: 2596.00 Matches: 501  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0

US-10-014-101-4 (1-501) x ABK28625 (1-1506)

Qy 1 MetAlaAsnLeuArgLeuMetIleThrLeuIleThrValLeuMetIleThrLysSer 20  
Db 1 ATGGCTAATCTTCGTTAATGATCACTTTAATCAGGGTTTATGATCACCATAATCA 60  
Qy 21 AsnGlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSer 40  
Db 61 AACGGTATTAAATGATTGATTTACCTAAATCCCTTAAACCTCACCTCTCTACCGATCTCTCC 120  
Qy 41 IleIleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyVal 60  
Db 121 ATCATCTCCGAGCCTCTCATGACTTCGGAACATACCAACCGTGACCCCGCGCGGCTA 180  
Qy 61 IleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGlyLys 80  
Db 181 ATCTGCCCTCTCTCCACCGCTGATATCTCTGCTCTCTCAATACGCGCAACGGAATA 240  
Qy 81 SerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal 100  
Db 241 AGTACATCTCAAGTAGCGGCTCGTGGCAAGCCACCTCTTAAACGGCCCAAGCTCGGTC 300  
Qy 101 SerGlyGlyValIleValAsnMetThrCysIleThrAspValValValSerLysAspLys 120  
Db 301 TCCGGCGAGTAATCGTCAACATCAGCTGATCATCTACGCTGGTGGTTTCAAAAGACAAG 360  
Qy 121 LysTyrAlaAspValAlaAlaGlyThrLeuTrpValAspValLeuLysThrAlaGlu 140  
Db 361 AAGTACGCTGACGTGGCGCGCGGACGTTATGGGTGGATGGCTTAAGAGACGGCGAG 420  
Qy 141 LysGlyValSerProValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeu 160  
Db 421 AAAGGGGTGTCGCGGTTCTTTGGACGATTATTTGCATATAACCGTCGGAGAACGTTG 480  
Qy 161 SerAsnGlyGlyIleGlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeu 180

Db 481 TCGAATCGTGAATTGGTGGTCAAGTGTTCGAAACGGTCTCTTGTGTTAGTAACGTCCTT 540  
Qy 181 GluLeuAspValIleThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnPro 200  
Db 541 GAATTGGACGTTATTACTGGGAAAGGTGAATGTTGACATGCTCGCGACAGCTAAACCCA 600  
Qy 201 GluLeuPheTyrGlyValLeuGlyGlyGlnPheGlyIleIleThrArgAlaArg 220  
Db 601 GAATTGTTCTATGAGTGTAGGAGGTTTGGGTCAATTTGGAATTATAACGAGAGCCAGA 660  
Qy 221 IleValLeuAspHisAlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPhe 240  
Db 661 ATTGTTTGGACCATGACCATTAACGGCCCAATGGTTTCGGATGCTCTACAGTGAITTC 720  
Qy 241 ThrThrPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAsp 260  
Db 721 ACAACTTTTACAAAGGACCAAGACGTTTATCAATGGCAACGATATGGAGTGCAC 780  
Qy 261 TyrLeuGluGlyGlnIlePheLeuSerAsnGlyValValAspThrSerPhePhePro 280  
Db 781 TATTAGNAGTCAAAATATTTCTATCAACGGTGTCTGTGACACCTCTTTTTTCCCACT 840  
Qy 281 SerAspGlnSerLysValAlaAspLeuValGlnHisGlyIleIleThrValLeuGlu 300  
Db 841 TCAGATCAATCAAAAGTCGCTGATCTAGTCAAGCAACACGATATCATCTATGTTCTTGA 900  
Qy 301 ValAlaLysTyrTyrAspAspProAsnLeuProIleIleSerLysValIleAspThrLeu 320  
Db 901 GTAGCCAAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGTTATTGACACATTA 960  
Qy 321 ThrLysThrLeuSerTyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAsp 340  
Db 961 ACGAAACATTAAGTTACTTCCCGGGTTCATATCAATGACGACGCTGGCTTCTTCGAT 1020  
Qy 341 PheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeu 360  
Db 1021 TCTTGAACCGTGTACATGTCGAAGAAATTAATCATGATCTTTGGATATGGGAATTT 1080  
Qy 361 ProHisProTrpLeuAsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGly 380  
Db 1081 COTCATCTTGGCTTAACCTCTACGTTCTCTAAATCTCGGATTCCTCGATTTTCTAAGCGT 1140  
Qy 381 ValValLysAspIleLeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrPro 400  
Db 1141 GTTGTCAAGACATTTCTTTAAGCAAAATCAGCTTCGGACCTCGGCTCTTCTCTTATCCA 1200  
Qy 401 ThrAsnArgAsnLysTrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAsp 420  
Db 1201 ACARACCGGAATAAATGGCAATCGTATGTCGGCGATGATACCAAGATCGATGAAGAT 1260  
Qy 421 ValIleTyrIleIleGlyLeuGlnSerAlaThrProLysAspLeuProGluValGlu 440  
Db 1261 GTTATATATATATCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAGTGGAG 1320  
Qy 441 SerValAsnGluLysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyr 460  
Db 1321 AGCGTTAAGCAAGATTAATAGGTTTTCGAAAGGATTCAGGTATTAGATTAAAGCAATAT 1380  
Qy 461 LeuMetHisTyrThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAsp 480  
Db 1381 CTAATGCAATTACTAGTAAAGAGATTGGATTGGATTTTGGATCAAAATGGGATGAT 1440  
Qy 481 PheSerLysArgLysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIle 500  
Db 1441 TTTTCCAGAGAAAGATCTATTGATCCCAAGAACTGTTATCTCTCCAGGCGACAGATC 1500  
Qy 501 Phe 501  
Db 1501 TTT 1503

RESULT 2  
ACC85294  
ID ACC85294 standard; cDNA; 1506 BP.

XX AC C85294;  
 XX AC 18-SEP-2003 (first entry)  
 XX DE Arabidopsis cytokinin oxidase-like protein 2 cDNA.  
 XX KW Maize; root growth; root geotropism; cytokinin oxidase; seed size;  
 XX KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.  
 XX OS Arabidopsis thaliana.  
 XX PN WO2003050287-A2.  
 XX PD 19-JUN-2003.  
 XX PF 10-DEC-2002; 2002WO-EP013990.  
 XX PR 10-DEC-2001; 2001US-00014101.  
 XX PA (SCHM/) SCHMULLING T.  
 XX PA (WERN/) WERNER T.  
 XX PI Schmulling T, Werner T;  
 XX DR WPI; 2003-541577/51.  
 XX ST Stimulating root growth, enhancing lateral or adventitious root formation  
 PT or altering root geotropism comprises increasing plant cytokinin oxidase  
 PT levels or other protein or nucleic acid that reduces active cytokinins in  
 PT a plant.  
 XX PS Claim 3; Page 167-168; 177pp; English.  
 XX CC The present invention relates to a method for stimulating root growth or  
 CC enhancing the formation of lateral or adventitious roots or altering root  
 CC geotropism, which comprises increasing in a plant or plant part the level  
 CC of a plant cytokinin oxidase or other protein that reduces the level of  
 CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and  
 CC coding sequences from Arabidopsis thaliana are also provided. The method  
 CC is useful in modifying plant morphological, biochemical and physiological  
 CC properties, such as in modifying the initiation, stimulation or  
 CC enhancement of root growth, adventitious root formation, lateral root  
 CC formation, root geotropism, shoot growth, apical dominance, branching,  
 CC timing of senescence, timing of flowering, flower formation, seed  
 CC development and/or seed yield. The present sequence is a coding sequence  
 CC shown in the invention  
 XX SQ Sequence 1506 BP; 431 A; 328 C; 324 G; 423 T; 0 U; 0 Other;

Db 181 ATCTGCCCTCTCCACCGCTGATATCTCTCTCTCCATACGCCCAACCGGAAA 240  
 Qy 81 SerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal 100  
 Db 241 AGTACATTCCAAAGTAGCGCTCGTGGCCAAAGCCACTCTCTTAACGGCCACCGCTCGTGC 300  
 Qy 101 SerGlyValValValValValMetThrCysIleThrAspValValValSerValSerVal 120  
 Db 301 TCCGGCGGAGTAATCGTCAACATGACGTGTATCATCTGACGTGTGTGTGTTCCTCAACAGCA 360  
 Qy 121 LysTyrAlaAspValAlaAlaGlyThrLeuTyrValAlaAspValValLeuValSerVal 140  
 Db 361 AAGTACGCTGACGTGGCGCGCGGACGTTATGGTGGATGTCTTAAAGAGACGGCGAG 420  
 Qy 141 LysGlyValSerProValSerThrThrThrThrThrThrThrThrThrThrThrThrThr 160  
 Db 421 AAAGGGGTGTGGCGGTCTTCTGGACGGATTAATTTGCATATTAACCGTCCGAGCAAGCTTG 480  
 Qy 161 SerAsnGlyGlyIleGlyGlnValPheArgAsnGlyProLeuValSerValSerVal 180  
 Db 481 TCGAATGGTGGAAATGGTGTCAAGTGTTCGAAACGGTCTCTTGTAGTAACGCTCTT 540  
 Qy 181 GluLeuAspValIleThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnPro 200  
 Db 541 GAATTCGACGTTATTAATCGGAAAGGTGAATGTTCACATGCTCGGACAGCTAAACCCA 600  
 Qy 201 GluLeuPheTyrGlyValLeuGlyGlyGlnPheGlyIleIleThrArgAlaArg 220  
 Db 601 GAATTTCTATCGAGTGTAGGAGGTTTGGGTCAATTTGGAAATATAACGAGAGCCAGA 660  
 Qy 221 IleValLeuAspHisAlaProLysArgAlaLysTyrPheArgMetLeuTyrSerAspPhe 240  
 Db 661 ATTGTTTGGACCATCAGTCAATCAACGGGCAATGGTTTCGGATGCTCTACAGTATTTTC 720  
 Qy 241 ThrThrPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAsp 260  
 Db 721 ACAACATTTTCAAGGACCAAGACGTTGATATCAATGCGCAACCGATATGGAGTCGAC 780  
 Qy 261 TyrLeuGluGlyGlnIlePheLeuSerAsnGlyValValAspThrSerPhePhePro 280  
 Db 781 TATTAGAGGTCAATATTTCTATCAACGGGTGCTGTGACACCTCTTTTTCACACCT 840  
 Qy 281 SerAspGlnSerLysValAlaAlaPheValLysGlnHisGlyIleIleThrValLeuGlu 300  
 Db 841 TCAGATCAATCTAAAGTCGCTGATCTAGTCAACCAACAGGATCATCTATGTTCTTGA 900  
 Qy 301 ValAlaLysTyrTyrAspAspProAsnLeuProIleIleSerLysValIleAspThrLeu 320  
 Db 901 GTAGCCCAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTATTATGACACATTA 960  
 Qy 321 ThrLysThrLeuSerTyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAsp 340  
 Db 961 ACAGAAACATTAAGTTACTTCCCGGCTTCATATCAATGCGACGCTGGCTACTTCGAT 1020  
 Qy 341 PheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTyrGluLeu 360  
 Db 1021 TCTTGAACCGTGTACATGTGGAAGAAATAAACTCAGATCTTTGGGATTATGGGAACCT 1080  
 Qy 361 ProHisProThrLeuAsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGly 380  
 Db 1081 CCTCATCTTGGCTTAACCTCTACGTTCTTAAATCTCGGATCTCGATTTTCATACGGT 1140  
 Qy 381 ValValLysAspIleLeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrPro 400  
 Db 1141 GTTGTCAAGACATCTCTTAAAGCAAAATCAGTTCGGGACTCGCTCTCTCTATCCA 1200  
 Qy 401 ThrAsnArgAsnLysTyrAspAsnArgMetSerAlaMetIleProGluIleAspGluAsp 420  
 Db 1201 ACAACCGGAATTAATGGGCAATCGTATGTCGGCGATGATACGAGAGATCGATGAAGAT 1260  
 Qy 421 ValIleTyrIleIleGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGlu 440

Alignment Scores:  
 Pred. No.: 2,19e-265 Length: 1506  
 Score: 2596.00 Matches: 501  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 8 Gaps: 0  
 US-10-014-101-4 (1-501) x ACC85294 (1-1506)  
 Qy 1 MetAlaAsnLeuArgLeuMetIleThrLeuIleThrValLeuMetIleThrLysSerSer 20  
 Db 1 ATGGCTAACTTCGTTTATGATCACTTAAATACCGGTTTTAATGATCACCACCAATCATCA 60  
 Qy 21 AsnGlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSer 40  
 Db 61 AACGGTATTAAATTTGATTTTACCTAAATCCCTTAACCTCACCTCTCTACCGATCTCTCC 120  
 Qy 41 IleIleSerAlaAlaSerHisAspPheGlyValIleThrThrValThrProGlyGlyVal 60  
 Db 121 ATCATCTCGGACGCTCTCATGACTTCGGAACATACACCGTGNACCCCGCGGCGGTA 180  
 Qy 61 IleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGlyLys 80

Db 1261 GTTATATATATTCGGACTACTACAATCCGCTACCCCAAGGATCTTCCAGAGTGAG 1320  
Qy 441 SerValAsnGluLysIleArgPheCysLysAspSerGlyLeuLysGlnTyr 460  
Db 1321 AGCGTTAACGAGAGATAATTAGGTTTTCGAAGGATTCAGGTATTAAAGCAATAT 1380  
Qy 461 LeuMetHisTyrThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAsp 480  
Db 1381 CTAATGCATTACTAGTAAGAGATTGGATTGAGCAATTTGGATCAAAATGGATGAT 1440  
Qy 481 PheSerLysArgLysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIle 500  
Db 1441 TTTTCGAGAGAGAAAGATCTATTTCATCCCAAGAACTGTTATCTCCAGGCGAAGACATC 1500  
Qy 501 Phe 501  
Db 1501 TTT 1503  
RESULT 3  
AAC43214  
ID AAC43214 standard; DNA; 1548 BP.  
XX  
AC AAC43214;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38443.  
XX  
KW Hybridisation assay; genetic mapping; gene expression control;  
KW protein identification; signal transduction pathway; metabolic pathway;  
KW promoter; termination sequence; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
XX  
PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 16-APR-1999; 99US-0128714P.  
PR 19-APR-1999; 99US-0129845P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 28-APR-1999; 99US-0130891P.  
PR 30-APR-1999; 99US-0131449P.  
PR 30-APR-1999; 99US-0132048P.  
PR 04-MAY-1999; 99US-0132407P.  
PR 05-MAY-1999; 99US-0132484P.  
PR 06-MAY-1999; 99US-0132485P.  
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PR 07-MAY-1999; 99US-0132487P.  
PR 11-MAY-1999; 99US-0132863P.  
PR 14-MAY-1999; 99US-0134256P.  
PR 14-MAY-1999; 99US-0134218P.  
PR 14-MAY-1999; 99US-0134219P.  
PR 14-MAY-1999; 99US-0134221P.  
PR 14-MAY-1999; 99US-0134370P.  
PR 18-MAY-1999; 99US-0134768P.  
PR 19-MAY-1999; 99US-0134941P.  
PR 20-MAY-1999; 99US-0135124P.  
PR 21-MAY-1999; 99US-0135353P.  
PR 24-MAY-1999; 99US-0135629P.  
PR 25-MAY-1999; 99US-0136021P.  
PR 27-MAY-1999; 99US-0136392P.  
PR 28-MAY-1999; 99US-0136782P.  
PR 01-JUN-1999; 99US-0137222P.  
PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 21-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145085P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145089P.  
PR 22-JUL-1999; 99US-0145132P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145913P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 02-AUG-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.





Db 901 GTAGCCAAAGTATTATGATGATCCCATCTCCCATCATCAGCAAGGTTATTGACACATTA 960  
 QY 321 ThrLysThrLeuSerTyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAsp 340  
 Db 961 ACGAAACATTAAGTTACTTGCCTGGGTTTCATATCAATGACGACGTGGCTTACTTCGAT 1020  
 QY 341 PheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTyrGluLeu 360  
 Db 1021 TTCCTGAACCGGTGATCATGTCGAGAAATAAATCAATCAGATCTTTGGGATTATGGAACTT 1080  
 QY 361 ProHisProTyrLeuAsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGly 380  
 Db 1081 CCTCATCTCTGGCTTAACTCTACGTTCTAAATCTCGAATCTCGAATCTCGAATCTTTCATAACGGT 1140  
 QY 381 ValValLysAspIleLeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrPro 400  
 Db 1141 GTTGICAAAGACATCTTCTTAAAGCAAAATCAGCTTCGGGACTCGCTCTTCTCTATCA 1200  
 QY 401 ThrAsnArgAsn-----LysTyr 406  
 Db 1201 ACAACCGGAATAAGTACATATCTCTCTCATTCATATTTATCTTCAAGAACCAAAATGG 1260  
 QY 407 AspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIleGly 426  
 Db 1261 GACATCGTATGTCGGCGGATGATACAGAGATCGATGAAGATGTTATATATATTATTCGGA 1320  
 QY 427 LeuLeuGlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGluLysIle 446  
 Db 1321 CTACTACAATCCGCTACCCCAAGGATCTTCAGAAAGTCGAGAGCGTTAAACGAGAAGATA 1380  
 QY 447 IleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyrThrSer 466  
 Db 1381 ATTAGGTTTTGCAAGGATTCAGGTATTAAGATTAAGCAATATCTTAATGATTATATCTAGT 1440  
 QY 467 LysGluAspTyrIleGluHisPheGlySerLysTyrAspAspPheSerLysArgLysAsp 486  
 Db 1441 AAAGAAGATGGATTGGACATTTTGGATCAAAATGGGATGATTTTCGAAGAGGAAGAT 1500  
 QY 487 LeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501  
 Db 1501 CTATTTGATCCCAAGAACTGTTATCTCCAGGGCAAGACATCTTT 1545  
 RESULT 4  
 ID ABK28607 standard; DNA; 2991 BP.  
 AC ABK28607;  
 XX  
 DT 09-APR-2002 (first entry)  
 DE DNA encoding A. thaliana cytokinin oxidase AtCKX2.  
 XX Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;  
 KW root growth; lateral root; adventitious root; root geotropism; herbicide;  
 KW root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ds.  
 XX Arabidopsis thaliana.  
 OS  
 XX W0200196580-A2.  
 PN  
 XX 20-DEC-2001.  
 PD  
 XX 18-JUN-2001; 2001WO-EP006833.  
 PF  
 XX 16-JUN-2000; 2000EP-00670132.  
 PR 27-DEC-2000; 2000US-0258415P.  
 PR 16-MAR-2001; 2001EP-00670053.  
 XX (SCHM/) SCHMULLING T.  
 PA (WERN/) WERNER T.  
 XX  
 PI Schmullling T, Werner T;

XX WPI: 2002-130736/17.  
 DR P-PSDS; AAU81968.  
 XX  
 PT Polynucleotide encoding novel plant protein having cytokinin oxidase  
 PT activity and the protein useful for stimulating root growth, enhancing  
 PT the formation of lateral or adventitious roots, altering root geotropism.  
 XX  
 PS Claim 3; Page 128-129; 154pp; English.  
 XX  
 CC The invention relates to an isolated polynucleotide (I) encoding a novel  
 CC plant protein (II) having cytokinin oxidase activity. (I) is useful for  
 CC production of transgenic plants, plant cells or tissues; for production  
 CC of altered plants, plant cell or tissues; and for effecting the  
 CC expression of (II) where (I) is operably linked to one or more control  
 CC sequences. The methods further comprises regenerating a plant from the  
 CC plant cell. (I) and (II) are useful for stimulating root growth;  
 CC enhancing the formation of lateral or adventitious roots; altering root  
 CC geotropism, leading to an increase in yield; and for screening growth  
 CC promoting chemical of herbicides. (I) is useful for increasing the size of  
 CC of the root meristem; increasing root size; increasing the size of the  
 CC shoot meristem; delaying leaf senescence and altering leaf senescence;  
 CC increasing leaf thickness; reducing or increasing the vessel size;  
 CC inducing parthenocarp; improving standability of the seedlings;  
 CC increasing branching and for improving lodging resistance. Antibody (III)  
 CC to (II) is useful for identifying and obtaining proteins interacting with  
 CC (II) comprising a screening assay, preferably a two-hybrid screening  
 CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase  
 CC coding sequences and PCR primers of the invention  
 XX  
 SQ Sequence 2991 BP; 920 A; 522 C; 521 G; 1028 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 1.06e-225 Length: 2991  
 Score: 2226.50 Matches: 499  
 Percent Similarity: 50.00% Conservative: 0  
 Best Local Similarity: 50.00% Mismatches: 2  
 Query Match: 85.77% Indels: 499  
 DB: 6 Gaps: 4  
 US-10-014-101-4 (1-501) x ABK28607 (1-2991)  
 QY 1 MetAlaAsnLeuArgLeuMetIleThrLeuIleThrValLeuMetIleThrLysSerSer 20  
 Db 1 ATGGCTAATCTTCGTTTAAATGATCATTAAATCAGCGTTTAAATGATCAGCAATCATCA 60  
 QY 21 AsnGlyIleLysIleAspLeuProLysSerLysLeuAsnLeuThrLysSerThrAspProSer 40  
 Db 61 AACGGTATTAAATTTGATTTACCTAAATCCCTTAACTCACCCTCTCTACCGATCTCTCC 120  
 QY 41 IleIleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyVal 60  
 Db 121 ATCATCTCCGAGGCTCTCATGACTTCGGAACATATACCAACCGTGACCCCGCGCGGTA 180  
 QY 61 IleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGlyLys 80  
 Db 181 ATCTGCCCTCTCTCCACCGCTGATATCTCTGCTCTCTCCAAATACGCGGCAACGGAATA 240  
 QY 81 SerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal 100  
 Db 241 AGTACATTCGAAGTAGCGGCTCTGGCCCAAGGCCACTCTTAAACGCCAAGCCTCGGTC 300  
 QY 101 SerGlyGlyValIleValAsnMetThrCysIleThrAspValValValSerLysAspLys 120  
 Db 301 TCCGCGCGGAGTAATCGTCAACATGACGTGATATCATGACGTGGTGGTGGTTTCAAAAGACAAG 360  
 QY 121 LysTyrAlaAspValAlaAlaGlyThrLeuTyrValAspValLeuLysLysThrAlaGlu 140  
 Db 361 AAGTACGCTGACGTGGCGCGCGGACGTTATGGGTGATGTGCTTAAAGACGCGCGGAG 420  
 QY 141 LysGlyValSerProValSerTyrThrAspTyrLeuHisIleThrValGlyGlyThrLeu 160  
 Db 421 AAAGGGGTGTCGCCGGTTTCTTGACGCGATTATTTGCATATATACCGTCGGAGGAACGTTG 480

QY 161 SerAsnGlyGlyIleGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeu 180  
DB 481 TCGATGTTGGAAATTTGGTGGTCAAGTGTTCGAACGGTCTCTTTGTAGTAACGTCCTT 540  
QY 181 GluLeuAspValIleThr----- 186  
DB 541 GAATTTGGACGTTATTACTGGTACGCGATCTCTAAACCTTTGTATGATACATACACAA 600  
QY 186 ----- 186  
DB 601 ACTGTTTTGTTTTATAGTATTTTTCATTTTTTTGTACCATAGGTTTTATGTTTTATAGTT 660  
QY 186 ----- 186  
DB 661 GTGCTAAACCTTCTGCACCACACGTAAGTCTTCGAAACACAAATGGCGTAACGCATCTAT 720  
QY 186 ----- 186  
DB 721 ATGTTTTTTGTACATATTGAATGTTGTTTCATGAGAAATAAAGTAATTACATATACACA 780  
QY 186 ----- 186  
DB 781 TTTATTTGCGTACATATATAAATAATTAAAGACAAATTTTTCACAAATGGTAGCGTTAA 840  
QY 186 ----- 186  
DB 841 TTTGGGAATTTTGTAAATGATACATGATGACGATGATATGAGGCTTTTCGGTTTTCTTA 900  
QY 186 ----- 186  
DB 901 GATTTGTTGATGATTTCAAATATATCATTTATTTTCTTCGAATAAAGAGGTGATATT 960  
QY 186 ----- 186  
DB 961 TTTAAATAGCAACATTTTCAGAAATTTTCTTTGAAATTTACACTTTTAAATTTGTTATGT 1020  
QY 187 ----- GlyLysGlyGluMetLeuThrCysSerArgG1 197  
DB 1021 TAATATGATTTTGAATAAATAATTTTCAGGGAAGGTGAATTTGATGATGCTCGGACA 1080  
QY 197 nLeuAsnProGluLeuPheThrGlyValLeuGlyGlyLeuGlnPheGlyIleIleTh 217  
DB 1081 GCTAAACCCAGAAATTTCTATGGAGTGTAGGAGGTTTGGTCAAATTTGGAATTAATAC 1140  
QY 217 rArgAlaArgIleValLeuAspHisAlaProLys----- 228  
DB 1141 GAGAGCCAGATTTGTTGGACCAATGACCTTAACGGGTACGTATCATATTTTACCA 1200  
QY 228 ----- 228  
DB 1201 TTTGTTTTAGTCAGCATTCATTTTTCAATAGTAATTCGGTTTCAATTTCTAAATTTTTT 1260  
QY 228 ----- 228  
DB 1261 AGTCAATAGAAAATGATTTCTTATGTCAGAGCTTGATATTTATGATGATTTTATGAGATA 1320  
QY 228 ----- 228  
DB 1321 AAATAAATAATAACCTAACGGAATAAATTTTACTTAATCGGATAATGCTCGATTAA 1380  
QY 228 ----- 228  
DB 1381 CATTATGATATTACTAAGAGAGTTAGAGCGTATGGATCACAACAAACATGAAGCTTT 1440  
QY 228 ----- 228  
DB 1441 CTTAGATGATTCCTAAACCTAAAGTTAGGTACAAAGTTTGGNAATTTAGTCAAAATGCTTA 1500  
QY 228 ----- 228  
DB 1501 AGTTGCATTAATTTGAACAAATCTATGCATTTGAATAAATAAAGATATGGATTATTATTA 1560

QY 228 ----- 228  
DB 1561 TAAAGTATAGTCTCTTGTAAATCCTAGGACTTGTTGTCTAATCTTGTCTTATGGTCAAAAT 1620  
QY 228 ----- 228  
DB 1621 CTTTTTGATGTCAATATATAAATCCCTTTGTTTATTAGAGTCAAGCTCTTTTCATTAGTCAACT 1680  
QY 228 ----- 228  
DB 1681 ACTCAAAATATATCCAAAGTTTGAATAATAGTCTTCTGACTAATTAGAATCTTACAACCG 1740  
QY 228 ----- 228  
DB 1741 ATAAAGTTTACAATTTGGTTATCATTTTAAAAACAGATTTGGTCAATAATATACGATGAC 1800  
QY 228 ----- 228  
DB 1801 GTTCTGTTTGTCTCTATCTATTCACAAATTTTATATAATTATTTTCAAGAAAAATATTGA 1860  
QY 228 ----- 228  
DB 1861 AATACTATATCTGTAATATGTTTCTTTATATATGTGTATAAATTTAAATGGGATTTGTT 1920  
QY 229 ----- ArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrTh 242  
DB 1921 TCTCTAAATGAATTTGTGTAGGCC-AAATGGTTTCGATGCTCTACAGTGATTTTCAAC 1979  
QY 242 rPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLe 262  
DB 1980 TTTTACAAAGGACCAAGAACGTTTGATATCAATGCGCAACAGATATTGGAGTGCACATTT 2039  
QY 262 uGluGlyGlnIlePheLeuSerAsnGlyValValLeuThrSerPhePheProSerAs 282  
DB 2040 AGAAGTCAAAATTTTCTATCAACGGTGTGTTGACCTCTTTTTTCCACCTTCAGA 2099  
QY 282 pGlnSerLysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAl 302  
DB 2100 TCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAAGTAGC 2159  
QY 302 aLysTyrTyrAspAspProAsnLeuProIleIleSerLys----- 315  
DB 2160 CAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTACTACACATTTACATTTT 2219  
QY 315 ----- 315  
DB 2220 CATCATCGTTTTTATCATACCATAAGATATTAAATGATTTCATTCATTGCACCACATTAAG 2279  
QY 315 ----- 315  
DB 2280 ATATTCATCATCATCATCGTTACATTTTTTTTTTGCACTTTATGCTTCTCATATCTACTA 2339  
QY 316 ----- ValIleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPheIleSerM 333  
DB 2340 TTGTGTAGTTATTGACATTAACGAAACATTAAGTTACTTGCCTGGGTTTCATATCAA 2399  
QY 333 eThiAspValAlaTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeuA 353  
DB 2400 TGCACGACGTGGCCTACTTCGATTTCTTGAAACCGTGTACATGTCTGAAGAAAAATAACTCA 2459  
QY 353 rGSerLeuGlyLeuTyrGluLeuProHisProTrpLeuAsnLeuTyrValProLysSerA 373  
DB 2460 GATCTTTGGGATTTAGGAACCTTCTCATCTTTGGCTTTAACCTCTACGTTCTCTTAATCTC 2519  
QY 373 rGileLeuAspPheHisAsnGlyValValLysAspIleLeuLeuLysGlnLysSerAlas 393  
DB 2520 GGATTTCTCGATTTTCAACGGTGTGTCAAGACATTTCTTCTTAAGCAAAAAATCAGCTT 2579  
QY 393 eRgGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 405  
DB 2580 CGGACTCGCTCTTCTCTATCCAAACACCGGAATAA-GTACATACTTCTCTTCATTCAT 2638  
QY 405 ----- 405





XX 17-OCT-2000 (first entry)  
 DT Arabidopsis thaliana DNA fragment SEQ ID NO: 37588.  
 DE Hybridisation assay; genetic mapping; gene expression control;  
 DE Protein identification; signal transduction pathway; metabolic pathway;  
 DE Promoter; termination sequence; ss.  
 KW Arabidopsis thaliana.  
 OS Arabidopsis thaliana.  
 PN EP1033405-A2.  
 PP 06-SEP-2000.  
 XX 25-FEB-2000; 2000EP-00301439.  
 XX 25-FEB-1999; 99US-0121825P.  
 PR 05-MAR-1999; 99US-0123180P.  
 PR 09-MAR-1999; 99US-0123548P.  
 PR 23-MAR-1999; 99US-0125788P.  
 PR 25-MAR-1999; 99US-0126264P.  
 PR 29-MAR-1999; 99US-0126785P.  
 PR 01-APR-1999; 99US-0127462P.  
 PR 06-APR-1999; 99US-0128234P.  
 PR 08-APR-1999; 99US-0128714P.  
 PR 16-APR-1999; 99US-0129845P.  
 PR 19-APR-1999; 99US-0130077P.  
 PR 21-APR-1999; 99US-0130449P.  
 PR 23-APR-1999; 99US-0130510P.  
 PR 28-APR-1999; 99US-0130891P.  
 PR 30-APR-1999; 99US-0131449P.  
 PR 30-APR-1999; 99US-0132048P.  
 PR 04-MAY-1999; 99US-0132407P.  
 PR 05-MAY-1999; 99US-0132484P.  
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 PR 07-MAY-1999; 99US-0132863P.  
 PR 11-MAY-1999; 99US-0134256P.  
 PR 14-MAY-1999; 99US-0134218P.  
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 PR 18-MAY-1999; 99US-0134768P.  
 PR 19-MAY-1999; 99US-0134941P.  
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 PR 28-MAY-1999; 99US-0136782P.  
 PR 01-JUN-1999; 99US-0137222P.  
 PR 03-JUN-1999; 99US-0137528P.  
 PR 04-JUN-1999; 99US-0137502P.  
 PR 07-JUN-1999; 99US-0137724P.  
 PR 08-JUN-1999; 99US-0138059P.  
 PR 10-JUN-1999; 99US-0138540P.  
 PR 10-JUN-1999; 99US-0138847P.  
 PR 14-JUN-1999; 99US-0139119P.  
 PR 16-JUN-1999; 99US-0139452P.  
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 PR 17-JUN-1999; 99US-0139492P.  
 PR 18-JUN-1999; 99US-0139454P.  
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 PR 01-JUL-1999; 99US-0141842P.  
 PR 02-JUL-1999; 99US-0142055P.  
 PR 02-JUL-1999; 99US-0142154P.  
 PR 06-JUL-1999; 99US-0142390P.  
 PR 08-JUL-1999; 99US-0142803P.  
 PR 09-JUL-1999; 99US-0142920P.  
 PR 12-JUL-1999; 99US-0142977P.  
 PR 13-JUL-1999; 99US-0143542P.  
 PR 14-JUL-1999; 99US-0143624P.  
 PR 15-JUL-1999; 99US-0144005P.  
 PR 16-JUL-1999; 99US-0144085P.  
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 PR 19-JUL-1999; 99US-0144325P.  
 PR 19-JUL-1999; 99US-0144331P.  
 PR 19-JUL-1999; 99US-0144332P.  
 PR 19-JUL-1999; 99US-0144333P.  
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 PR 19-JUL-1999; 99US-0144335P.  
 PR 20-JUL-1999; 99US-0144352P.  
 PR 20-JUL-1999; 99US-0144632P.  
 PR 20-JUL-1999; 99US-0144884P.  
 PR 21-JUL-1999; 99US-0144814P.  
 PR 21-JUL-1999; 99US-0145086P.  
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 PR 22-JUL-1999; 99US-0145085P.  
 PR 22-JUL-1999; 99US-0145087P.  
 PR 22-JUL-1999; 99US-0145089P.  
 PR 22-JUL-1999; 99US-0145192P.  
 PR 23-JUL-1999; 99US-0145145P.  
 PR 23-JUL-1999; 99US-0145218P.  
 PR 23-JUL-1999; 99US-0145224P.  
 PR 26-JUL-1999; 99US-0145276P.  
 PR 27-JUL-1999; 99US-0145913P.  
 PR 27-JUL-1999; 99US-0145918P.  
 PR 27-JUL-1999; 99US-0145919P.  
 PR 28-JUL-1999; 99US-0145951P.  
 PR 02-AUG-1999; 99US-0146386P.  
 PR 02-AUG-1999; 99US-0146388P.  
 PR 02-AUG-1999; 99US-0146389P.  
 PR 03-AUG-1999; 99US-0147038P.  
 PR 04-AUG-1999; 99US-0147204P.  
 PR 05-AUG-1999; 99US-0147302P.  
 PR 05-AUG-1999; 99US-0147260P.  
 PR 06-AUG-1999; 99US-0147303P.  
 PR 06-AUG-1999; 99US-0147416P.  
 PR 09-AUG-1999; 99US-0147493P.  
 PR 09-AUG-1999; 99US-0147935P.  
 PR 10-AUG-1999; 99US-0148171P.  
 PR 11-AUG-1999; 99US-0148319P.  
 PR 12-AUG-1999; 99US-0148341P.  
 PR 13-AUG-1999; 99US-0148565P.  
 PR 13-AUG-1999; 99US-0148684P.  
 PR 16-AUG-1999; 99US-0149368P.  
 PR 17-AUG-1999; 99US-0149175P.  
 PR 18-AUG-1999; 99US-0149436P.  
 PR 20-AUG-1999; 99US-0149722P.  
 PR 20-AUG-1999; 99US-0149723P.  
 PR 20-AUG-1999; 99US-0149923P.  
 PR 23-AUG-1999; 99US-0149902P.  
 PR 23-AUG-1999; 99US-0149930P.  
 PR 25-AUG-1999; 99US-0150566P.  
 PR 26-AUG-1999; 99US-0150884P.



QY 406 TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIle 425  
 Db 1285 TGGAAACACCGCATGTCAACGATGACACCG-----GACGAAGATGTTTTTATGTGATC 1338  
 QY 426 GlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSerValAsnGlu 444  
 Db 1339 GGATTACTCAATCAGCTGGTGATCTCAAAATGGCAAGAACTTGAAATCTCAACGAC 1398  
 QY 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr 464  
 Db 1399 AAGGTATTACGTTTTGTGAAACTCGGAAATTAAGATTAAGAAATATTGATGACATAT 1458  
 QY 465 ThrSerLeuGluAspTrpIleGluHisPheGlySerLysTrpAspAspPheSerLysArg 484  
 Db 1459 ACAAGAAAGAGATGGGTGTTAAACATTTTGACCAAAATGGGATGATTTTTTAAGAAAG 1518  
 QY 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501  
 Db 1519 AAAATTATGTTGATCCCAAGACATATTGTTCTCAGGACAAACATATTT 1569

RESULT 7

ABZ14284  
 ID ABZ14284 standard; DNA; 1575 BP.  
 XX AC ABZ14284;  
 XX DT 21-JAN-2003 (first entry)  
 XX DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2089.  
 XX KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.  
 XX KW Arabidopsis thaliana.  
 XX OS Arabidopsis thaliana.  
 XX DN WO200216655-A2.  
 XX PD 28-FEB-2002.  
 XX PF 24-AUG-2001; 2001WO-US026685.  
 XX PR 24-AUG-2000; 2000US-0227866P.  
 XX PR 26-JAN-2001; 2001US-0264847P.  
 XX PR 22-JUN-2001; 2001US-0300111P.  
 XX PA (SCRI ) SCRIPPS RES INST.  
 XX PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX PI Harper JF, Kreps J, Wang X, Zhu T;  
 XX PS WPI; 2002-304127/34.

Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.  
 Claim 144; SEQ ID NO 2089; 577bp + Sequence Listing; English.

The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office

Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.78e-183 Length: 1575

Score: 1822.00 Matches: 345  
 Percent Similarity: 80.08% Conservative: 69  
 Best Local Similarity: 66.73% Mismatches: 79  
 Query Match: 70.18% Indels: 24  
 DB: 6 Gaps: 5  
 US-10-014-101-4 (1-501) x ABZ14284 (1-1575)  
 QY 7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21  
 Db 25 CTCATCACCCATAAAGCTTTTATAAGTTTAAACCCCAACCTTAATCAATCAGATGAG 84  
 QY 22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41  
 Db 85 GGCATTGATGTTTCTACCATATCACCACTTACGGTCTCAACCGATCCTTCTCC 144  
 QY 42 IleSerAlaIleSerHisAspPheGlyAsnIleThrValThrProGlyGlyValIle 61  
 Db 145 ATCTCTCCCGCTTCTCAGACTTCGGTAAACATAACCGAAGAAATCCCGCGCGCTC 204  
 QY 62 CysProSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly----- 79  
 Db 205 TGCCCTTCTCCACCGAGGAGTGGCTCTCTCTCGGTTTCGTAACGGAGGATCTCT 264  
 QY 80 -----LysSerThrPheGlnValAlaIleAlaIleArgGlyGlnGly 91  
 Db 265 TACAATAAAGGCTCAACACGCGCGGCTCTACTTTCAAAGTGGCTGCTCGAGGCCAAGC 324  
 QY 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle 111  
 Db 325 CACTCCCTCCGTGCGCAAGCTCTGACCCCGGAGGTGCTGCTGTAACATGACGTGTCTC 384  
 QY 112 -----ThrAspValValSerLysAspLysIleTyrAlaAspVal 125  
 Db 385 GCCATGCGGCTAAACACGCGCGGTTGTTATCTCGGCACAGCGGACTTACGCTGACGTG 444  
 QY 126 AlaIleGlyThrLeuTrpValAspValLeuLysThrAlaGluLysGlyValSerPro 145  
 Db 445 GCTCGCGGACGATGTGGTGGATGTTCTGAAGCGCGCGTGGATAGAGGGCTCTCGCCG 504  
 QY 146 ValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle 165  
 Db 505 GTTACATGGACGGATTTATTTGTATCTCAGCGTTCGCGGAGCGTGTGCGAACGCTGGAATC 564  
 QY 166 GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle 185  
 Db 565 GGTGTGTCAGACGTTTAGACACGCGGCTCAGATTAGTAAACCTGAACCTGAATGTTCTATGGA 624  
 QY 186 ThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGly 205  
 Db 625 ACCGGAAGGTGAATGATGATGATGCTCTCCAAAGTTAAACCTGAATGTTCTATGGA 684  
 QY 206 ValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHis 225  
 Db 685 GTTTTAGGAGGTTTGGGTCAATTCCGTTATTATAACGAGGCGGAGGATTCGCTTGAATCAT 744  
 QY 226 AlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLys 245  
 Db 745 GCACCCCAAGGGTGAATGCTCGCATACTCTACAGTACTTCTCGGCTTTTAAAAAGA 804  
 QY 246 AspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLeuGluGlyGln 265  
 Db 805 GACCAAGAGCGTTTAATATATCAATGACCAATGATCTCGAGTTGACTTTTGAAGGTCAA 864  
 QY 266 IlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLys 285  
 Db 865 CTATGATGTCAATGGCTTCGTAGACACCTCTTTTCTCCACTCTCCGATCAACAAGA 924  
 QY 286 ValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAlaLysTyrTyr 305  
 Db 925 GTCCGATCTCTGTGATGACACCGGATCATCTATGTTCTCGAAGTAGACCAAGTATTAT 984  
 QY 306 AspAspProAsnLeuProIleIleSerLysValIleAspThrLeuThrLysThrLeuSer 325



Db 985 GACAGAACACCCCTTCCCATTTATGACAGGATGATGACAGTTAAGTAGAAGCTCTAGGT 1044

Qy 326 TyrLeuProGlyPheHisSerMetHisAspValAlaTyrPheAspPheLeuAsnArgVal 345

Db 1045 TTCGCTCCAGGTTTATGTCGTACAGATGTCGTATTCGATTTTCGATTTTCGACCGTGC 1104

Qy 346 HisValGluGluAsnLeuArgSerLeuGlyLeuTyrGluLeuProHisProTyrLeu 365

Db 1105 CGAAACGAGAGAGATTAACATCGATCTTTAGACATCGGAGATTCCTCATCCATGGCTT 1164

Qy 366 AsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIle 385

Db 1165 AACATCTTTGTCGCGGTCTCGAATCCAAAGATTTTCATGATGGTGTATTAAATGGCCTT 1224

Qy 386 LeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys 405

Db 1225 CTTCTAAACCAACCTCACTTCTGGTGTACTCTTCTATCTCCACAAACCGAACAACAA 1284

Qy 406 TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIle 425

Db 1285 TGGACACACCGCATGTCACGATGACACCG-----GACGAGATGTTTTTATGTGATC 1338

Qy 426 GlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSerValAsnGlu 444

Db 1339 GGATTTACTGCAATCAGCTGGTGGATCTCAAAATTCGCAAGAACCTTGAAATCTCAACGAC 1398

Qy 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr 464

Db 1399 AAGGTATTTCAGTTTGTGAAACCTCGGAATTAAGATTAAAGATATTGATGACATAT 1458

Qy 465 ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAspPheSerLysArg 484

Db 1459 ACAAGAAAAGAGATTGGGTAAACATTTTGGACCAAAATGGGATGATTTTTTAAGAAAG 1518

Qy 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501

Db 1519 AATAATTGTTTGATCCCAAGACATTTGTTCTCCAGGACAAGACATATTT 1569

RESULT 8

ID ABK28627

XX ABK28627 standard; cDNA; 1575 BP.

AC ABK28627;

XX 09-APR-2002 (first entry)

XX cDNA encoding A. thaliana cytokinin oxidase AtCKX4.

XX Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;

XX root growth; lateral root; adventitious root; root geotropism; herbicide;

XX root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ss.

XX Arabidopsis thaliana.

XX WO200196580-A2.

XX 20-DEC-2001.

XX 18-JUN-2001; 2001WO-BP006833.

XX 16-JUN-2000; 2000EP-00870132.

XX 27-DEC-2000; 2000US-0258415P.

XX 16-MAR-2001; 2001EP-00870053.

XX (SCHM/) SCHMULLING T.

XX (WERN/) WERNER T.

XX Schmullling T, Werner T;

XX WPI; 2002-130736/17.

XX Polynucleotide encoding novel plant protein having cytokinin oxidase

PT activity and the protein useful for stimulating root growth, enhancing

XX the formation of lateral or adventitious roots, altering root geotropism.

PS Claim 2; Page 147-148; 154pp; English.

XX

CC The invention relates to an isolated polynucleotide (I) encoding a novel

CC plant protein (II) having cytokinin oxidase activity. (I) is useful for

CC production of transgenic plants, plant cells or tissues; for production

CC of altered plants, plant cell or tissues; and for effecting the

CC expression of (II), where (I) is operably linked to one or more control

CC sequences. The methods further comprises regenerating a plant from the

CC plant cell. (I) and (II) are useful for stimulating root growth;

CC enhancing the formation of lateral or adventitious roots; altering root

CC geotropism, leading to an increase in yield; and for screening growth

CC promoting chemical of herbicides. (I) is useful for increasing the size

CC of the root meristem; increasing root size; increasing the size of the

CC shoot meristem; delaying leaf senescence and altering leaf senescence;

CC increasing leaf thickness; reducing or increasing the vessel size;

CC inducing parthenocarp; improving standability of the seedlings;

CC increasing branching and for improving lodging resistance. Antibody (III)

CC to (II) is useful for identifying and obtaining proteins interacting with

CC (II) comprising a screening assay, preferably a two-hybrid screening

CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase

CC coding sequences and PCR primers of the invention

XX

SQ Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3,78e-183 Length: 1575

Score: 1822.00 Matches: 345

Percent Similarity: 80.08% Conservative: 69

Best Local Similarity: 66.73% Mismatches: 79

Query Match: 70.18% Indels: 24

DB: 6 Gaps: 5

US-10-014-101-4 (1-501) x ABK28627 (1-1575)

Qy 7 MettleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21

Db 25 CTATCATCCCTAATACGCTTTTATAGTTTAAACCAACCTTATCAATCAGATGAG 84

Qy 22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41

Db 85 GGCATTGATGTTTCTTTACCATATCACTCAACCTTACGGTCTTAAACCGATCCTCTCC 144

Qy 42 IleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyValIle 61

Db 145 ATCTCTCCCGCTTCTCAGACTTCGGTAACATAACCGAATAATCCCGCGCGCTCTC 204

Qy 62 CysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly----- 79

Db 205 TGGCTTCTCCACACGAGGTGGTCTCTCTCTCGTTTCGCTAACCGAGGATTTCTCT 264

Qy 80 -----LysSerThrPheGlnValAlaAlaArgGlyGlnGly 91

Db 265 TACAATAAAGGCTCAACACGCGCGCTCTACTTTCAAGTGGCTGTCGAGGCCAAGGC 324

Qy 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle 111

Db 325 CACTCCCTCCGTGGCCAAAGCTCTGCACCGGAGGTGTCGTCGTGAACATGACGTGCTC 384

Qy 112 -----ThrAspValValValSerLysAspLysLysTyrAlaAspVal 125

Db 385 GCCATGGCGGCTAAACACGCGCGTGTGTTATCTCCGCAGACGCGGACTTACGCTGACGTG 444

Qy 126 AlaAlaGlyThrLeuTyrValAspValIleLysLysThrAlaGluLysGlyValSerPro 145

Db 445 GCTCCGGGACGATGTGGTGGATGTTCTGAGCGCGCGGTGGATAGAGCGTCTCCCGC 504

Qy 146 ValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle 165

Db 505 GTTACATGACCGATTTATTTGTATCTCAGCGTCCGCGGACGTTGTGTCGACGCTGAATC 564

QY 166 GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValle 185  
DB 565 GGTGGTCAGAGCTTTAGACAGCGCCCTCAGATTAGTAAGCTTCATGAGCTTACGCTTAT 624  
QY 186 ThrGlyGlyGlyMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGly 205  
DB 625 ACCGNAAGGTGAATGATGACTTCCTCAAGTTAAACCTGAATGTTCTATGGA 684  
QY 206 ValLeuGlyGlyLeuGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHis 225  
DB 685 GTTTTAGGAGGTTTGGGTCAATTCGGTATTATAACGAGGCCGAGGATTCGGTGGATCAT 744  
QY 226 AlaProLyArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLys 245  
DB 745 GCACCACAGGGTGAAATGGTCTCGCATCTCTACAGTACCTTCGCGCTTTAAAGA 804  
QY 246 AspGlnLysArgLeuLeuSerMetAlaAsnAspIleGlyValAspTyrLeuGluGln 265  
DB 805 GACCAAGAGGTTTAAATATCAATGACCAATGATCTCGAGTTCGACTTTTGGAGGTCAA 864  
QY 266 IlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLys 285  
DB 865 CTTATGATGTCAAATGGCTTCGTAGACACTCTTTCTCCCACTCTCCGATCCAAACAAGA 924  
QY 286 ValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAlaLysTyrTyr 305  
DB 925 GTGCGATCTCTTGTGAATGACCAACCGGATCATCTATGTTCTCGAAGTAGCCAAAGTATTAT 984  
QY 306 AspAspProAsnLeuProIleLeuSerLysValIleAspThrLysThrLysSer 325  
DB 985 GACAGAACCAACCTTCCCATTTATGACAGGTGATGACAGTTAAGTAGAAGTCTAGGT 1044  
QY 326 TyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArgVal 345  
DB 1045 TTCGCTCCAGGTTTATGTTGCTGACAAAGATGTTCCGTTATTCGATTTCTTGAACCGTGC 1104  
QY 346 HisValGluLysAsnLysLeuArgSerLeuGlyLeuTyrGluLeuProHisProTyrLeu 365  
DB 1105 CGAAACGAGAGAAATAAATCAGATCTTTAGGACTATGGAGATTCCTCATCCATGGCTT 1164  
QY 366 AsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIle 385  
DB 1165 AACATCTTGTCCGGGGTCTCGAATCCAGATTTTCATGATGGTGTATTATGCGCTT 1224  
QY 386 LeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys 405  
DB 1225 CTTCTAAACCAACCTCAACTCTGTTGTTACTCTCTTATCCCAACCAACCGAACA 1284  
QY 406 TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIle 425  
DB 1285 TGAACAAACCGATGTCACGATGACACCG-----GACGAGATGTTTTTATGTGATC 1338  
QY 426 GlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSerValAsnGlu 444  
DB 1339 GGATTACTGCAATCAGCTGGTGGATCTCAAAATTTGGCAAGAACTTGAAATCTCAACGAC 1398  
QY 445 LysIleIleArgPheCysLysAspSerGlyIleValIleLysGlnTyrLeuMetHisTyr 464  
DB 1399 ARGTTATTCAGTTTGTGAAACTCGGAATTAAGATTAAAGAAATTTATGTCACATAT 1458  
QY 465 ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspPheSerLysArg 484  
DB 1459 ACAAGAAAGAGAGATTGGTTAAACATTTTGGACCAAAATGGGATGATTTTTTAAGAAAG 1518  
QY 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501  
DB 1519 AAAATTATGTTGATCCCAAAAGACTATTGTTCTCCAGGCAAGACATATTT 1569  
RESULT 9  
ADA68648  
ID ADA68648 standard; DNA; 1575 BP.  
XX  
AC ADA68648;

XX 20-NOV-2003 (first entry)  
DE Arabidopsis thaliana gene, SEQ ID 428.  
XX  
KW Plant; bacterial infection; fungal infection; viral infection; ds.  
XX Arabidopsis thaliana.  
XX WO2003000898-A1.  
XX 03-JAN-2003.  
XX 22-JUN-2001; 2001WO-1B001105.  
XX 22-JUN-2001; 2001WO-1B001105.  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
XX WPI; 2003-175290/17.  
XX Identifying at least one gene involved in plant resistance or response to  
PT pathogenic infection for conferring resistance or tolerance to a plant to  
PT bacterial, fungal or viral infection by determining or detecting plant  
PT gene expression.  
XX Claim 6; SEQ ID NO 428; 899pp; English.  
XX The present invention relates to a method (M1) for identifying genes  
CC involved in plant resistance or response to pathogenic infection. M1  
CC comprises identifying a gene whose expression is significantly altered in  
CC the incompatible interaction of plant gene expression relative to  
CC expression of the gene in an uninfected plant, in a mutant plant that  
CC does not express a gene associated with response to pathogenic infection,  
CC or in a corresponding incompatible or compatible interaction. (M1) is  
CC useful for conferring resistance to resistance or tolerance to a plant to  
CC bacterial, fungal or viral infection. The present sequence was used to  
CC illustrate the invention.  
XX  
SQ Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 3,78e-183 Length: 1575  
Score: 1822.00 Matches: 345  
Percent Similarity: 80.08% Conservative: 69  
Best Local Similarity: 66.73% Mismatches: 79  
Query Match: 70.18% Indels: 24  
DB: Gaps: 5  
  
US-10-014-101-4 (1-501) x ADA68648 (1-1575)  
QY 7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21  
DB 25 CTCATCACCTTAATAACGCTTTTATAAGTTTAAACCCCAACCTTAATCAAAATCAGATGAG 84  
QY 22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41  
DB 85 GCGATTGATGTTTCTTACCCATATCACTCACTCACTCACTCACTCACTCACTCACTCACT 144  
QY 42 IleSerAlaAlaSerHisAspPheGlyAsnIleThrValThrProGlyGlyValIle 61  
DB 145 ATCTCTCGCGCTTCTCAGACTTCGGTAAACATAACCGACGAAATCCGCGCGCTCCTC 204  
QY 62 CysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly----- 79  
DB 205 TGCCCTTCTCCACACGAGGTGGCTGCTCTCTCGTTTCGTTACGGAGGATTTCTCT 264  
QY 80 -----LysSerThrPheGlnValAlaAlaArgGlyGlyGly 91  
DB 265 TACATAAAGGCTCAACACGACCCCGCTCTACTTCAAAGTGGCTGCTCGAGGCCAAGGC 324

QY 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyValIleValIleValAsnMetThrCysIle 111  
 Db 325 CACTCCCTCCGTGGCCAAAGCCTCTCACCGGAGGTGCTGCGTGAACATGACGCTGCTC 384  
 QY 112 -----ThrAspValValSerLysAspLysLysValValValValValVal 125  
 Db 385 GCCATGGCGGTAAACACGCGCGGTGTTGTTATCGGACGACGGGACTTACGCTGACGTG 444  
 QY 126 AlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerPro 145  
 Db 445 GCTGCGGACGATGCTGGTGGATGTTCTGAAGCGCGGTGATAGAGCGGTCTCGCGC 504  
 QY 146 ValSerTrpThrAspLysLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle 165  
 Db 505 GTTACATGACGGATATTGTTATCTCAGCGTGGCGGAGCTTGTGCAACGCTGGAATC 564  
 QY 166 GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle 185  
 Db 565 GGTGTCAGAGCTTTAGACAGCGCCCTCAGATTAGTACGTTTCATGACGTTGAGTTATT 624  
 QY 186 ThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTrpGly 205  
 Db 625 ACCGAAAGGTGAATGATGATGCTCTCCAAAGTTAAACCTGGAATTGTTCTATGGA 684  
 QY 206 ValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHis 225  
 Db 685 GTTTTAGAGGTTTGGTCAATTCGGTATTATACAGGCGCAGGATTGCGTTGATCAT 744  
 QY 226 AlaProLysArgAlaLysTrpPheArgMetLeuTrpSerAspPheThrThrPheThrLys 245  
 Db 745 GCACCCACAAGGTCGAAATGGTCTCGCATCTCTACAGTACTTCTCGGCTTTTAAAGA 804  
 QY 246 AspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTrpLeuGluGlyCln 265  
 Db 805 GACCAAGAGCGTTTAAATCAATGACCAATGATCTCGGAGTTGACTTTTGAAGGTGCA 864  
 QY 266 IlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLys 285  
 Db 865 CTTATGATGTCAAATGGCTTCGTAGACACCTCTTCTCCCACTCTCGATCAACAAGA 924  
 QY 286 ValAlaAspLeuValLysGlnHisGlyIleIleTrpValLeuGluValAlaLysTrpTyr 305  
 Db 925 GTCCGATCTCTTGTGAATGACCAACCGGATCACTATGTTCTGGAAGTAGCAAGTATTAT 984  
 QY 306 AspAspProAsnLeuProIleIleSerLysValIleAspThrLeuTrpLysThrLeuSer 325  
 Db 985 GACAGAACCCCTTCCCATTTATTGACCAAGGTGATTGACAGTTAAGTAGACTTAGT 1044  
 QY 326 TyrLeuProGlyPheIleSerMetHisAspValAlaLysTrpPheAspPheLeuAsnArgVal 345  
 Db 1045 TTCGCTCCAGGTTTATGTTCTGCAAGATGTTCCGTTATTCGATTTCTTGAACCGTGC 1104  
 QY 346 HisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeu 365  
 Db 1105 CGAAACGAGAGATAACTAGTCTTTTAGACTATGGAGTTCCTCATCCATGGCTT 1164  
 QY 366 AsnLeuTrpValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIle 385  
 Db 1165 AACATCTTTGTCGCGGCTCTCAATCCAAAGATTTTCATGATGGTGTATTATTAATGGCCTT 1224  
 QY 386 LeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTrpProThrAsnArgAsnLys 405  
 Db 1225 CTTCTAAACCAACCTCAACTCTGGTGTACTCTCTTATCCCAACACCGAACA 1284  
 QY 406 TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleIleIle 425  
 Db 1285 TGGAAACACCGCATGTCAACGATGACACCG-----GACGAAGATGTTTTTTTATGTGATC 1338  
 QY 426 GlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSerValAsnGlu 444  
 Db 1339 GGATTACTCAATCAGCTGGTGGATCTCAAAATTCGCAAGACTTGAATAATCTCAACGAC 1398

QY 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTrpLeuMetHisTrp 464  
 Db 1399 AAGTTATTTCAGTTTGTGAAACCTCGGATTAAGATTAAAGAAATATTGATGCACTAT 1458  
 QY 465 ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAspPheSerLysArg 484  
 Db 1459 ACAGAAAGAGATTTGGTTAAACATTTTGGACCAAAATGGATGATTTTAAAGAAAG 1518  
 QY 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501  
 Db 1519 AAAATTATGTTGATCCCAAAAGACTATTGTCTCCAGGACAAGACATATTT 1569  
 RESULT 10  
 ACC85296  
 ID ACC85296 standard; cDNA; 1575 BP.  
 XX  
 AC ACC85296;  
 DT 18-SEP-2003 (first entry)  
 XX  
 DE Arabidopsis cytokinin oxidase-like protein 4 cDNA.  
 XX  
 KW Maize; root growth; root geotropism; cytokinin oxidase; seed size;  
 KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN W02003050287-A2.  
 XX  
 PD 19-JUN-2003.  
 XX  
 PF 10-DEC-2002; 2002WO-EP013990.  
 XX  
 PR 10-DEC-2001; 2001US-00014101.  
 XX  
 PA (SCHM/) SCHMULLING T.  
 PA (WERN/) WERNER T.  
 PI  
 PI Schumulling T, Werner T;  
 XX  
 DR WPI; 2003-541577/51.  
 XX  
 FT Stimulating root growth, enhancing lateral or adventitious root formation  
 FT or altering root geotropism comprises increasing plant cytokinin oxidase  
 FT levels or other protein or nucleic acid that reduces active cytokinins in  
 FT a plant.  
 XX  
 PS Claim 2; Page 169-170; 177pp; English.  
 XX  
 CC The present invention relates to a method for stimulating root growth or  
 CC enhancing the formation of lateral or adventitious roots or altering root  
 CC geotropism, which comprises increasing in a plant or plant part the level  
 CC of a plant cytokinin oxidase or other protein that reduces the level of  
 CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and  
 CC coding sequences from Arabidopsis thaliana are also provided. The method  
 CC is useful in modifying plant morphological, biochemical and physiological  
 CC properties, such as in modifying the initiation, stimulation or  
 CC enhancement of root growth, adventitious root formation, lateral root  
 CC formation, root geotropism, shoot growth, apical dominance, branching,  
 CC timing of senescence, timing of flowering, flower formation, seed  
 CC development and/or seed yield. The present sequence is a coding sequence  
 CC shown in the invention  
 XX  
 SQ Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 3,78e-183 Length: 1575  
 Score: 1822.00 Matches: 345  
 Percent Similarity: 80.08% Conservative: 69  
 Best Local Similarity: 66.73% Mismatches: 79  
 Query Match: 70.18% Indels: 24  
 DB: Gaps: 5

US-10-014-101-4 (1-501) x ACC85296 (1-1575)

Qy		7	MelIleThrLeuIleThrValLeuMet-----IlleThryLysSerAsn	21
Dd		25	CTCATCACCCATAACGCTTTTATTAAGTGTAAACCCCACCTTAAATCAAAATCAGATGAG	84
Qy		22	GlyileYsileAspLeuProLYsSerLeuAasnLeuThrLeuSerThrAspProserIle	41
Dd		85	GGCATTGATGTTTTCTTACC CATATCACTCAACTTACCGTCCTAACCCGATCCCTTCTCC	144
Qy		42	IIserAlalaSerHisAspPheGlyAsnIleThrThrValThrProGlyValIle	61
Dd		145	ATCTCTGCCGCCTCTCTACGACTTCGGTAAACATAACCGACGAATAATCCCCGGCGCTCTC	204
Qy		62	CyaProSerSerThrAlaAspIleSeraArgLeuLeuGlnTyraLaalaaSnGly-----	79
Dd		205	TGCGCTTCTCCACCA CGGAGGTGCTGCTCTCTCGTTTCGCTAACGAGGATTCTCT	264
Qy		80	-----LysSerThrPheInValalalaargGlyGlnGly	91
Dd		265	TACAATAAAGGCTCAACACCGCGCGCTTCTTCAAAGTGCTGCTCGAGCCAAAGC	324
Qy		92	HISerLeuAasnglyGlnAlaserValSerGLyLyValIleValAasnMetThrCySille	111
Dd		325	CAC TCCCTCGTGSCCAAGCTCTG CACCCGGAGGTGCTGCTGTAACATGACGTGCTC	384
Qy		112	-----ThrAspValvalValSerlysAsplyslystYrAlaaspVal	125
Dd		385	GCCATGCGGCTAAACCAGCGCGGTGTATTCTCGCACACGGGACTTAGCGTGACGTG	444
Qy		126	AlaAlaglyThrLeuTrpValAspValLeuLYsLysThrAlaglUysGlyValSerPro	145
Dd		445	GCTCGCGGACGATGTGGTGGATGTTCTCAAGCGCGCGTGGATAGAGCGCTCGCGG	504
Qy		146	ValsertPrAspyrLeuHsisIleThrValGlyGlyThrLeusxandnglyGlylle	165
Dd		505	GTTACATGGACGGAATTATTGTATCTCAGGCTCGCGGACGTTGTCGAACGCTGAATC	564
Qy		166	GlyglyGlnValPheArsgAnslprOeuValserAsnValLeuGlueuAspValIle	185
Dd		565	GGTGGTCAGACGTTTAGACGGGCCCTCAGATTAGTAACGTTGATGAGCTTGACGTTAT	624
Qy		186	ThrGLyLYSGlyGluMetLeuThrCYseArsglnLeuAasnProgluLeuPheTYrGly	205
Dd		625	ACCGAAAAGGTGAATGATGACTTCTCTCCAANGTTAAACCTGNAATTGTTCTATGGA	684
Qy		206	ValLeuglyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHis	225
Dd		685	GTTTTAGAGGTTTTGGGTCAATTTCG GTATTATAACGAGGGCCAGGATGGGTGGATCAT	744
Qy		226	AlaProLYsArgAlalytVtpPheArsgMetLeuTYrSerAspPheThrThrPheThrLYs	245
Dd		745	GCACCACAAGGGTGAATGTCTCGCATACTCTACAGTGACTTCTCGGCTTTTAAAGA	804
Qy		246	AspGlnGluArgLeulleSerMetAlaasnAsplegLYValAsptyrLeuGluGlyGln	265
Dd		805	GACCAAGAGCGTTTAAATATCAATGACCAATGATCTCGAGGTGACTTTTTGGAGGTCAA	864
Qy		266	IlePheLeuSerAnslYValValAspThrSerPhePheProProSerAspGlnSerLYs	285
Dd		865	CTTATGATGTCAAMPGGTTCGTAGACACCTCTTTTCTCCCATCTCTCCGATCAACAAAGA	924
Qy		286	ValAlaAspLeuValLYsGlnHiSLyIleIleTYrValLeuGluValAlalytyrTYr	305
Dd		925	GTCGCATCTCTTGTGAATGACACCGGATCATCTATGTTCTCGAAGTAGCAAGTATTAT	984
Qy		306	AspAspProAsnLeuProIleIleSerLYsValIleAspThrLeuThrLYsThrLeuSer	325
Dd		985	GACAGAACCCTTCCCATTATTGACCGACGTGATTGACGTTTAAGTAGAACTTAGGT	1044
Qy		326	TyrLeuproGlyPheIleSerMethisAspValAlatyrrPheAspPheLeuasArgVal	345
Dd		1045	TTCGTCTCAGGGTTATGCTGCTACAGATGTCGGTATTTCGATTTCGATTCTTGAAACCGGTGTC	1104

Qy	346	HisValGluClnAsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeu	365
Db	1105	CGAAACGAAGAGATAAATCAGATCTTTAGGACTATGGGAGTCTCTCATCCATGGCTT	1164
Qy	366	AsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIle	385
Db	1165	AACATCTTTGTCGCGGGTCTCGAAATCCAAGATTTTCATGATGGTGTATTAAATGGCCTT	1224
Qy	386	LeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys	405
Db	1225	CTTCTAAACAAACCTCAACTCTGGGTGTACTCTCTCTATCCCAAAACCGAACA	1284
Qy	406	TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIle	425
Db	1285	TGGAACACACCGCATGTCAACGATGACACCG-----GACCAAGATGTTTTTATGTGATC	1338
Qy	426	GlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSerValAsnGlu	444
Db	1339	GGATTACTGCAATCAGCTGTGTGATCTCAAAATGGCAAGAACTTGAATACTCAACGAC	1398
Qy	445	LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr	464
Db	1399	AAAGTTATTCAATTTGTGAAACTCGGAATTAAGATTAAAGGAATATTTTATGTCACAT	1458
Qy	465	ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAspPheSerLysArg	484
Db	1459	ACRAGAAAAAGAGATTGGGTAAACATTTTGGACCAAAATGGGATGATTTTAAAGAAAG	1518
Qy	485	LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe	501
Db	1519	AAATTAATGTTGATCCCAAGACATTTGTCCTCCAGACAAGACATATTT	1569
RESULT	11		
ID	ABK28609	standard; DNA; 2782 BP.	
XC	AC	ABK28609;	
XX	AC	ABK28609;	
DT	09-APR-2002	(first entry)	
DE	XX	DNA encoding A. thaliana cytokinin oxidase AtCKX4.	
KW	XX	Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;	
KW	XX	root growth; lateral root; adventitious root; root geotropism; herbicide;	
KW	XX	root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ds.	
OS	XX	Arabidopsis thaliana.	
XX	XX	WO200196580-A2.	
FN	XX	20-DEC-2001.	
PD	XX	18-JUN-2001; 2001WO-EP006833.	
PF	XX	16-JUN-2000; 2000EP-00870132.	
PR	XX	27-DEC-2000; 2000US-0258415P.	
PR	XX	16-MAR-2001; 2001EP-00870053.	
XX	XX	(SCHM//) SCHMULLING T.	
PA	XX	(WERN//) WERNER T.	
XX	XX	Schmulling T, Werner T;	
PI	XX	WPI; 2002-130736/17.	
XX	XX	P-PSDB; AAU81970.	
DR	XX	Polynucleotide encoding novel plant protein having cytokinin oxidase	
PT	XX	activity and the protein useful for stimulating root growth, enhancing	
PT	XX	the formation of lateral or adventitious roots, altering root geotropism.	
XX	XX	Claim 2; Page 134-135; 154pp; English.	
XX	XX		

Claim 2; Page 134-135; 154pp; English.

polynucleotide encoding novel plant protein having cytokinin oxidase activity and the protein useful for stimulating root growth, enhancing the formation of lateral or adventitious roots, altering root geotropism.

CC The invention relates to an isolated polynucleotide (I) encoding a novel  
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for  
CC production of transgenic plants, plant cells or tissues; for production  
CC of altered plants, plant cell or tissues; and for effecting the  
CC expression of (II) where (I) is operably linked to one or more control  
CC sequences. The methods further comprises regenerating a plant from the  
CC plant cell. (I) and (II) are useful for stimulating root growth;  
CC enhancing the formation of lateral or adventitious roots; altering root  
CC geotropism, leading to an increase in yield; and for screening growth  
CC promoting chemical of herbicides. (I) is useful for increasing the size  
CC of the root meristem; increasing root size; increasing the size of the  
CC shoot meristem; delaying leaf senescence and altering leaf senescence;  
CC increasing leaf thickness; reducing or increasing the vessel size;  
CC inducing parthenocarp; improving standability of the seedlings;  
CC increasing branching and for improving lodging resistance. Antibody (III)  
CC to (II) is useful for identifying and obtaining proteins interacting with  
CC (II) comprising a screening assay, preferably a two-hybrid screening  
CC assay. ABX28606-ABX28633 represent Arabidopsis thaliana cytokinin oxidase  
CC coding sequences and PCR primers of the invention  
XX

SQ Sequence 2782 BP; 826 A; 538 C; 507 G; 911 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8,896-153 Length: 2782  
Score: 1539.50 Matches: 344  
Percent Similarity: 44.89% Conservative: 69  
Best Local Similarity: 37.39% Mismatches: 80  
Query Match: 59.30% Indels: 429  
DB: 6 Gaps: 9

US-10-014-101-4 (1-501) x ABX28609 (1-2782)

QY 7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21  
DB 25 CTCAATCACCTTAATAACGGCTTTTATAGTTTAAACCCCAACCTTAATCAATCAGATGAG 84  
QY 22 GlyIleLysIleAspLeuProLysLeuAsnLeuThrLeuSerThrAspProSerIle 41  
DB 85 GGCATGTAGTGTCTTACCCATATACCTCAACCTTACGGTCTTAAACCGATCCCTTCCTC 144  
QY 42 IleSerAlaAspHisAspPheGlyAsnIleThrValThrProGlyGlyValIle 61  
DB 145 ATCTCTGCGCTTCACAGACTTCGGTAACATACCGACGAAATCCGCGCGCTCCTC 204  
QY 62 CysProSerSerThrAlaAspIleSerArgLeuLeuGlnThrAlaAlaAsnGly----- 79  
DB 205 TGCCTTCTCCACACGAGGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 264  
QY 80 -----LysSerThrPheGlnValAlaAlaArgGlyGlnGly 91  
DB 265 TACAATAAGGCTCAACACGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 324  
QY 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle 111  
DB 325 CACTCCCTCCGTGGCCAGCCCTCTGACCGGAGGTGCTGCTGTAACATGACGCTGTCTC 384  
QY 112 -----ThrAspValValValSerLysAspLysLysThrAlaAspVal 125  
DB 385 GCCATGGCGGCTAAACACGCGGCTTGTATCTCTGCGACGCGGACTTACGCTGACGCTG 444  
QY 126 AlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerPro 145  
DB 445 GCTGCGCGGACGATGTGGGTGGATGTTCTGAAGGCGCGGCGGTGGATAGAGCGCTCTCG 504  
QY 146 ValSerThrAspThrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle 165  
DB 505 GTTACATGACGCGATTTATTGTATCTATCATCGCGCGGCGGACGTTGTCGAACCTCGAATC 564  
QY 166 GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle 185  
DB 565 GGTGGTTCAGACGTTTAGACACGCGCTCAGATTAGTAACTGTTTCTGACGCTTCTTAT 624  
QY 186 Thr----- 186

DB 625 AC-CGGTACGTAAATACCAAACTTCCTAACTCGTTACAATTTTAAATTTTGGTA 683  
QY 186 ----- 186  
DB 684 ATATAAATTTGTACGGCTCAACTCTTAATAAGAAATGAACAGTATCTATGATCTCTA 743  
QY 186 ----- 186  
DB 744 GATGCTCTTTTGTCTGCAAGCTTTAATTGTAGTAACATCAGCGATATATATACACA 803  
QY 186 ----- 186  
DB 804 TGCATGTGTTATTGATGATAATATAATATGTTTAGTTACAAATTTGATTTCAAGGT 863  
QY 186 ----- 186  
DB 864 AAAACTCACAGCCATACCAAGTATRAAACTCAAAAATCAGGTTTGGTCAGAAATACA 923  
QY 186 ----- 186  
DB 924 TATCCTTCATTAACAGTAGTTATGCTATAAATTTGTGATTATAAATAAATCCGAGTTGT 983  
QY 187 -----GlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnPro 200  
DB 984 TCACAATACATAATTTTCAGGAAAGGTGAATGATGACTTGCTCTCCAAAGTTAAACCTT 1043  
QY 201 GluLeuPheThrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArg 220  
DB 1044 GAATTGTTCTATGAGGTTTATAGGAGGTTTGGTCAATTCGGTATTATAACGAGGCGCAG 1103  
QY 221 IleValLeuAspHisAlaProLys----- 228  
DB 1104 ATTGCGTTGGATCATGCACCCCAAGGATGATGATCATGCATCTATAGTGTAAATCAATTT 1163  
QY 228 ----- 228  
DB 1164 ATAAATTAATGTAGTGGTCTTAATCCAAATTTGATTTGTTGGTGAACGACGT 1223  
QY 228 ----- 228  
DB 1224 ATATAATAAGTCAAAAGGCTGATTTGAAGACGAATTTATATATATCTTTTGTGAATTA 1283  
QY 228 ----- 228  
DB 1284 ATCTGATTTGCTTACGTTTATTAGATTCGCTGCGTAATAAATCCTAGGACTTGCTCGAGT 1343  
QY 228 ----- 228  
DB 1344 GTAATCTTGCTTATGCTTGCRAAATCTTGTGATGTCAATATCTAATCTTTTATTATA 1403  
QY 228 ----- 228  
DB 1404 TTTCCCTACGTAAGTTTATAGATATAGTATTATTTAAACTGCTATAAATTTGTGTAGTAG 1463  
QY 228 ----- 228  
DB 1464 ACITTAGATAAAAGTTGTGCTGCTTGACCTATTGTTTATCGCTATAGTAGTATCAAA 1523  
QY 228 ----- 228  
DB 1524 GGTCTATATAGTATCTTGTGTTTCTTTTGTGAAATAAATAGACCATACAAATCCAAAGAA 1583  
QY 229 -----ArgAlaLys 231  
DB 1584 GATGATCTTAATGGACTAATTTATGGATATAAATGATATACAAATCTCGAGGTG-AAA 1642  
QY 232 TrpPheArgMetLeuThrSerAspPheThrPheThrLysAspGlnGluArgLeuIle 251  
DB 1643 TGGTCTCGCATACTCTACAGTGACTTCTCGGCTTTTAAAGAGACCAAGAGCGTTTAAATA 1702  
QY 252 SerMetAlaAsnAspIleGlyValAspThrLeuGlyGlnIlePheLeuSerAsnGly 271  
DB 271 ----- 271

Db 1703 TCAATGACCAATGATCTCGAGTTGACTTTTGGAGGTCAACTTATGATGTCARATGGC 1762  
Qy 272 valValAspThrSerPheProSerProSerAspGlnSerLysValAlaAspLeuValLys 291  
Db 1763 TTGCTAGACACCTCTTCTTCCACTCTCCGATCAACAAGAGTGCATCTCTTGTAAT 1822  
Qy 292 GlnHisGlyLeuLeuValLeuGluValAlaLysTyrAspAspProAsnLeuPro 311  
Db 1823 GACCACCGATCATCTATGTTCTGAGTAGCCAGTATTATGACAGAACCCTTCC 1882  
Qy 312 IleIleSerLys----- 315  
Db 1883 ATTATTGACCAAGGTACTAAATCCATTATTCATGATGATTATCTTCACACAATCAGTATC 1942  
Qy 315 ----- 315  
Db 1943 ATCACCACCAATACCATCATCTGTTGTCATATATGATCCAAAGTAATATATCATCATAT 2002  
Qy 315 ----- 315  
Db 2003 AAATAAATCGTTCAAAATCTTTTAAAGATAAAGATCAATTTTCAAGCATTAATCTC 2062  
Qy 315 ----- 315  
Db 2063 ATACATCTACGAATCAGGTGACCATATATACCATAGCTTATTAATATCATTTT 2122  
Qy 316 -----ValIleAspThrLeuThrLysThrLysLeuSerTyrLeuProGlyPheIleSer 332  
Db 2123 TGTGTTGAGTGATTCACAGCTTAAGTAGAATCTAGTTCCTCCAGGGTTATGTTTC 2182  
Qy 333 MetHisAspValAlaTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeu 352  
Db 2183 GTACAGATGTTCCGATTTCGATTCTTGAACCGTGTCCGAACGGAAGAATATAACTC 2242  
Qy 353 ArgSerLeuGlyLeuTyrGluLeuProHisProTyrLeuAsnLeuTyrValProLysSer 372  
Db 2243 AGATCTTTAGACTATGGAGTTCCTCATCCATGCTTAACATCTTTCGCGGGTCT 2302  
Qy 373 ArgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLysGlnLysSerAla 392  
Db 2303 CGAATCAAGATTTTCATGATGTTGTTATTAATGGCCCTCTTCTAAACCAACCTCACT 2362  
Qy 393 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys----- 405  
Db 2363 TCTGGTGTACTCTCTCTATCCCAACCAACCAAGTAATATTTACTTTTGTATT 2422  
Qy 405 ----- 405  
Db 2423 TGTTTTATTTGAAAGTATATCCCAATAATGTTAAATTTGTTAAACAAGAAATTTATTT 2482  
Qy 406 -----TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIle 422  
Db 2483 ATTAATAGATGGACACACCGCATGTCAACGATGACACCG-----GACGAGATGTTT 2536  
Qy 423 TyrIleLeuGlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSer 441  
Db 2537 TATGTGATCGGATTTACGCAATCAGCTGGTGGATCTCAAAATTTGGCAAGAACTTGAAAT 2596  
Qy 442 ValAsnGluLysIleIleArgPheCysValAspSerGlyIleLysIleLysGlnTyrLeu 461  
Db 2597 CTCACGACAGAGTTATTCAGTTTGTGAAACCTCGGAATTAGATTAGGATATTG 2656  
Qy 462 MethIstYrThrSerLysGluAspTyrIleGluHisPheGlySerLysTrpAspAspPhe 481  
Db 2657 ATGCACATATACAGAAAGAAGATTGGGTTAAACATTTTGGACCAAAATGGGATGATTT 2716  
Qy 482 SerLysArgLysAspLeuPheAspProLysLysLeuSerProGlyGlnAspIlePhe 501  
Db 2717 TTAAGAAAGAAATTAATGTTTATGATCCCAAAAGACTATTTGTTCTCAGGACCAAGACATATT 2776

RESULT 12  
ACC85278  
ID ACC85278 standard; DNA; 2782 BP.

XX ACC85278;  
XX 18-SEP-2003 (first entry)  
XX Arabidopsis cytokinin oxidase-like protein 4 gene.  
XX Maize; root growth; root geotropism; cytokinin oxidase; seed size;  
XX embryo size; cotyledon size; transgenic plant; herbicide; gene; ds.  
XX Arabidopsis thaliana.  
XX WO2003050287-A2.  
XX 19-JUN-2003.  
XX 10-DEC-2002; 2002MO-EP013990.  
XX 10-DEC-2001; 2001US-00014101.  
XX (SCHM/) SCHMULLING T.  
XX (WERN/) WERNER T.  
XX Schmullling T, Werner T;  
XX WPI; 2003-541577/51.  
XX P-PSDB; ABR63571.  
XX Stimulating root growth, enhancing lateral or adventitious root formation  
XX or altering root geotropism comprises increasing plant cytokinin oxidase  
XX levels or other protein or nucleic acid that reduces active cytokinins in  
XX a plant.  
XX Claim 2; Page 153-154; 177pp; English.  
XX The present invention relates to a method for stimulating root growth or  
XX enhancing the formation of lateral or adventitious roots or altering root  
XX geotropism, which comprises increasing in a plant or plant part the level  
XX of a plant cytokinin oxidase or other protein that reduces the level of  
XX active cytokinins in a plant or plant part. Cytokinin oxidase protein and  
XX coding sequences from Arabidopsis thaliana are also provided. The method  
XX is useful in modifying plant morphological, biochemical and physiological  
XX properties, such as in modifying the initiation, stimulation or  
XX enhancement of root growth, adventitious root formation, lateral root  
XX formation, root geotropism, shoot growth, apical dominance, branching,  
XX timing of senescence, timing of flowering, flower formation, seed  
XX development and/or seed yield. The present sequence is a coding sequence  
XX shown in the invention  
SQ Sequence 2782 BP; 826 A; 538 C; 507 G; 911 T; 0 U; 0 Other;  
  
Alignment Scores:  
Pred. No.: 8.89e-153 Length: 2782  
Score: 1539.50 Matches: 344  
Percent Similarity: 44.89% Conservative: 59  
Best Local Similarity: 37.39% Mismatches: 80  
Query Match: 59.30% Indels: 429  
DB: 8 Gaps: 9  
  
US-10-014-101-4 (1-501) x ACC85278 (1-2782)  
Qy 7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21  
Db 25 CTCATCACCCCTAATAACCTTTTATTAAGTTTAAACCCCACTTAATCAATCATGATGAG 84  
Qy 22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41  
Db 85 GGCATTGATGTTTCTTACCCTATCATCAACCTTACGGTCTTAACCGATCCCTTCTCC 144  
Qy 42 IleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyValIle 61  
Db 145 ATCTCTGCGGTTTCTACGACTTCGGTAACATAACCGACGAAATCCCGGGCGGCTCTC 204

Qy	62	CysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly-----	79
Db	205	TGSCCTTCCTCCACCGAGGTGGTCTGCTCTCGTTTCGCTAACGAGAGATTCTCT	264
Qy	80	-----LysSerThrPheGlnValAlaAlaAspGlyGlnGly	91
Db	265	TACAATAAAGGCTCAACACCGCCGCTTACTTTTCAAAGTGGCTGCTCGAGGCCAAGC	324
Qy	92	HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle	111
Db	325	CACCTCCCTCGTGGCCAAAGCCTCTGACCCGGAGGTGTCGTGTAACATGAGCGTGTCTC	384
Qy	112	-----ThrAspValValSerIleAspIleSerIleAspVal	125
Db	385	GCCATGGCGCTAAACACGGCGCGTGTATCTCGCACACGGACTTACGCTGACGTG	444
Qy	126	AlaAlaGlyThrLeuTrpValAspValLeuIleSerThrAlaGluIleValSerPro	145
Db	445	GCTGCCGGGACGATGTGGTGGATGTTCTCAAGCGCGCTGGATAGAGCGCTCGCCG	504
Qy	146	ValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyIle	165
Db	505	GTACATGGACGATATTATTGTATCTCAGCGTCGGCGGACGTTGTTCGAACGCTGGAATC	564
Qy	166	GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle	185
Db	565	GGTGGTCAGACGTTTAGACACGCGCCTCAGATTAGTACCGTTTCATGAGCTTGACGTATT	624
Qy	186	Thr-----	186
Db	625	AC-CGGTACGTAAATACCAAACTTCACTAATCTCGTTACAATTTTTTAAATTTTTGGTA	683
Qy	186	-----	186
Db	684	ATATAAATTTTGACGCTCAACTCTTAATTAGAATGAACACAGTATCTATGATCTCTA	743
Qy	186	-----	186
Db	744	GATGCTCTTTTTTGTCTGCAAGCTTTAATTGTAGTAACATCAGCGATATATATACCA	803
Qy	186	-----	186
Db	804	TGCATGTGTAATTATGATGATAATATAATAGTTTGTAGTTACAAATTTGATTCTCAAGT	863
Qy	186	-----	186
Db	864	AAAACACACGCCATACCAACAGTATAAACTCCAAAAATCACGTTTTTGGTCAGAAATACA	923
Qy	186	-----	186
Db	924	TATCCTTCATTAACAGTAGTTATGCTATAATTTGTGATTATAATAACTCCGGAGTTGT	983
Qy	187	-----GlyIleGlyGluMetLeuThrCysSerArgGlnLeuAsnPro	200
Db	984	TCACAACTAAATTTTCAGGAAAGGTGAATGATGACTTGTCTCCAAAGTTAAACCTT	1043
Qy	201	GluLeuPheTyrGlyValLeuGlyGlyLeuGlnPheGlyIleIleThrArgAlaArg	220
Db	1044	GAATTGTCTATGGAGTTTTAGGAGGTTTGGGTCAATTGCGTATTATACGAGGGCCAGG	1103
Qy	221	IleValLeuAspHisAlaProLys-----	228
Db	1104	ATTCCGTTGGATCATGCCCAACCAAGGGTATGATCATGCACTATAGTGTATCAATTT	1163
Qy	228	-----	228
Db	1164	ATAATTTTAAATGTAGTGTCTCTAAATCCAAAAATTTGATTTGGTTGGACGTACGT	1223
Qy	228	-----	228
Db	1224	ATATATAAATAGTCAAAAGGCTGATTTTGAAGACGAATTTATATACATTTTGTTCGAATTA	1283
Qy	228	-----	228

1284	ATCTGATTTTGGCTTAGCTTTTATTAGATCTCGGTAAATAAATCCTAGGACTTGCTCGAGT	1344
228	-----	228
1344	GTAATCTTGTTGTTATGCTTGCAAATCTTGTTGATGTCATATCAATCTTTTATTATTA	1403
228	-----	228
1404	TTTCCCTACGTAAGTTTATAGATATAGTATTTTAAACTGCTATAAAATTGTTGACGTATAG	1463
228	-----	228
1464	ACTTTAGATAAAAAAGTTGTGCTTGCACCTATTGTTTATCGTATAGTGAATCAAA	1523
228	-----	228
1524	GGTCTATATATGATCTTGTTGTTTCTTTTGAATAAATAGACCATACAAATCCAAGGAA	1583
229	-----	231
1584	GATGATCTTAAATGACTAAATTTATGGATATAAAATGATATACAAATCTGCAGGTG-AAA	1642
232	TTPPheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGlnGluArgLeuLeu	251
1643	TGGTCTCGCATACTCTACAGTGACTTCTCGGCTTTAAAGAGACCAAGAGCGTTTAATA	1702
252	SerMetAlaAsnAspIleGlyValAspTyrLeuGluGlyGlnIlePheLeuSerAsnGly	271
1703	TCAATGACCAATGATCTCGGAGTGACTTTTGGAAAGTCAACTTATGATGTCAAAATGGC	1762
272	ValValAspThrSerPhePheProProSerAspGlnSerLysValAlaAspLeuValLys	291
1763	TTCGTAGACACCTCTTTCTTCCCACTCTCGATCAACAAAGAGTCGATCTCTGTGGAAT	1822
292	GlnHisGlyIleIleTyrValLeuGluValAlaLysTyrTyrAspAspProAsnLeuPro	311
1823	GACCACGGATCATCTATGTTCTCGAAGTAGCCAAAGTATTATGACAGAACCCCTTCCC	1882
312	IleIleSerLys-----	315
1883	ATTATTGACCAGGTACTAAATCCATTATTCATGATGATTATCTTCACAAATCAGTATC	1942
315	-----	315
1943	ATCACCAAATTACCATCATCATCTTGTCATATATGATCCAAAGTAAATATATCATCATGATAT	2002
315	-----	315
2003	AAATAAATCGTTCAAATCTTTTTTTTAAAGATAAAAGAATCATTTTCAAGCATTACTC	2062
315	-----	315
2063	ATACACATCTACGAATCACCGTGACCATATATAACCATACGCTTTATTAAATAATCATTTT	2122
316	-----ValIleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPheIleSer	332
2123	TGTTTGTAGGTGATTGACGTTTAAGTAGAACTCTAGGTTTCGCTCCAGGGTTATGTGTC	2182
333	MetHisAspValAlaTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeu	352
2183	GTACAGAATGTTCCGTATTTTCGATTTCTTGAAACCGTCTCCGAAACGAGAAGATAAACTC	2242
353	ArgSerLeuGlyLeuTrpGluLeuProHisProThrLeuAsnLeuTyrValProLysSer	372
2243	AGATCTTTTAGGACTATGGGAAGTTCTCTCAFCATGGCTTAACATCTTTGTCGCCGGGTCT	2302
373	ArgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLeuLysGlnLysSerAla	392
2303	CGAATCCAAGATTTTCATGATGGTGTATTAAATGGCCTTCTTCTAAACCAAACTCAACT	2362
393	SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys-----	405
	:::	

Db 2363 TCCTGGTGTACTCTCTCTATCCACAAACCGAACAAGTAATATTTACTTTTGTATTT 2422  
Qy 405 ----- 405  
Db 2423 TGTTTATTTGAAAGTATATCCCAATAATGTATGTTAAATTTGTTAAAGAAATTTATTTT 2482  
Qy 406 -----TTPAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIle 422  
Db 2483 ATTAATAGATGGAAACCAACCATGTCTAAGATGACACCG-----GACGAAATGTTTTT 2536  
Qy 423 TyrIleIleGlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSer 441  
Db 2537 TATGTGATCGGATTACTGCAATCAGCTGGTGGATCTCAAAATTTGGCAAGAACTTGAAAT 2596  
Qy 442 ValAspGluIleIleArgPheCysLeuAspSerClyIleIleLysGlnTyrLeu 461  
Db 2597 CTCAACGACAGAGTTATTCAGTTTGTGAAACTCGGAATTAAGATTAAAGAAATTTG 2656  
Qy 462 MetHisTyrThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspPhe 481  
Db 2657 ATGCACATATCAAGAAAGAAAGATTGGTTAAACATTTTGGACCAAAATGGGATGATTTT 2716  
Qy 482 SerLysArgLysAspLeuPheAspProLysLysLeuSerProGlyGlnAspIlePhe 501  
Db 2717 TTAAGAAAGAAATATGTTTGTATCCCAAGAACTATTGTTCCAGCAAGACATATTT 2776  
RESULT 13  
ID ABK28626 standard; cDNA; 1572 BP.  
XX AC ABK28626;  
XX DT 09-APR-2002 (first entry)  
XX DE cDNA encoding A. thaliana cytokinin oxidase AtCKX3.  
XX KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;  
XX KW root growth; lateral root; adventitious root; root geotropism; herbicide;  
XX KW root meristem; shoot meristem; leaf senescence; parthenocarpy; gene; ss.  
XX OS Arabidopsis thaliana.  
XX PN WO200196580-A2.  
XX PD 20-DEC-2001.  
XX PF 18-JUN-2001; 2001WO-EP006833.  
XX PR 16-JUN-2000; 2000EP-00870132.  
XX PR 27-DEC-2000; 2000US-0258415P.  
XX PR 16-MAR-2001; 2001EP-00870053.  
XX (SCHM/) SCHMULLING T.  
XX (WERN/) WERNER T.  
XX PI Schmulling T, Werner T;  
XX PI WPI, 2002-130736/17.  
XX PT Polynucleotide encoding novel plant protein having cytokinin oxidase  
XX PT activity and the protein useful for stimulating root growth, enhancing  
XX PT the formation of lateral or adventitious roots, altering root geotropism.  
XX PS Claim 3; Page 147; 154pp; English.  
XX CC The invention relates to an isolated polynucleotide (I) encoding a novel  
XX CC plant protein (II) having cytokinin oxidase activity. (I) is useful for  
XX CC production of transgenic plants, plant cells or tissues; for production  
XX CC of altered plants, plant cell or tissues; and for effecting the  
XX CC expression of (II) where (I) is operably linked to one or more control  
XX CC sequences. The methods further comprises regenerating a plant from the  
XX CC plant cell. (I) and (II) are useful for stimulating root growth;  
XX CC enhancing the formation of lateral or adventitious roots; altering root

CC geotropism, leading to an increase in yield; and for screening growth  
CC promoting chemical of herbicides. (I) is useful for increasing the size  
CC of the root meristem; increasing root size, increasing the size of the  
CC shoot meristem; delaying leaf senescence and altering leaf senescence;  
CC increasing leaf thickness; reducing or increasing the vessel size;  
CC inducing parthenocarpy; improving standability of the seedlings;  
CC increasing branching and for improving lodging resistance. Antibody (III)  
CC to (II) is useful for identifying and obtaining proteins interacting with  
CC (II) comprising a screening assay, preferably a two-hybrid screening  
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase  
CC coding sequences and PCR primers of the invention  
XX Sequence 1572 BP; 461 A; 327 C; 348 G; 436 T; 0 U; 0 Other;  
SQ  
Alignment Scores:  
Pred. No.: 7, 41e-127 Length: 1572  
Score: 1292.00 Matches: 251  
Percent Similarity: 59.05% Conservative: 106  
Best Local Similarity: 48.55% Mismatches: 138  
Query Match: 49.77% Indels: 22  
DB: 6 Gaps: 6  
US-10-014-101-4 (1-501) x ABK28626 (1-1572)  
Qy 3 AsnLeuArgLeuMetIleThrLeuIleThr-----ValLeuMetIleThrLysSer 19  
Db 13 AATCTCGTTTCAAGATTTCGCTTTATAGCAATAACAATAGTATCATCACTACTCTCTCA 72  
Qy 20 SerAsnGlyIleLysIleAspLeuProLysSerLeuAsnLeu----- 33  
Db 73 ACTCCGATCACACCAACACATCACCAACCATGGAATATCTTTCACACACGAATTC 132  
Qy 34 -----ThrLeuSerThrAspProSerIleIleSerAlaAlaSerHisAspPheGlyAsn 51  
Db 133 GCGGAAAACTCACCTCTCTCTCTCGTCTGAAATCAGCCGACACAGATTTGGCCAC 192  
Qy 52 IleThrValThrProGlyGlyValIleCysProSerSerThrAlaAspIleSerArg 71  
Db 193 GTCACAAAATCTCCCTTCGCGCTTAATCTCTCTCGTTCGTTGAGACATCACAGAT 252  
Qy 72 LeuLeuGlnTyrAlaAlaAsnGlyLysSerThrPheGlnValAlaAlaArgGlyGlnGly 91  
Db 253 CTCATAAAACTCTCTTTGACTCTCACTGTCTTTTCTTTAGCGGCTCGGTGACGGA 312  
Qy 92 HisSerLeuAsnGlyLysAlaSerValSerGlyGlyValIleValAsnMetThrCysIle 111  
Db 313 CACAGCCACCGTGGCCAAAGCTTCGGCTAAAGACGAGTTGGTCAACATCGGTCCATG 372  
Qy 112 ThrAsp-----ValValSerLysAspLysThrAlaGlyLysGlyValSerProValSer 127  
Db 373 GTAAACCGGATCGAGGTATCAAGGTGTCTAGGACCTGTTTATATATGTTGACGTGACGCT 432  
Qy 128 GlyThrLeuTrpValAspValLeuLysThrAlaGlyLysGlyValSerProValSer 147  
Db 433 GCGTGGCTATGATTGAGGTGTTGAATAAACTTTGGAGTTAGGTTAAACCGCGTTTCT 492  
Qy 148 TrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIleGlyGly 167  
Db 493 TGGACGGATTATTTGTTAATTAACATCGGTGGAGCTTATCAACCGCGGAATAGTGA 552  
Qy 168 GlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThrGly 187  
Db 553 CAACAGTTTCGGTACGGTCCACAGATCACTAATGTCTTAGAGATGGATGTTATTACTGA 612  
Qy 188 LysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheThrGlyValLeu 207  
Db 613 AAAGGAGATTGCAACTTTTCCAGGACATGAATCGGATCTTTCTTCGCGGTGTTA 672  
Qy 208 GlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaAlaGlyIleValLeuAspHisIlePro 227  
Db 673 GGAGGTTTGGTCAATTCGGCATTTATAACAGAGCCAGAAATTAACATTTGAAGTAGTCTCG 732  
Qy 228 LysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGln 247



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Db 733 AAAGGGCCAGTGGTTAAAGTTCTATACATAGATTTCCTCGAATTCACAGAGATCAA 792
Qy 248 GluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLeuGluGlyGlnIlePhe 267
Db 793 GAACGAGTGATATCGAAACCGAC-----GGTGTAGATTCTTTAGAGGTTCCATTATG 846
Qy 268 LeuSerAsnGlyValValAsp-----ThrSerPheProProSerAspGlnSer 284
Db 847 GTGGACCATGGCCACCGGATAACTGGAGATCCAGCTATTATCCACCGTCGCATCACTTG 906
Qy 285 LysValAlaAspLeuValGlnHisGlyLeuIleLeuValLeuGluValAlaLysTyr 304
Db 907 AGGATCGCTCAATGGTCAAAACGACATCGTGTCTACTCTACCTGCTGAAGTGTCAAGTAT 966
Qy 305 TyrAspAspProAsnLeuProIleIleSerLysValIleAspThrLeuThrLysThrLeu 324
Db 967 TACGACGAAACTTCTCATACAGCTCAACGAGGAAATGGAGGATTAAGCGATAGTTTA 1026
Qy 325 SerTyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArg 344
Db 1027 AACCATGTAAAGAGGTTTATGTACGAGAAAGATGTGACGTATATGGAATTCCTAAACCGA 1086
Qy 345 ValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTyrGluLeuProHisProTyr 364
Db 1087 GTCGAACCGGAGAGCTAAACCTGAAATCCAAAGCCCAATGGAGTGTCCACATCCATGG 1146
Qy 365 LeuAsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAsp 384
Db 1147 CTTAATCTCTCGTACCAAAACTCAAAATCTCCAAATTTGATGATGGTGTTTTAAAGGTT 1206
Qy 385 IleLeuLeuLysGlnLysSerAlaSerLysLeuAlaLeuLeuTyrProThrAsnArgAsn 404
Db 1207 ATTATCTCAAGAAATAACATCACTAGCGGTCTGTCTGTGTATCTTATCTATGATCGCAAC 1266
Qy 405 LysTyrAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIle 424
Db 1267 AAGTGGAGTATCGATGTCTCCGCTATACCGAG-----GAAGATGATTTTATCGG 1320
Qy 425 IleGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGlu 444
Db 1321 GTAGGTTTTTAAATCCCGCGGTTTGAATTTGGAGGCTTTTGTGACAAAGAAACATG 1380
Qy 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr 464
Db 1381 GAAATCTCAAGTTTGTGAGATGCTATATATGGGGTTATACATATCTTCTTATCAT 1440
Qy 465 ThrSerLysGluAspTrpIleGluHisPheGlySerLysTyrAspAspPheSerLysArg 484
Db 1441 TCATCACAAGAGGATGGGTAGACATTTTGGTCCGAGGTGGAATATTTTTCGTAGAGAGA 1500
Qy 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db 1501 AATATAAATATGATCCCAAAATGATATATATCACCGGGCAAAATATATTT 1551
RESULT 14
ID ACC85295
XX ACC85295 standard; cDNA; 1572 BP.
XX
XX ACC85295;
XX
XX
DT 18-SEP-2003 (first entry)
XX
DE Arabidopsis cytokinin oxidase-like protein 3 cDNA.
XX
KW Maize; root growth; root geotropism; cytokinin oxidase; seed size;
KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.
XX
OS Arabidopsis thaliana.
XX
SS WO2003050287-A2.
XX
PD 19-JUN-2003.

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XX 10-DEC-2002; 2002NO-EP013990.
XX
XX 10-DEC-2001; 2001US-00014101.
XX
XX (SCHM/) SCHMULLING T.
XX (WERN/) WERNER T.
XX
XX Schnulling T, Werner T;
XX
XX WPI; 2003-541577/51.
XX
XX Stimulating root growth, enhancing lateral or adventitious root formation
XX or altering root geotropism comprises increasing plant cytokinin oxidase
XX levels or other protein or nucleic acid that reduces active cytokinins in
XX a plant.
XX
XX Claim 3; Page 168-169; 177pp; English.
XX
XX The present invention relates to a method for stimulating root growth or
XX enhancing the formation of lateral or adventitious roots or altering root
XX geotropism, which comprises increasing in a plant or plant part the level
XX of a plant cytokinin oxidase or other protein that reduces the level of
XX active cytokinins in a plant or plant part. Cytokinin oxidase protein and
XX coding sequences from Arabidopsis thaliana are also provided. The method
XX is useful in modifying plant morphological, biochemical and physiological
XX properties, such as in modifying the initiation, stimulation or
XX enhancement of root growth, adventitious root formation, lateral root
XX formation, root geotropism, shoot growth, apical dominance, branching,
XX timing of senescence, timing of flowering, flower formation, seed
XX development and/or seed yield. The present sequence is a coding sequence
XX shown in the invention
XX
SQ Sequence 1572 BP; 461 A; 327 C; 348 G; 436 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 7,41e-127 Length: 1572
Score: 1292.00 Matches: 251
Percent Similarity: 69.05% Conservative: 106
Best Local Similarity: 48.55% Mismatches: 138
Query Match: 49.77% Indels: 22
DB: 8 Gaps: 6

US-10-014-101-4 (1-501) x ACC85295 (1-1572)

Qy 3 AsnLeuArgLeuMetIleThrLeuIleThr-----ValLeuMetIleThrLysSer 19
Db 13 AATCTTCGTTCAAGAAGTTCGTTATAGCAATTAACATAGTAATCATATCTCTCA 72
Qy 20 SerAsnGlyIleLysIleAspLeuProLysSerLeuAsnLeu----- 33
Db 73 ACTCCGATCAACCAACACATCACCAACCATGGAATATCTTTCACAAACGAATTC 132
Qy 34 -----ThrLeuSerThrAspProSerIleIleSerAlaIleSerHisAspPheGlyAsn 51
Db 133 GCGGAAAACCTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 192
Qy 52 IleThrThrValThrProGlyGlyValIleCysProSerSerThrAlaAspIleSerArg 71
Db 193 GTACCAAAATCTCCCTTCGCGGTCTTAATCCCTCTCTCTCTCTCTCTCTCTCTCT 252
Qy 72 LeuLeuGlnTyrAlaAlaAsnGlyLysSerThrPheGlnValAlaAlaArgGlyGlnGly 91
Db 253 CTCATAAAATCTCTCTTTGACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 312
Qy 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle 111
Db 313 CACAGCCACCGTGGCCAAAGCTCGGTAAAGACGGAGTTGTGTGTCACATTCGGTCCATG 372
Qy 112 ThrAsp-----ValValSerLysLysLysLysLysLysLysLysLysLysLys 127
Db 373 GTAAACCGGGATCGAGGTATCAAGGTGTCTAGGACCTGTTTATATGTGTGACGTGGCGCT 432

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QY 128 GlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerProValSer 147  
 DB 433 GCGTGGCTATGATTGAGGTGTGAATAAACTTTGGAGTTAGGGTTAAACCGCGTTCTT 492  
 QY 148 TrpThrAspTyrLeuHisThrValGlyGlyThrLeuSerAsnGlyGlyIleGlyGly 167  
 DB 493 TGGACGGATTATTTGTTATTAACAGTCGGTGGAGCGTTATCAAACGGCGGAGTATAGTGA 552  
 QY 168 GluValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThrGly 187  
 DB 553 CAAACGTTTCGGTACGGTCCACAGATCACTAATGTTCTAGAGATGGATGTTATTACTGGA 612  
 QY 188 LysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGlyValLeu 207  
 DB 613 AAAGGAGAGATTGCAACTGTTTCCAGGACATGAATCGATCTTTTCTCGCGGTGTTA 672  
 QY 208 GlyGlyLeuGlyGlnPheGlyIleThrArgAlaArgIleValLeuAspHisAlaPro 227  
 DB 673 GGAGGTTTGGGTCAATTGGCATATTAAACAGAGCCAGATTAACACTTGAAGTAGTCCG 732  
 QY 228 LysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGln 247  
 DB 733 AAAGGCCCAAGTGTGAAGTTTCTATACATAGATTTCTCCGAATTCACAGAGATCAA 792  
 QY 248 GluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLeuGluGlyGlnIlePhe 267  
 DB 793 GAACGAGTATATCGAAACCGAC-----GTGTGATGTTTCTTAGAAGGTTCATTATG 846  
 QY 268 LeuSerAsnGlyValValAsp-----ThrSerPhePheProProSerAspGlnSer 284  
 DB 847 GTGGACCATGCGCCACCGGATAACTGGAGATCCACGTATTATCCACCGTCGCATCTG 906  
 QY 285 LysValAlaAspLeuValLysGlnHisGlyIleThrValLeuGluValAlaLysTyr 304  
 DB 907 AGATCGCTCAATGGTCAACAGCATCGTGTCACTACTGCTTGAAGTCTCAAGTAT 966  
 QY 305 TyrAspAspProAsnLeuProIleLeuSerLysValIleAspThrLeuThrLysThrLeu 324  
 DB 967 TAGCAGAACTCTCAATACACAGTCAACAGGAAATGGAGAGTTTAAGCGATAGTTTA 1026  
 QY 325 SerTyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArg 344  
 DB 1027 AACCATGTAAGAGGTTTATGTACGAGAAGATGTGACCTATATGATTTCTTAACCGA 1086  
 QY 345 ValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrp 364  
 DB 1087 GTTCGAACCGAGAGCTAAACCTGAAATCCAAAGGCCAATGGGATGTTCCACATCCATCG 1146  
 QY 365 LeuAsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAsp 384  
 DB 1147 CTTAATCTCTGTACCAAACTCAAACTCCAAATTTGATGGTGGTGTGTTTAAAGGT 1206  
 QY 385 IleLeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsn 404  
 DB 1207 ATTATCTTAAGAATAAATCACTACGCGTCTGTTCTTCTTATCTTATCTTATGATCG 1266  
 QY 405 LysTrpAspAsnArgMetSerAlaMetIleProGluLysAspGluAspValIleTyrIle 424  
 DB 1267 AAGTGAATGATCGGATGTCGCGGTATACCCGAG-----GAAGATGATTTTATCGG 1320  
 QY 425 IleGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGlu 444  
 DB 1321 GTAGGGTTTTAAGATCCGCGGTTTGAATTTGGAGGCTTTTATCAAGAAACATG 1380  
 QY 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr 464  
 DB 1381 GAAATCTGAAGTTTGTGAGGATGTAATATGGGGTTTATCAATATATCTTCTTATCAT 1440  
 QY 465 ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspPheSerLysArg 484  
 DB 1441 TCATCACAAGAGATGGGTAGACATTTTGGTCCGAGGTGGAATATTTTCTAGAGAGA 1500  
 QY 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501

DB 1501 AAATATAATATGATCCCAAAATGATATTATCACCAGGACAAATATATTT 1551

## RESULT 15

ABK28628

ID ABK28628 standard; cDNA; 1611 BP.

XX ABK28628;

XX 09-APR-2002 (first entry)

XX cDNA encoding A. thaliana cytokinin oxidase AtCKX5.

XX Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;  
 KW root growth; lateral root; adventitious root; root geotropism; herbicide;  
 KW root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ss.

XX Arabidopsis thaliana.

XX W0200196580-A2.

XX 20-DEC-2001.

XX 18-JUN-2001; 2001WO-EP006833.

XX 16-JUN-2000; 2000EP-00870132.

PR 27-DEC-2000; 2000US-0258415P.

PR 16-MAR-2001; 2001EP-00870053.

XX (SCHM/) SCHMULLING T.

FA (WERN/) WERNER T.

XX Schmullling T, Werner T;

XX WPI; 2002-130736/17.

XX Polynucleotide encoding novel plant protein having cytokinin oxidase  
 PT activity and the protein useful for stimulating root growth, enhancing  
 PT the formation of lateral or adventitious roots, altering root geotropism.

XX Claim 3; Page 148-149; 154pp; English.

XX The invention relates to an isolated polynucleotide (I) encoding a novel  
 CC plant protein (II) having cytokinin oxidase activity. (I) is useful for  
 CC production of transgenic plants, plant cells or tissues; for production  
 CC of altered plants, plant cell or tissues; and for effecting the  
 CC expression of (II) where (I) is operably linked to one or more control  
 CC sequences. The methods further comprises regenerating a plant from the  
 CC plant cell. (I) and (II) are useful for stimulating root growth;  
 CC enhancing the formation of lateral or adventitious roots; altering root  
 CC geotropism, leading to an increase in yield; and for screening growth  
 CC promoting chemical of herbicides. (I) is useful for increasing the size  
 CC of the root meristem; increasing root size; increasing the size of the  
 CC shoot meristem; delaying leaf senescence and altering leaf senescence;  
 CC increasing leaf thickness; reducing or increasing the vessel size;  
 CC inducing parthenocarp; improving standability of the seedlings;  
 CC increasing branching and for improving lodging resistance. Antibody (III)  
 CC to (II) is useful for identifying and obtaining proteins interacting with  
 CC (II) comprising a screening assay, preferably a two-hybrid screening  
 CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase  
 CC coding sequences and PCR primers of the invention

XX Sequence 1611 BP; 416 A; 379 C; 409 G; 407 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	2,27e-115	Length:	1611
Score:	1184.00	Matches:	233
Percent Similarity:	66.46%	Conservative:	84
Best Local Similarity:	48.85%	Mismatches:	142
Query Match:	45.61%	Indels:	18
DB:	6	Gaps:	7

US-10-014-101-4 (1-501) x ABK28628 (1-1611)





GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 7, 2004, 05:53:12 ; Search time 5849 Seconds  
(without alignments)  
3712.577 Million cell updates/sec

Title: US-10-014-101-4  
Perfect score: 2596  
Sequence: 1 NANLRLMITLITVLMTKSS.....SKRKDLFPKLLSPGQDIF 501

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model/US10014101/runat\_05042004\_154154\_8576/app\_query.fasta\_1.647  
-Q=/cgn2\_1/USPTO.spool/US10014101/runat\_05042004\_154154\_8576/app\_query.fasta\_1.647  
-DB=GenEmbl -OPMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blcsum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=DOT -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pcio -NORM=ext -HEARSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10014101@cgn\_1\_1\_2496@runat\_05042004\_154154\_8576 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.\*

1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_ov.\*  
5: gb\_ov.\*  
6: gb\_ov.\*  
7: gb\_ov.\*  
8: gb\_ov.\*  
9: gb\_ov.\*  
10: gb\_ro.\*  
11: gb\_ro.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vt.\*  
15: gb\_vt.\*  
16: em\_fun.\*  
17: em\_fun.\*  
18: em\_fun.\*  
19: em\_fun.\*  
20: em\_fun.\*  
21: em\_fun.\*  
22: em\_fun.\*  
23: em\_fun.\*  
24: em\_fun.\*  
25: em\_fun.\*  
26: em\_fun.\*  
27: em\_fun.\*  
28: em\_fun.\*

29: em\_vt.\*  
30: em\_vt.\*  
31: em\_vt.\*  
32: em\_vt.\*  
33: em\_vt.\*  
34: em\_vt.\*  
35: em\_vt.\*  
36: em\_vt.\*  
37: em\_vt.\*  
38: em\_vt.\*  
39: em\_vt.\*  
40: em\_vt.\*  
41: em\_vt.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Length	DB ID	Description
1	2596	100.0	1506	6	AX339729 Sequence
2	2596	100.0	1506	6	AX785077 Sequence
3	2596	100.0	1537	8	BT005653 Arabidops
4	2596	100.0	1687	8	BT004107 Arabidops
5	2588	99.7	1506	8	AF303978 Arabidops
6	2226.5	85.8	2991	6	AX339706 Sequence
7	2226.5	85.8	2991	6	AX785054 Sequence
8	2226.5	85.8	92822	8	AC005917 Arabidops
9	1822	70.2	1575	6	AX339731 Sequence
10	1822	70.2	1575	6	AX507394 Sequence
11	1822	70.2	1575	6	AX651615 Sequence
12	1822	70.2	1575	6	AX785079 Sequence
13	1822	70.2	1655	8	BT000179 Arabidops
14	1822	70.2	1863	8	AY054460 Arabidops
15	1820	70.1	1575	8	AF303980 Arabidops
16	1539.5	59.3	2782	6	AX339710 Sequence
17	1539.5	59.3	2782	6	AX785058 Sequence
18	1539.5	59.3	88011	8	AT11614 Arabidops
19	1292	49.8	1572	6	AX339730 Sequence
20	1292	49.8	1572	6	AX785078 Sequence
21	1292	49.8	1572	8	AF303979 Arabidops
22	1221	47.0	1740	8	DSO294542 Dendrobu
23	1184	45.6	1611	6	AX339732 Sequence
24	1184	45.6	1611	6	AX785080 Sequence
25	1184	45.6	1620	6	AX339737 Sequence
26	1184	45.6	1620	6	AX785085 Sequence
27	1178	45.4	1623	8	AF303982 Arabidops
28	1152	44.4	1776	8	ZMY18377 Y18377 Zea mays mr
29	1141.5	44.0	1608	6	AX039923 Sequence
30	1141	44.0	1605	6	AR150952 Sequence
31	1141	44.0	1605	6	AR399211 Sequence
32	1135	43.7	1930	8	AK101022 Oryza sat
33	1108.5	42.7	13183	2	AP004181 Oryza sat
34	1108.5	42.7	136967	8	AP004996 Oryza sat
35	1108.5	42.7	156879	2	AP004887 Oryza sat
36	1091	42.0	1566	6	AX654568 Sequence
37	1091	42.0	1593	6	AX652883 Sequence
38	1076	41.4	1677	6	AX653630 Sequence
39	1074	41.4	1587	6	AX653027 Sequence
40	1063.5	41.0	1590	6	AX653226 Sequence
41	1060	40.8	1857	8	AF540382 Hordeum v
42	1056.5	40.7	1728	6	AX339728 Sequence
43	1056.5	40.7	1728	6	AX785076 Sequence
44	1056.5	40.7	2328	8	AK121317 Oryza sat
45	1056.5	40.7			

# ALIGNMENTS

RESULT 1

AX339729 AX339729 1506 bp DNA linear PAT 10-JAN-2002  
 LOCUS Sequence 26 from Patent WO0196580.  
 DEFINITION AX339729  
 ACCESSION AX339729  
 VERSION AX339729.1 GI:18135722  
 KEYWORDS Arabidopsis thaliana (thale cress)  
 SOURCE Arabidopsis thaliana  
 ORGANISM Arabidopsis thaliana  
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1  
 Schmuelling, T. and Werner, T.  
 Method for modifying plant morphology, biochemistry and physiology  
 Patent: WO 0196580-A 26 20-DEC-2001;  
 Schmuelling, Thomas (DE); Werner, Tomas (DE)  
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 Best Local Similarity: 100.00% Indels: 0  
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US-10-014-101-4 (1-501) x AX339729 (1-1506)

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 SOURCE Arabidopsis thaliana  
 ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

## REFERENCE

Schmulling, T. and Werner, T.  
Method for modifying plant morphology, biochemistry and physiology  
Patent: WO 03050287-A 26 19-JUN-2003;

## JOURNAL

Schmulling, Thomas (DE); Werner, Tomas (DE)

## FEATURES

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Alignment Scores:  
Pred. No.: 2,896-213 Length: 1506  
Score: 2596.00 Matches: 501  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
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ACCESSION BT005653  
VERSION BT005653.1 GI:28973496  
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SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
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1 (bases 1 to 1537)  
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M.,  
Oncidera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wong, C., Wu, H.C.,  
Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y.,

Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M.,  
 Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P.,  
 Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W.,  
 Ecker,J.R. and Theologis,A.  
 Arabidopsis Open Reading Frame (ORF) Clones  
 Unpublished

#### TITLE JOURNAL REFERENCE AUTHORS

2 (bases 1 to 1537)  
 Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Huan,V.W., Lee,J.M.,  
 Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C.,  
 Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Kawai,J., Kim,C.J., Narusaka,M.,  
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 Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P.,  
 Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W.,  
 Ecker,J.R. and Theologis,A.  
 Direct Submission

#### TITLE JOURNAL COMMENT

Submitted (15-MAR-2003) Plant Gene Expression Center, 800 Buchanan  
 Street, Albany, CA 94710, USA  
 The RIKEN Genomic Sciences Center (GSC) members carried out the  
 collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN  
 Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,  
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,  
 Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members constructed and  
 sequenced the PUNI (ORF) clones using the RAFL cDNAs: Yamada,K.,  
 Chan,M.M., Chang,C.H., Dale,J.M., Huan,V.W., Lee,J.M.,  
 Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C.,  
 Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M.,  
 Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W.,  
 Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally  
 to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP  
 /PGEC) contributed equally to this work as PIs.

Annotation based on July 2002 version of the Arabidopsis genome  
 submitted to Genbank.

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 Best Local Similarity: 100.00% Mismatches: 0

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 KEYWORDS Arabidopsis thaliana (thale cress)  
 SOURCE Arabidopsis thaliana  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; eucosids II; Brassicales; Brassicaceae; Arabidopsids.  
 1 (bases 1 to 1687)  
 Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Heuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.  
 Arabidopsis Full Length cDNA Clones  
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 Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Heuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.  
 Arabidopsis Full Length cDNA Clones  
 Unpublished  
 TITLE Arabidopsis Full Length cDNA Clones  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE Submitted (14-FEB-2003) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA  
 JOURNAL  
 REFERENCE  
 AUTHORS  
 COMMENT RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,

Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.  
 The Salk, Stanford, PGECC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Heuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Narusaka,M., Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W., Ecker,J.R. and Theologis,A.  
 Yamada,K. (SSP/PGECC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGECC) contributed equally to this work as PIs.  
 Annotation based on July 2002 version of the Arabidopsis genome submitted to Genbank.  
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 REFERENCE 1 (bases 1 to 1506)  
 AUTHORS Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and  
 Morris, R.O.  
 TITLE A family of cytochrome oxidases from Arabidopsis thaliana  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1506)  
 AUTHORS Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and  
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 JOURNAL Submitted (11-SEP-2000) University of Missouri, 210 Waters Hall,  
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REFERENCE 1  
 AUTHORS Schmueling, T. and Werner, T.  
 TITLE Method for modifying plant morphology, biochemistry and physiology  
 JOURNAL Patent: WO 0196580-A 3 20-DEC-2001;  
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SEQUENCE 3 from Patent WO03050287.
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ACCESSION AX785054
VERSION AX785054.1 GI:32952890
KEYWORDS
SOURCE
ORGANISM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
1 Schmulling, T. and Werner, T.
METHOD for modifying plant morphology, biochemistry and physiology
PATENT: WO 03050287-A 3 19-JUN-2003;
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LOCATION/Qualifiers
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DEFINITION Arabidopsis thaliana chromosome 2 clone F3P11 map C1C06E08,
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VERSION AC005917.3 GI:20197478
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1. (bases 1 to 92822)
REFERENCE
AUTHORS Lin, X., Kaul, S., Shea, T.P., Fujii, C.Y., Shen, M., VanAken, S.E.,
Barnstead, M.E., Mason, T.M., Bowman, C.L., Ronning, C.M.,
Benito, M.-I., Carrera, A.J., Creasy, T.H., Buell, C.R., Town, C.D.,
Nierman, W.C., Fraser, C.M. and Venter, J.C.
JOURNAL Unpublished
2. (bases 1 to 92822)
REFERENCE
AUTHORS Lin, X.
JOURNAL Direct Submission
TITLE Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
3. (bases 1 to 92822)
REFERENCE
AUTHORS Town, C.D. and Kaul, S.
JOURNAL Direct Submission
TITLE Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA, cdtnw@igrr.org
COMMENT On Apr 18, 2002 this sequence version replaced gi:6598497.
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 DEFINITION Sequence 28 from Patent WO0196580.  
 ACCESSION AX339731  
 VERSION AX339731.1 GI:18135724  
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 ORGANISM Arabidopsis thaliana  
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 REFERENCE 1  
 AUTHORS Schmulling,T. and Werner,T.  
 TITLE Method for modifying plant morphology, biochemistry and physiology  
 JOURNAL Patent: WO 0196580-A 28 20-DEC-2001;  
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Query Match:	70.18%	Indels:	24
DB:	6	Gaps:	5

US-10-014-101-4 (1-501) x AX339731 (1-1575)

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DB	85	GGGATTGATGTTTCTTACCACATATCATCACTTACCGTCTCAACCGATCCCTTCTCC	144
QY	42	IleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyValIle	61
DB	145	ATCTCTGCCGCTCTCACGACTTCGGTAAACATAACGACGACGAAAAATCCGCGCGCTCTC	204
QY	62	CysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly-----	79
DB	205	TGCGCTTCTCCACACGAGGTGGCTGCTCTCTCGTTTTCGCTAACCGAGATTCCTCT	264
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DB	385	GCCATGGCGGCTAAACACGCGCGGTGTTATCTCGCAGACGCGGACTTACGCTGACGTG	444
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QY	166	GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle	185
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QY	286	ValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAlaLysTyrTyr	305
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DEFINITION	Sequence 2089 from Patent WO0216655.		
ACCESSION	AX507394		
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SOURCE	Arabidopsis thaliana		
ORGANISM	Arabidopsis thaliana		
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AUTHORS	Harper,J.F.; Krops,J.; Wang,X. and Zhu.T.		
TITLE	Stress-regulated genes of plants, transgenic plants containing same, and methods of use		
JOURNAL	Patent: WO 0216655-A 2089 28-FEB-2002; The Scripps Research Institute (US) ; Syngenta Participations AG (CH)		
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Score:	1822.00	Matches:	345
Percent Similarity:	80.06%	Conservative:	69
Best local Similarity:	66.73%	Mismatches:	79
Query Match:	70.18%	Indels:	24
DB:	6	Gaps:	5

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 VERSION AX785079.1 GI:32952910  
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 SOURCE Arabidopsis thaliana  
 ORGANISM Arabidopsis thaliana  
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 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi  
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 REFERENCE 1  
 AUTHORS Schmulling, T. and Werner, T.  
 TITLE Method for modifying plant morphology, biochemistry and physiology  
 JOURNAL Patent: WO 03050287-A 28 19-JUN-2003;  
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DEFINITION mRNA, complete cds.
ACCESSION BT000179
VERSION BT000179.1 GI:23197941
KEYWORDS FLI_CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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REFERENCE 1 (bases 1 to 1655)
AUTHORS Nguyen,M., Karlin-Neumann,G., Southwick,A., Tripp,M., Miranda,M.,
Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
Sakano,H., Sakurai,T., Satou,M., Seki,M., Shinn,P., Yamada,K.,
Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
Direct Submission
JOURNAL Submitted (19-SEP-2002) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA
COMMENT e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGENC (SSP) Consortium members constructed and
sequenced the pENTR (ORF) clones using the RAFL cDNAs: Nguyen,M.,
Southwick,A., Tripp,M., Palm,C.J., Jones,T., Wu,T., Chen,H.,
Cheuk,R., Chan,M.M., Chang,C.H., Dale,J.M., Deng,J.M., Huan,V.W.,
Lee,J.M., Kim,C.J., Quach,H.L., Shinn,P., Tang,C.C., Toriumi,M.,
Wallender,E.K., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S.,
Ecker,J., Theologis,A. and Davis,R.W.

Nguyen,M., (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W.
(SSP/Stanford) contributed equally to this work as PIs.

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ORIGIN

Alignment Scores:  
Pred. No.: 8,81e-147 Length: 1655  
Score: 1822.00 Matches: 345  
Percent Similarity: 80.08% Conservative: 69  
Best Local Similarity: 66.73% Mismatches: 79  
Query Match: 70.18% Indels: 24  
DB: 8 Gaps: 5

US-10-014-101-4 (1-501) x BT000179 (1-1655)

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DB	85	GGCATTGTATGTTTACCATATCACTCAACCTTACCGTCTCAACCATCCCTTCTCC	144
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DB	145	ATCTGCGCTTCTCAGCATTCTCGGTATCAATACCGACGAAATCCCGCGCGCTCTC	204
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QY	146	ValSerTrpThrAspTyLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle	165
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QY	166	GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle	185
DB	565	GGTGGTCAGACGTTTAGACACGCGCTCTCAGATTAGTAACGTTTCATGAGCTTACGTTAT	624
QY	186	ThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyGly	205
DB	625	ACCGAAAGGTAATGATGACTTGTCTCCAAAGTTAAACCTGAAATTGTTCTATGGA	684
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DB	685	GTTTTAGGAGGTTTGGGTCAAATTCGGTATTATAACGAGGCCAGGATTCGGTTGGATCAT	744
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DB	805	GACCAAGAGGTTTAAATATCAATGACCAATGATCTCGAGTTGACTTTTGGAGGTCAA	864
QY	266	IlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLys	285
DB	865	CTTATGATGCAATAGGCTTCGTAGACACTCTTCTTCTCCACTCTCCGATCAACAAGA	924
QY	286	ValAlaAspLeuValLysGlnHisGlyIleIleTyValLeuGluValAlaLysTyTr	305
DB	925	GTGCGATCTCTTGTGAATGACCAACCGGATCATCTATGTTCTCGAAGTAGCAAGTATTAT	984
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QY	445	LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyTrLeuMetHisTyTr	464
DB	1399	AAGTTATTGATTTTGTGAAACTCGGAAATTAAGATTAAAGGATATTATGATGACATAT	1458
QY	465	ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspPheSerLysArg	484
DB	1459	ACAAGAAAGAAAGATTGGGTAAACATTTTGGACCAAAATTTGGATGATTTTAAAGAAAG	1518
QY	485	LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe	501
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ACCESSION  
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VERSION  
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ORGANISM  
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REFERENCE  
1 (bases 1 to 1863)

## AUTHORS

Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Cheuk, R., Chung, M.K., Hayashizaki, Y., Ienida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.

TITLE  
JOURNAL

Direct Submission  
Submitted (28-AUG-2001) DNA Sequencing and Technology Center,  
Stanford University, 855 California Avenue, Palo Alto, CA 94304,  
USA

## COMMENT

e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salik, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen, M., Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M.K., Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.

Southwick, A., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W. (SSP/Stanford) contributed equally to this work as PIs.

## FEATURES

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## ORIGIN

## Alignment Scores:

Pred. No.: 1 04e-146 Length: 1863  
Score: 1822.00 Matches: 345  
Percent Similarity: 80.08% Conservative: 69  
Best Local Similarity: 66.73% Mismatches: 79  
Query Match: 70.18% Indels: 24  
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US-10-014-101-4 (1-501) x AV054460 (1-1863)

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DEFINITION Arabidopsis thaliana (thale cress)
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VERSION AF303980.1 GI:11120511
KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1. (bases 1 to 1575)
Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickie, S. and
Morris, R.O.
A family of cytokinin oxidases from Arabidopsis thaliana
Unpublished
2. (bases 1 to 1575)
Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickie, S. and
Morris, R.O.
Direct Submission
Submitted (11-SEP-2000) University of Missouri, 210 Waters Hall,
Columbia, MO 65211, USA
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gene
CDS
ORIGIN

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Alignment Scores: 1.22e-146 Length: 1575
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Best Local Similarity: 66.73% Mismatches: 80
Query Match: 70.11% Indels: 24
DB: Gaps: 5

US-10-014-101-4 (1-501) x AF303980 (1-1575)
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1045 TTCGCTCCAGGGTTTATGTTCTGACAGATGTTCCGTTATTCGATTTCCTGAACCGTGTG 1104
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Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1105 CGAAACGAAGAAGATAAATCTAGATCTTTAGGACTATGGAGATTCCTCATCCATGGCTT 1164
QY 366 AsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIle 385
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1165 AACATCTTTGTCCTCGGGTCTCGAATCCAAGATTTTCATGATGGTGTATTATTAATGGCCTT 1224
QY 386 LeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys 405
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1225 CTTCTAAACCAACCTCAACTTCTGGTGTACTCTCTTCTATCCACAAACCGAAACAAA 1284
QY 406 TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIle 425
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1285 TGGAAACACCGCATCTCACGATGACACCG-----GACGAGATGTTTTTTATGTGATC 1338
QY 426 GlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSerValAsnGlu 444
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1339 GGATTACTGCAATCAGCTGGTGATCTCAAAATTCGCAAGAACTTGAAAATCTCAACGAC 1398
QY 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr 464
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1399 AAGTTATTTCAGTTTGTGAAAACTCGGGAATTAGATTAGGAATATTGTATGCACATAT 1458
QY 465 ThrSerLysGluAspTyrIleGluHisPheGlySerLysTyrTrpAspAspPheSerLysArg 484
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1459 ACAAGAAAAGAAAGATTGGGTTAAACATTTTGACCAAAATGGGATGATTTTAAAGAAAG 1518
QY 485 LysAspLeuPheAspProLysLysLeuSerProGlyGlnAspIlePhe 501
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1519 AAAATTATGTTGATCCCAAGACATATTGTCTCAGGACAAAGACATATTT 1569
```

Search completed: April 7, 2004, 09:35:32  
Job time : 5923 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 7, 2004, 07:23:26 ; Search time 3777 Seconds  
(without alignments)  
3961.068 Million cell updates/sec

Title: US-10-014-101-4  
Perfect score: 2596  
Sequence: 1 MANURLMTLITVLMITKSS.....SKRKDLDPKLLSPGQDIP 501

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters: -DEV=xlh  
-Q/cgn2\_1/USPTO\_spool/US10014101/runat\_05042004\_154154\_8588/app\_query.fasta\_1.647  
-DB=EST -Qfmt=fasta -Suffix=p2n.rst -MINMATCH=0.1 -LOOPEXT=0 -DOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10014101.CCN 1.1 1906 @runat\_05042004\_154154\_8588 -NCPU=3  
-NO WMAP -LARGEQUERY -NEG SCORE=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pin:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pto:\*  
25: em\_gss\_rtd:\*  
26: em\_gss\_rtd:\*  
27: em\_gss\_vrt:\*  
28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	893	34.4	1776	11	AY112108 Zea mays
2	808	31.1	561	9	AU236872 AU236872
3	785	30.3	838	28	BH575041 BOGHT82TR
4	765	29.5	689	14	CD813279 BN15.019B
5	690	26.6	688	28	BZ006516 Oeg06a08
6	685.5	26.4	811	14	CF439478 EST875823
7	598.5	23.1	809	14	CF209921 CAB20005
8	598	23.0	626	14	CB922686 VVD086G02
9	584	22.5	792	28	BZ078445 11f25a03
10	583	22.5	969	29	CG289653 OGWPN30TV
11	577	22.2	601	13	BU025625 QHG10G19
12	561	21.6	948	29	CG460090 FUIJV92TD
13	560	21.6	582	12	BMI43498 saj44h08
14	557	21.5	635	10	BE330968 so91g01.Y
15	555.5	21.4	566	13	BU084470 sar19h02
16	551	21.2	876	29	CG445712 OGVHS26TV
17	543.5	20.9	707	14	CD843876 RFO2.134G
18	538	20.7	852	28	BZ528348 OGAKW21TC
19	526.5	20.3	436	9	AU227876 AU227876
20	525	20.2	553	10	AW623777 EST131722
21	523.5	20.2	510	14	CF607152 GEMMA01.0
22	521.5	20.1	963	29	CG351153 OG2BM20TV
23	519	20.0	741	14	CF210007 CAB20005
24	514.5	19.8	895	29	CG316304 OG3DC28TV
25	514	19.8	552	12	BM528151 sal15a02
26	508.5	19.6	995	29	CG287021 OG0DU53TV
27	507	19.5	667	9	AI731492 BNLGH1996
28	507	19.5	807	14	CA766652 AF53-RP6
29	506.5	19.5	857	29	CG445707 OGVHS26TV
30	501.5	19.3	683	28	BZ006156 Oeg06a08
31	499	19.2	813	28	BZ542127 OGAIU60TC
32	498.5	19.2	806	14	CF393540 RTDR3.13
33	496.5	19.1	870	29	CG351143 OG2BM20TH
34	496	19.1	451	13	BQ588342 E012308-0
35	495.5	19.1	677	12	B1931101 EST550990
36	494	19.0	699	28	BZ340096 1c36904.D
37	493.5	19.0	753	29	CC693605 OGULX22TH
38	493	19.0	488	10	AW429072 EST306444
39	492.5	19.0	638	9	AI728095 BNLGH1995
40	491.5	18.9	748	14	CF451378 EST687723
41	489	18.8	802	29	CG451590 OGVGM89TH
42	485	18.7	750	29	CG322138 OGXC022TH
43	484.5	18.7	697	14	CF398227 RTDSF.24
44	484	18.6	911	29	CG268306 OG3BV28TV
45	484	18.6	917	29	CG322151 OGXC022TV

# ALIGNMENTS

RESULT 1  
LOCUS AY112108 1776 bp mRNA linear HTC 17-OCT-2002  
DEFINITION Zea mays CL1532\_1 mRNA sequence.  
ACCESSION AY112108  
VERSION AY112108.1 GI:21216698  
KEYWORDS HTC.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE 1 (bases 1 to 1776)

**AUTHORS** Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whittitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.  
**TITLE** Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes  
**JOURNAL** Unpublished (2002)  
**REFERENCE** 2 (bases 1 to 1776)  
**AUTHORS** Coe, E.H.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA  
**COMMENT** If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSR, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

**FEATURES**  
 source  
 1. 1776  
 Location/Qualifiers  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4577"  
 /clone\_lib="Maize Mapping Project/DuPont Consensus Library"  
 /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

## ORIGIN

**Alignment Scores:**  
 Pred. No.: 2,598-96 Length: 1776  
 Score: 893.00 Matches: 199  
 Percent Similarity: 54.18% Conservative: 67  
 Best Local Similarity: 40.53% Mismatches: 197  
 Query Match: 34.40% Indels: 28  
 DB: 11 Gaps: 11

US-10-014-101-4 (1-501) x AV112108 (1-1776)

QY 35 LeuSerThrAspProSerIleIleSerAlaAlaSerHisAspPheGlyAsnIleThr 54  
 DB 176 CTCGGACCGACAGCAACGCGCGCGCGCTCGACGACCTTCGGCAACATCANNNN 235  
 QY 55 ValThrProGlyGlyValIleCysProSerThrAlaAspIleSerArgLeuGln 74  
 DB 236 NNN 295  
 QY 75 TyrAlaAlaAsnGlyLysSer-----ThrPheGlnValAlaAlaArgGlyGlnGlyHis 92  
 DB 296 ---GGGGCAACTCCACCCCGGGGTGGCCCTACACCATCGGCTTCGGCGCGCGGCAC 352  
 QY 93 SerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIleThr 112  
 DB 353 TCCTCATGGCGCAGNN 412  
 QY 113 AspValVal-----ValSerLysAspLysLysTyrAlaAspValala 126  
 DB 413 NNN 472  
 QY 127 AlaGlyThrLeuTrpValAspValIleLysLysThrAlaGluLysGlyValSerProVal 146  
 DB 473 GCGGACGAGGTGTGATGACGTGCTGGCGCGTNNNNNNNNNNNNNNNNNNNNNN 532  
 QY 147 SerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIleGly 166  
 DB 533 NNNNGGACCGACTACTCTACCTACCTCGCGCGCACGCTGTCCACAGCAGGCATCAGC 592  
 QY 167 GlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThr 186

DB 593 GGCAGGGGTTCCGCCACGGCCACAGATATCTAACGTGTGGAGATGGACGTTATCACC 652  
 QY 187 GlyLysGlyGluMetLeuThrCysArgGlnLeuAsnProGluLeuPheTyrGlyVal 206  
 DB 653 GGCATGGGGAGATGGTGACGTCTCCAAGCAGCTGAACGCGACCTGTTTCAGANNNNNN 712  
 QY 207 LeuGlyGlyLeuGlyGlnPheGlyIleThrArgAlaArgIleValLeuAspHisAla 226  
 DB 713 NNN 772  
 QY 227 ProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAsp 246  
 DB 773 NNN 832  
 QY 247 GlnGluArgLeuIleSerMetAlaAsnAspIleGly-----ValAsp 260  
 DB 833 CAGGACGGCGNN 892  
 QY 261 TyrLeuGluGlyGlnIlePhe-----LeuSerAsnGlyValValAspThrSer 276  
 DB 893 TACGTGAAGAGGTGGTGTCTGTGAACAGACGCTGGCGACCGACCTGGCAACACGGGG 952  
 QY 277 PhePheProSerAspGlnSerLysValAlaAspLeuValLysGlnHisGly----- 294  
 DB 953 TTCTTCCACGACGCGCGCTGCGCGGATCGTGGCGTTCGGCGGGAGCGGAACGCCACC 1012  
 QY 295 IleIleTyrValLeuGluValAlaLysTyrTyrAsp-----AspProAsnLeuProIle 312  
 DB 1013 ACCGTGTACAGCATCGAGCGCACGCTCAACTACGACNNNNNNNNNNNNNNNNNN 1072  
 QY 313 IleSerLysValIleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPheIleSer 332  
 DB 1073 NNNNCCAGAGCTCGCGTGGCGACGCTGAGCTAGTGGAGGGGTTCGCGTTC 1132  
 QY 333 MetHisAspValAlaLysPheAspPheLeuAsnArgValHisValGluGluAsnLysLeu 352  
 DB 1133 CAGCGCGAGCTGGCTTACCGCGCGTTCCTTGACCGGTGCACGGCGAGAGGTGCGCTC 1192  
 QY 353 ArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeuAsnLeuTyrValProLysSer 372  
 DB 1193 AACAAAGCTGGGGTGTGGCGGTGGCGCACCGCTGCTCAACATGTTGTCGCGCGCTCG 1252  
 QY 373 ArgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLysGlnLysSerAla 392  
 DB 1253 CGCATCGCGCATTCGACCGCGCGTGTTCAGGGCATC---CTGACGGGACCGACATC 1309  
 QY 393 SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLysTrpAspAsnArgMetSerAla 412  
 DB 1310 GTCGGCGCGCTCATGCTCTANNNNNTCAACAAATCCATGTGGGACGACGCGCATGTGCGG 1369  
 QY 413 MetIleProGluIleAspGluAspValIleTyrIleIleGlyLeuLeu---GlnSerAla 431  
 DB 1370 GGCACGCGG-----TCTGAGGACGTGTCTACGGGTGTCTGCTCTTCTTCGCGGTG 1423  
 QY 432 ThrProLysAspLeuProGluValGluSerValAsnGluLysIleIleArgPheCysLys 451  
 DB 1424 GCGCCCAACGACCTGGCGAGGTGCGAGGAGCAGAACAGGAGGATCTCGCTTCGCGAC 1483  
 QY 452 AspSerGlyIleLysIleLysGlnTyrLeuMetHisTyrThrSerLysGluAspTrpIle 471  
 DB 1484 CTCGCGCGGATCCAGTACAGACCTACCTGCGCGGCGCACCGACCGAGTACTGGGTG 1543  
 QY 472 GluHisPheGly---SerLysTrpAspPheSerLysArgLysAspLeuPheAspPro 490  
 DB 1544 CGCCACTTCGGCGCCCAAGTGAATCGTCTGTGGAGATGAAGAACAAAGTACGACCC 1603  
 QY 491 LysLysLeuSerProGlyGlnAspIlePhe 501  
 DB 1604 AAGAGGTGCTCTNNNNNGCCAGGACATCTTC 1636

RESULT 2  
 AU236872  
 LOCUS

AU236872 561 bp mRNA linear EST 01-APR-2002

DEFINITION AU236872 RAPL15 Arabidopsis thaliana cDNA clone RAPL15-29-H04 5', mRNA sequence.

ACCESSION AU236872

VERSION AU236872.1 GI:19876041

KEYWORDS EST

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 561)

AUTHORS Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Akiyama, K., Enju, A., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y., and Shinozaki, K.

TITLE Large scale analysis of Arabidopsis full-length cDNA

JOURNAL Unpublished (2002)

COMMENT Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: mseki@tc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1999). cDNA cleaved with BamHI and XhoI was ligated to modified lambda FIC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pluscript vector. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

## FEATURES

source

1..561 Location/Qualifiers

/organism="Arabidopsis thaliana"

/mol\_type="mRNA"

/db\_xref="taxon:3702"

/clone="RAPL15-29-H04"

/tissue\_type="mixture of silique and flower"

/lab\_host="DH103"

/clone\_lib="RAPL15"

/note="Site\_1: BamHI; Site\_2: SalI"

## ORIGIN

Alignment Scores:

Pred. No.:	6,94e-87	Length:	561
Score:	808.00	Matches:	166
Percent Similarity:	97.65%	Conservative:	0
Best Local Similarity:	97.65%	Mismatches:	2
Query Match:	31.12%	Indels:	2
DB:	9	Gaps:	0

US-10-014-101-4 (1-501) x AU236872 (1-561)

QY 1 MetAlaAsnLeuArgLeuMetIleThrLeuIleThrValLeuMetIleThrLysSer 20

DB 55 ATGCTAATCTCTGTTTAAATGATCACTTTAATCAGGTTTAAATGATCACTCA 114

QY 21 AsnGlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSer 40

DB 115 AACGGTATTAATGATTGATTACCTAAATCCCTTAACCTCAACCTCTCTACCGATCCTTC 174

QY 41 IleIleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyVal 60

DB 175 ATCATCTCCGAGGCTCTCATGACTTCGAAATACCAACCCGTCACCCCGCGCGTA 234

QY 61 IleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnIleThrAlaAlaAsnGlyLys 80

DB 235 ATCTGCCCTCTCTCCACCGCTGATATCTCTCGTCTCTCTCAATACCGCGCAACGGA 294

QY 81 SerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal 100

DB 295 AGTACATTCCAAAGTAGCGGCTCGTGGCCAAAGGCCACTCTTAACCGGCCAAGCTCGGTC 354

QY 101 SerGlyGlyValIleValAlaAsnMetThrCysIleThrAspValValValSerLysAspLys 120

DB 355 TCCGGCGGAGTAATCGTCAACATGACGTGATCACTGACGTGGTGTTCATAAAGCAAG 414

QY 121 LysTyrrAlaAspValAlaAlaGlyThrLeuTyrValAspValLeuLysLysThrAlaGlu 140

DB 415 AAGTACCTGACGTGGCGCGGACGTTATGCTGGATGCTGTTAAGNAGACGGCGAG 474

QY 141 LysGlyValSerProValSerThrThrAspTyrLeuHisIleThrValGlyGlyThrLe 160

DB 475 AAAGGGGTGTCGGCGTTCCTTGACGATTAATTGCATATAACCCGTCGGNAGACGTT 534

QY 160 userAsnGlyGly-IleGlyGlyGln 168

DB 535 NTCNAATGGTGGAAATGGTGICAA 560

## RESULT 3

BH575041/c

LOCUS

DEFINITION

BOGTR82TR BOGB Brassica oleracea genomic clone BOGTR82, genomic

survey sequence.

ACCESSION

BH575041

VERSION

BH575041.1 GI:17827114

KEYWORDS

GSS.

SOURCE

Brassica oleracea

ORGANISM

Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

1 (bases 1 to 838)

AUTHORS

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

TITLE

Whole genome shotgun sequencing of Brassica oleracea

JOURNAL

Unpublished (2001)

COMMENT

Other GSSs: BOGTR82TF

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: Sheared ends.

Location/Qualifiers

1..838

/organism="Brassica oleracea"

/mol\_type="Genomic DNA"

/strain="T01000DH3"

/db\_xref="taxon:3712"

/clone="BOGTR82"

/clone\_lib="BOGB"

/note="Vector: pPOS1; Site\_1: BstXI; 2-3 kb sheared

genomic DNA inserted into pPOS1 using BstXI linkers"

## ORIGIN

Alignment Scores:

Pred. No.:	6,56e-84	Length:	838
Score:	786.00	Matches:	154
Percent Similarity:	79.62%	Conservative:	14
Best Local Similarity:	72.99%	Mismatches:	16
Query Match:	30.28%	Indels:	28
DB:	28	Gaps:	2

US-10-014-101-4 (1-501) x BH575041 (1-838)

QY 316 ValIleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPheIleSerMetHisAsp 335

DB 638 GTGATTGACAAAGTTAACTAAACCCCTAGTTACCTGCCCGGTTTATATCAATGCACAC 579

QY 336 ValAlaTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeu 355

DB 578 GTGCTCTACTTTGATTTCTGAAACCGTGTACAGTTGAGAGATATAACTCAGATCTCTG 519

```

Qy 356 GyleUtrpLuleuProHisProTrrpLeuAsnLeuTyrValProLysSerArgIleLeu 375
Db 518 GCATTATGGAAGTCTCTATCCATCGCTTAACCTATATGTCCTCTAAACACTCAGATACTA 459
Qy 376 AspPheHisAsnGlyValValLysAspLleLeuLysGlnLysSerAlaSerGlyLeu 395
Db 458 GATTTCATACGGTGTGTAAAGACATCTCTTCTAAGCGAATCGACTCTGCGGT 399
Qy 396 AlaLeuLeuTyrProThrAsnAsgAsnLys- 405
Db 398 GCTCTCTCTATCCCAACCAACCGGAATAA-GTAAGGTTATTCATCAATACTTCAAGAAC 340
Qy 406 -----TrpAsnAsgMet 410
Db 339 AAGTAACAGATCTGACATAAATGTTTTCTGTTATTATTAGATGGGACAAATGATG 280
Qy 411 SerAlaMetIleProGluLleAspGluAspValIleIleIleGlyLeuLysGlnSer 430
Db 279 TCGCGGATGATACCA-----GATGAAGATGTTTCTATGTCGTGGACTACTACAGGCA 226
Qy 431 AlaThrProLysAspLeuProGluValGluSerValAsnGluLysIleIleArgPheCys 450
Db 225 GCTAGCTCACAAATGTCGAAGAGTGAGAGTGTAACAGAGCGCATCTATTAGTTTTC 166
Qy 451 LysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyrThrSerLysGluAspTrrp 470
Db 165 AAGGACTCGGTATTAGATTAGACATCTAATGCAATTCACAGAAAAGAGATTGG 106
Qy 471 IleGluHisPheGlySerLysTrrpAspPheSerLysArgLysAspLeuPheAspPro 490
Db 105 GTTGAACATTGTCATCTAAATGGGGTCTTTTCGAAGAGGAAAGATCTGTTTGTCTCT 46
Qy 491 LysLysLeuLeuSerProGlyGlnAspIlePhe 501
Db 45 AAGAACTATTATCTCCAGGCGCAAGATATTTT 13

RESULT 4
CD813279 689 bp mRNA linear EST 10-JUL-2003
LOCUS BN15.019B17F020122 BN15 Brassica napus cDNA clone BN15019B17, mRNA
DEFINITION
CD813279
CD813279.1 GI:32495219
EST.
Brassica napus (rape)
Brassica napus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 689)
Genopiante.
Genopiante, a major partnership french program in plant genomics
Unpublished (2003)
Contact: Genopiante
Genopiante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genopiante' (http://www.genopiante.com
and http://genopiante-info.infobiogen.fr).
FEATURES
Location/Qualifiers
1..689
/organism="Brassica napus"
/mol_type="mRNA"
/cultivar="Jet neuf"
/db_xref="taxon:3708"
/clone="BN15019B17"
/tissue_type="seed"
/clone_lib="BN15"
ORIGIN
Alignment Scores:

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Pred. No.: 1.64e-81 Length: 689
Score: 765.00 Matches: 149
Percent Similarity: 88.08% Conservative: 21
Best Local Similarity: 77.20% Mismatches: 17
Query Match: 29.47% Indels: 6
DB: 14 Gaps: 2
US-10-014-101-4 (1-501) x CD813279 (1-689)
Qy 1 MetAlaAsnLeuArgLeuMetIleThrLeuIleThrValLeuMet----- 15
Db 102 ATGGCTAATCTTCGTCTAATGATCACTCAATCAACCGTTTGGTTTATTATTTCCGAGC 161
Qy 16 IleThrLysSerSerAsnGlyIleLys---IleAspLeuProLysSerLeuAsnLeuThr 34
Db 162 TTGTCTAATCGTCAGAAAGCACATAAGTTATTCTCTACTTAAGTCCCTAAACCTCACC 221
Qy 35 LeuSerThrAspProSerIleIleSerAlaAlaSerHisAspPheGlyAsnIleThrThr 54
Db 222 CTCCTCACCGATCTCTCAACCATCTCCACCGCTCTCCGATTACGGAAACGTTACCACC 281
Qy 55 ValThrProGlyGlyValIleCysProSerSerThrAlaAspIleSerArgLeuGln 74
Db 282 GTGACACCGCGCGGCTCTCTGCGCTTCCTCCCGGAGATATCCGTCCTCTCAGC 341
Qy 75 TyrAlaAlaAsnGlyLysSerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeu 94
Db 342 TAGCGCGCAACGAGAGACTATATTCACGTGGCGCTCGCAGCCCAAGGCCACTCTTTA 401
Qy 95 AsnGlyGlnAlaSerValSerGlyValIleValAsnMetThrCysIleThrAspVal 114
Db 402 AACGCCCAAGCTCCGTATCAGTGGAGTGGTTATCAACATGACGTGTCCTCGTGACATA 461
Qy 115 ValValSerLysAspLysLysTyrAlaAspValAlaAlaGlyThrLeuTrrpValAspVal 134
Db 462 ACTGTTTCAGAAAGACAAAGAGTATGCTGACGTGGCAGCGGACGTTATGGGTGATGTG 521
Qy 135 LeuLysLysThrAlaGluLysGlyValSerProValSerProValSerThrAspTrrpLeuHisIle 154
Db 522 CTTAGAGAGACGGCGGAGCAAGCGGTTTCGCGCGGTTTCGTGGACGGATATTTCATATT 581
Qy 155 ThrValGlyGlyThrLeuSerAsnGlyIleGlyGlyGlnValPheArgAsnGlyPro 174
Db 582 ACGCTCGGAGGAACCTCTCGAATGCTGGATCGCGGTCAATGTTTAGAACGGTCTCT 641
Qy 175 LeuValSerAsnValLeuGluLeuAspValIleThrGly 187
Db 642 CAATTAGTAACGTCCTTGAGTTGGACGTTATAACTGTT 680

RESULT 5
BZ006516 688 bp DNA linear GSS 07-OCT-2002
LOCUS ceg06a08.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
DEFINITION
BZ006516
BZ006516.1 GI:23554774
GSS.
Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 688)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D., and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: ceg06 row: a column: 08
Seq primer: -28RfPOT reverse

```



California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:  
5'-AAGCATGGTATCAGCGAGATGCCATTCAGCGCGG-3' and  
5'-ATTGACGAGCGAGCGCGCATG-dT(30)-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

ORIGIN

Alignment Scores:  
Pred. No.: 3,43e-61 Length: 809  
Score: 599.50 Matches: 116  
Percent Similarity: 64.94% Conservative: 47  
Best Local Similarity: 46.22% Mismatches: 75  
Query Match: 23.05% Indels: 13  
DB: 14 Gaps: 5

US-10-014-101-4 (1-501) x CF209921 (1-809)

QY	260	AspTyrLeuGluGlyGlnIlePheLeuSerAsnGlyValValAsp-----ThrSer	276
DB	2	GACTATGTTGAGGGCTTGTTATAGTTGTGAAGGCCTTATCAACAACCTGGAGGTCTCCTCC	61
QY	277	PhePheProProSerAspGlnSerLysValAlaAspLeuValLysGlnHisGlyIlelle	296
DB	62	TTTTTCTCCCTCGCACCCCTGTAAATCTCTTTTNGAATAACCGGGGTGTGCTC	121
QY	297	TyrValLeuGlnValAlaLysTyrTyraSpAspProAsnLeuproIleIleSerLysVal	316
DB	122	TATGCTTAGAGTACCAGAAGTAACCATCAATCCATGCCGATATTATTCACCAAGAT	181
QY	317	IleAspThrLeuThrylserThrLeuSerTyrLeuProGlyPheIleSerMetHisAspVal	336
DB	182	GTAGAGGCTCTGCTGAAGAGACTAGATTTTATTCGTCATCGTCTTCCAACAGCATCTT	241
QY	337	AlaTyrrPheAspPheLeuAsnArgValHisValGluGlnAsnLysLeuArgSerLeuGly	356
DB	242	CCATATGTGTGATTTCCTGGACCGGGTTCACAGCGGAGCTCAAGCTCCGGTCGAAGGT	301
QY	357	LeuTipGluLeuProHisProTyrLeuAsnLeuTyrValProLysSerArgIleLeuAsp	376
DB	302	TTGTGGACGTGGCGACCCCTTGGCTCAACCTTTTGTCCCAGATCAAGGATTTGCTGAC	361
QY	377	PheHisasnGlyValValLysAspIleLeuLeuLysGlnLysSerAlaSerGlyLeuAla	396
DB	362	TTTGATGAAGCGGTATTCAAGGGCATTTTG-----GGGAATAAGACAAGTGCCCCCATC	415
QY	397	LeuLeuTyrProThrAsnArgAsnLysTyrAspAsnArgMetSerAlaMetIleProGlu	416
DB	416	CTCATCTACCCCTATGAACAAAACAAGTGGGACACCGCACATCGTGGTTCACGCCAGAG	475
QY	417	IleAspGluAspValIleTyrrilleIleGlyLeuLeuGlnSerAla-----	431
DB	476	-----GAGGACGTGTTTACCTTTGTGGCGTGTGCGGTTCAGTTTGATTCGGAGAC	529
QY	432	ThrProLysAspLeuProGluValGluSerValAsnGluLysIleIleArgPheCysLys	451
DB	530	GAGGCCACAGATTGGAGATCTCAGCAATCAGAACCGTCAGATCTCAGATTTCTGTGAC	589
QY	452	AspSerGlyIleLysIleLysGlnTyrrieuMethisTyrThrSerLysGluAspTrpIle	471
DB	590	GATGCTGGGATCAAGGTGAACAGTATCTGCCTCACTACACCGCAAGAGAGACTGGGTG	649
QY	472	GluHisPheGly----SerLysTyrAspAspPheSerLysArgLysAspLeuPheAspPro	490
DB	650	GACCACCTTTGTGTATGATCAAGTGGACTTTTGTTCGTATGATGAAAGATCGACTTCGACCC	709
QY	491	LysLysLeuLeuSerProGlyGlnAspilePhe	501
DB	710	CGGCGTATCTAGCCACCGGCAGCGCATTTT	742

RESULT B  
CB922686

378	TTTCGATTATGTTGAAGGATTTCTTATTGTTGATGAAGGACTGATCAATAAATCGGAGATCA	437
276	SerPheProProSerAspGlnSerLysValAlaAspLeuValLysGlnHisGly--	294
438	TTTCTTTCTTCTCTAGGATCTCTGAAGATAGTTCAATTAAACGGAGGAGGAGAG	497
295	IIeIIeTyValLeuGluValAlaLysTyTyTyAspAspProAsnLeuProIleLeSer	314
498	GTTCTTTACTGCTTAGAATACCAAGAATTACGACGATTTCTACTGCTAGCTTAGTGAT	557
315	LysValIleAspThrLeuThrLysThrLysLeuSerTyLeuProGlyPheIleSerMethis	334
558	CAGGAAGTGGATGGCATTTGTTGAAGAACTAAGATTATACCAAACTATTATTCACACT	617
335	AspValAlaTyT-PheAspPheLeuAsnArgValHisValGluGluAsnLysLeuArgSer	354
618	GACCTGCCATATGTAGACTTTCTAGACCGAGTTTCAAGAGCGAAGACTGAAGCTTAGGGGC	677
355	LeuGlyLeuTrpGluLeuProHisProTrpLeuAsnLeuTyTyValProLysSerArgile	374
678	AAAGGGCTTTGGAGGTGCCACACCCCTGGCTCCACCTGTTTGTGCGAAGCTCGCGCAT	737
375	LeuAspPheHisAsnGlyValValLysAspIleLeuLeuLysGlnLysSerAlaSerGly	394
738	ATTGAATTGCACCGGATATCCGTTGGATGTTGGGCACAGACTAGTGGGCCATCACAT	797
395	Leu 395	
798	CTA 800	
RESULT 7		
CF209921		
LOCUS	CF209921	
DEFINITION	809 bp mRNA linear EST 01-AUG-2003	
ACCESSION	CAB20005_IVb_Fb_G06 Cabernet Sauvignon Flower Bloom - CAB2 Vitis	
VERSION	vinifera cDNA clone CAB20005_IVb_Fb_G06 5', mRNA sequence.	
KEYWORDS	CF209921	
SOURCE	CF209921.1 GI:33404294	
ORGANISM	Vitis vinifera	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.	
AUTHORS	1 (bases 1 to 809) Goes da Silva, F., Iandolo, A., Lim, H., Baek, J., Jones, K. and Cook, D.	
TITLE	Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages	
JOURNAL	Unpublished (2003)	
COMMENT	Contact: Douglas Cook, PhD CAES Genome Facility UC Davis, Plant Pathology One Shields Ave., Davis, CA 95616, USA Tel: 530 754 6561 Fax: 530 754 6617 Email: drcook@ucdavis.edu Seq primer: ACGTACCGGACATATGCC. Location/Qualifiers	
FEATURES	1..809	
source	/organism="Vitis vinifera"	
	/mol_type="mRNA"	
	/cultivar="Cabernet Sauvignon"	
	/db_xref="taxon:29760"	
	/clones="CAB20005_IVb_Fb_G06"	
	/sex="Hermaphrodite"	
	/dev_stage="Bloom"	
	/clone_lib="Cabernet Sauvignon Flower Bloom - CAB2"	
	/note="Organ: Flower - Bloom; Vector: pDNR; Site 1: Sfil; Site 2: Sfil; CAB2 is a cDNA library of Vitis vinifera cv. 'Cabernet Sauvignon', Clone 8 berries. Samples were collected at full bloom (80 to 100% flowers showing dehiscence of calyptras or caps and anthers fully extended). Sampled vines were located at the University of	



LOCUS CB922686 626 bp mRNA linear EST 25-APR-2003  
DEFINITION VVD086G02.356005 An expressed sequence tag database for abiotic stressed berries of Vitis vinifera var. Chardonnay  
CDNA clone VVD086G02.5, mRNA sequence.  
ACCESSION CB922686  
VERSION CB922686.1 GI:30137348  
SOURCE EST.  
ORGANISM Vitis vinifera  
Vitis vinifera  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Vitaceae; Vitis.  
REFERENCE 1 (bases 1 to 626)  
Cushman, J.C.  
An expressed sequence tag database for abiotic stressed berries of Vitis vinifera var. Chardonnay  
Unpublished (2002)  
Contact: Cushman JC  
Department of Biochemistry  
University of Nevada  
MS200, Reno, NV 89557-0014, USA  
Tel: 775-784-1918  
Fax: 775-784-1650  
Email: jcushman@unr.edu  
PCR Primers  
FORWARD: T3 20mer  
BACKWARD: T7 21mer (backward)  
Plate: 086 row: G column: 02  
Seq primer: T3 20mer  
High quality sequence stop: 626.  
FEATURES  
source  
1..626  
/organism="Vitis vinifera"  
/mol\_type="mRNA"  
/db\_xref="taxon:29760"  
/clone="VVD086G02"  
/tissue\_type="berries"  
/dev\_stage="mixed; 8, 9, 11, 13, 15, 16 weeks daf"  
/clone\_lib="An expressed sequence tag database for abiotic stressed berries of Vitis vinifera var. Chardonnay"  
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site\_1: EcoRI; Site\_2: XhoI"  
ORIGIN  
Alignment Scores:  
Pred. No.: 2,51e-61 Length: 626  
Score: 598.00 Matches: 112  
Percent Similarity: 73.79% Conservative: 40  
Best Local Similarity: 54.37% Mismatches: 46  
Query Match: 23.04% Indels: 8  
DB: 14 Gaps: 3  
US-10-014-101-4 (1-501) x CB922686 (1-626)  
QY 107 AsnMetThrCysIleThrAspValValSerLysAspLys-----LysTVrAla 123  
DB 16 AACTGCAGCTGTGGAGTGAATCAGGGTTTACCAGAAATCCGATATGGGGTTCCTATGCT 75  
QY 124 AspValAlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyVal 143  
DB 76 GATGTCGGGGGTGAGCAGCAATGATGATGATGATGATGATGATGATGATGATGATGAT 135  
QY 144 SerProValSerTrpThrAspThrLeuHisIleThrValGlyThrLeuSerAsnGly 163  
DB 136 GCACCACTGTCGTGGAGTACTATTTGTACCTAACCAATTTGGTGTGATCTCTCTAATGCC 195  
QY 164 GlyIleGlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAsp 183  
DB 196 GGAATTAGCCGCCAGACATTCGCCCATGGTCCCTCAGATCAGCAACGTCATGAAATGGAT 255  
QY 184 ValIleThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPhe 203  
DB 256 GTTCTTACTGTAAGGGGAACCTGTGACTGTGTTCACAGACACAAACCTGTGAGCTGTTT 315

QY 204 TyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeu 223  
DB 316 TTTCGGCTTCTAGAGGCTCTCGGCGAGTTTGGGATTATATAACAGAGCAAGGATCGCTCTA 375  
QY 224 AspHisAlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPhe 243  
DB 376 GAACCGCACCAAGAGAGTAAATATGATACAGATGCTTTACGATGATGATCTCCACATTT 435  
QY 244 ThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspThrLeuGlu 263  
DB 436 TCTAGAGACCAAGACATTTGATTTCATCAAT-----GGACTGGACTATTGGAA 486  
QY 264 GlyGlnIlePheLeuSerAsnGlyValValAspThr-----SerPhePheProSer 281  
DB 487 GGTTCATCTCCCAAGAAATAGTCTCTCTAATAGTGGAGATCTCTTTCTCACCTCT 546  
QY 282 AspGlnSerLysValAlaAspLeuValLysGlnHisGlyIleIleThrValLeuGluVal 301  
DB 547 GATATACCCGAGATATCTTCACTAATATCCAGATGGCATCATCTACTGCTTNGATG 606  
QY 302 AlalysTrpTrpAspAsp 307  
DB 607 GTCAAGTATTACGATGAA 624  
RESULT 9  
BZ078445 792 bp DNA linear GSS 10-OCT-2002  
LOCUS 11f25a09.g1 B.oleracea002 Brassica oleracea genomic, genomic survey  
DEFINITION sequence.  
ACCESSION BZ078445  
VERSION BZ078445.1 GI:23702365  
KEYWORDS GSS.  
SOURCE Brassica oleracea  
ORGANISM Brassica oleracea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Brassicales; Brassicaceae; Brassica.  
REFERENCE 1 (bases 1 to 792)  
AUTHORS Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.  
Whole genome shotgun reads from Brassica oleracea  
Unpublished (2002)  
Contact: Richard K. Wilson  
Genome Sequencing Center  
Washington University School of Medicine  
Email: submissions@watson.wustl.edu  
Plate: 11f25 row: a column: 09  
Seq primer: -28RppOT reverse  
Class: Shotgun  
High quality sequence start: 12  
High quality sequence stop: 551.  
FEATURES  
source  
1..792  
/organism="Brassica oleracea"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:3712"  
/clone\_lib="B.oleracea002"  
/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T01000H3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."  
ORIGIN  
Alignment Scores:  
Pred. No.: 1.9e-59 Length: 792  
Score: 584.00 Matches: 120  
Percent Similarity: 81.99% Conservative: 12  
Best Local Similarity: 74.53% Mismatches: 21  
Query Match: 22.50% Indels: 8

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DB: 28 Gaps: 2
US-10-014-101-4 (1-501) x BZ078445 (1-792)
QY 1 MetAlaasnLeuArgLeuMetIleThrLeuIleThrValLeuMet----- 15
Db 495 ATGGCTGATCTTCTCTAATGATAACTTAATGACGGTTCGTGATTATTACTTCCAAGC 436
QY 16 IleThrLysSerSerAsnGlyLleLysLleAspLeuProLysSerLysLeuAsnLeuThrLeu 35
Db 435 TGTATCAAAATCGTCA-----GAGATTATTCTACCCAAATCGTTAAACCTCACCCCTC 385
QY 36 SerThrAspProSerIleLleSerAlaAlaSerHisAspPheGlyAsnIleThrVal 55
Db 384 CTAACCGATCTTCCGCCATCTCCGCCCTCTCACGATTGTTGGAACATCACTACCGTG 325
QY 56 ThrProGlyValLleCysProSerSerThrAlaAspIleSerArgLeuGlnThr 75
Db 324 ATACCCGGTGGCGTGTCTGCCCTCTCTCCCGCTGAGATATCCCGTCTCTCGCTAC 265
QY 76 AlaAlaAsnGlyLysSerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsn 95
Db 264 GCCTCAACGGAGAAGAAGTTCGAAGTGGAGCTCGGGCCCAAGGCCACTCTCTTGAAG 205
QY 96 GlyGlnAlaSerValSerGlyGlyValLleValAsnMetThrCysIleThrAspValVal 115
Db 204 GGTCAAGCAGCAGCTCTCAACGGAGTAATCGTCAACATGACGCTGTCTCGCTGGCGTAGTG 145
QY 116 ValSerLysAspLysLysValAlaAspValAlaAlaGlyThrLeuTrpValAspValLeu 135
Db 144 ATTTCAGATCAATGAAGTATGCTGACGTGGCGGTGGAGACGTTATGGGTGATGTCG 85
QY 136 LysLysThrAlaGlyLysGlyValSerProValSerTrpThrAspTyrLeuHisIleThr 155
Db 84 AAAAATACGGCGGAGAAAGCGTTTCGCCGTTTCTTGGACGGATTATTTCGATGTAGA 25
QY 156 Val 156
Db 24 ATT 22

RESULT 10
CG289653
LOCUS CGWFK30TV ZM 0.7-1.5 KB Zea mays genomic clone ZM566F12,
DEFINITION genomic survey sequence.
ACCESSION CG289653
VERSION CG289653.1 GI:34203867
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 969)
AUTHORS Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
JOURNAL Other_GSSs: CGWFK30TH
COMMENT Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: sheared ends.
FEATURES
Location/Qualifiers
source 1..969
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/strain="B73"

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/db xref="taxon:4577"
/clone_lib="ZM566F12"
/clone_lib="ZM 0.7-1.5 KB"
/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Alignment Scores: 3.58e-59 Length: 969
Pred. No.: 583.00 Matches: 132
Score: 54.63% Conservative: 45
Best Local Similarity: 40.74% Mismatches: 70
Query Match: 22.46% Indels: 78
DB: 29 Gaps: 7

US-10-014-101-4 (1-501) x CG289653 (1-969)
QY 173 GlyProLeuValSerAsnValLeuGluLeuAspValIleThrGly-Lys----- 188
Db 2 GGTCCGAGATCGCAACAGTGCATGAACCTCGATGTCGTACAGGTATCGATCGATCGATG 61
QY 188 ----- 188
Db 62 GTTACACTCCTGTGATAATTACATAGCAGCTAATCACACAGTAATGCTAATAATAGTT 121
QY 189 -----GlyGluMetLeuThrCysSerArgGlnLeuAs 199
Db 122 TATACATGTCATGAACAATGCAGGCACAGGTGAGATGTCGATGTCCTCCATGACCGTAA 181
QY 199 nProGluLeuPheTyrGlyValLeuGlyGlnPheGlyIleIleThrArgAl 219
Db 182 CTCGACCTGTTCTATGCGAGCTTAGCGCGGTAGGCAATTCCGGGTCTATACACAGGC 241
QY 219 aArgIleValLeuAspHisAlaProLysA:GAlaLysTTPheArgMetLeuTyrSerAs 239
Db 242 ACGGATCGGCTTTCAGCGCGGCCCAAGAGGGTGGCTGGTTCGACTTGCCTACACCGA 301
QY 239 pPheThrThrPheThrLysAspGlnGluArgLeuIleSer---MetAlaAsnAspIleG 258
Db 302 CGTGGCTACTTTTCCACCAAGGATCAGAGATTTCTCTATTCGACCGGACTAGCCAGTCGG 361
QY 258 yValAspTyrLeuGluGlyGlnIlePheLeuSerAsnGlyValValAsp----- 274
Db 362 GTTCGACTACGTCGAAGGCCAGGTCCAGCTCAACCGGTCTTGTGTGAAGTCCCAATC 421
QY 275 -ThrSerPhePheProSerAspGlnSerLysValAlaAspLeuValLysGlnHisG 294
Db 422 AACACCTTCTTCTCCGGCGCGGATCTTGTAGACTTGTGGACTCGCTCGCGTGGAGACCGG 481
QY 294 y-----IleIleTyrValLeuGluValAlaLysTyrTyrAspAspProAsnLeuProI 312
Db 482 ACCTACTCAATATACTACATCGAAGGCCCATGCTACTACACCGAGGACACCGGCATATC 541
QY 312 eIleSerLysVal-----IleAspThrLeuThrLysThr----- 323
Db 542 TGTGACAAAGGTACAGATCAGATCAGCTTGAACACACACACACACAACTTTATTATTGCTT 601
QY 323 ----- 323
Db 602 TCAATGCTTTGGACAAAGGAACTCATTCGTTGCTATATGATCGTTGCAGAAAT 661
QY 324 -----LeuSerTyrLeuProGlyPheIleSerMetHisAspValAl 337
Db 662 GAAAGGCACTCTCGATCAGCTGAGCTCGAGCCAGGGTTTCCGTTCCACCAAGGACGTGAC 721
QY 337 aTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeuGlyLe 357
Db 722 GTTCGTGCGATTTCTTCGACCGGTTGCGGAGAGAGAGGGTGTCTCGGTACGCGCGGC 781
QY 357 uTrpGluLeuProHisProTrpLeuAsnLeuTyrValProLysSerArgIleLeuAspPh 377
Db 782 GTGGGAGGTACACACACCATCGCTGAATCTCTTCGTCGCCGCGTCCGCGCATCTCTCGATT 841

```



[illegible]

library was prepared using the Stratagene pBluescript II  
DSK(+) library construction kit. Complementary DNA was  
synthesized from mRNA using a primer consisting of a  
poly(dT) sequence with an XhoI restriction site. EcoRI  
adaptors were ligated to the blunt-ended cDNA fragments  
followed by XhoI digestion. The cDNA insert is protected  
from XhoI digestion via methylation during first strand  
synthesis. The cDNA fragments were directionally cloned  
into the EcoRI-XhoI restriction site of the pBluescript  
vector. The ligated cDNA fragments were transformed into  
E. coli strain DH10B host cells. Plants were inoculated  
by Shuxian Li (Glen Hartman lab, University of Illinois,  
University of Illinois) and Steve Clough (Lila Vockin lab,  
University of Illinois). "

University Of Arkansas

ALIGNMENT SCORES:  
Unaligned Length: 582  
Score: 560.00 Matches: 582  
Percent Similarity: 72.68% Conservative: 37  
Best Local Similarity: 55.15% Mismatches: 44  
Query Match: 21.57% Indels: 6  
DB: 12 Gaps: 2

US-10-014-101-4 (1-501) x BM143498 (1-582)

QY	187	GlyLysGlyLeuMetLeuThrCysSerArgInLeuAsnProGluLeuPheTyrGlyVal	206
DB	1	GGAAAAGGAGAGTTCTTAACATGTCTTCACAGAAACTTGAGTATTCCACGCGGTT	60
QY	207	LeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaAargileValLeuAspHisAla	226
DB	61	CITTGAGGCTTGGACAANTTGGAGTTATAGCAAGGCCAGAAATGCTCTTGAGCCAGCA	120
QY	227	ProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLysAsp	246
DB	121	CCCCAAAGGGTTAAGTGGGTACAGACTACTTATAGTGACTTTCTCTTTATCCAAAGAC	180
QY	247	GlnGluArgLeuIleSerMet-----AlaAsnAspileGlyValaspTyrLeuGlu	263
DB	181	CAGAACGATTATCTCATCTCAATGAAGAAACAAAGAACCATTGGATTTCGGAA	240
QY	264	GlyGlnIlePheLeuSerAsnGlyValValasp-----ThrSerPhePheProPro	280
DB	241	GGGATGCTGTAATGAACCAAGGCCCATAAATAATTGGAGATCCCTCTTTCTTCCTCTTA	300
QY	281	SerAspGlnSerLysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGlu	300
DB	301	TCTGACCATCCCAGATAGCTCTCTTTAATAACTGAACATAGCATCTCTACTGCTTGA	360
QY	301	ValAlaLysTyrTyrAspAspProAsnLeuProIleIleSerLysValIleAspThrLeu	320
DB	361	GTGGCTAAATATTATGACGAACAAACCGAGTTAAATGTGGACAGGAAATGAGTTTTG	420
QY	321	ThrLysThrLeuSerTyrLeuProGlyPheIleSerMethHisAspValAlaTyrPheAsp	340
DB	421	CTCCAAGGACTAGCCTATATCCCTGGATTTAATTTATGAGAAAAATGTCTGCTAGTTGAG	480
QY	341	PheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeu	360
DB	481	TTCTTGAATAGGCTCGGAAGTGGAGATTTGAACTTCAGTGCACAGACCTGTGGGAAGTT	540
QY	361	ProHisProTrpLeuAsnLeuTyrValProLysSerArgile	374
DB	541	CCTCACCGCTGGCTTAATTTGTTATACCAAATACTCAAAATC	582

RESULT 14  
LOCUS BE330968 linear EST 04-DEC-2001  
DEFINITION B091901.y1 Gm-cl041 Glycine max CDNA clone GENOME SYSTEMS CLONE ID: Gm-cl041-745 5' similar to Tr:Q9ZUP1 Q9ZUP1 PUTATIVE CYTOKININ OXIDASE ; mRNA sequence.  
ACCESSION BE330968

```

VERSION      BE330968.1  GI:9204744
KEYWORDS
SOURCE      Glycine max (soybean)
ORGANISM    Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1 (bases 1 to 635)
AUTHORS    Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Corvett, V.,
            Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
            Beck, C., Wylie, F., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
            Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
            Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
            McCann, R., Waterston, R. and Wilson, R.
            Public Soybean EST Project
            Published (1999)
            Contact: Shoemaker R/Public Soybean EST Project
            Public Soybean EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available through: ResGen, Invitrogen Corp. 2130
            South Memorial Parkway Hunttsville, AL 35801 For further information
            call: (800)-533-4363 or contact via email: ccu@resgen.com
            High quality sequence stop: 423.
FEATURES             Location/Qualifiers
     1..635
         /organism="Glycine max"
         /mol_type="mRNA"
         /db_xref="taxon:3847"
         /clone="GENOME SYSTEMS CLONE ID: Gm-cl041-745"
         /tissue_type="Senescing leaves, mature plant, greenhouse
         grown"
         /lab_host="DH10B"
         /clone_lib="Gm-cl041"
         /note="vector: p773Pac (Pharmacia); Site 1: EcoRI;
         Site 2: HindIII; This library was constructed from mRNA
         isolated from senescing leaf tissue of mature greenhouse
         grown plants of the cultivar Williams. Complementary DNA
         was synthesized from mRNA using a 3' anchored poly(dT)
         primer. EcoRI adapters were ligated to the blunt-ended
         cDNA fragments followed by digestion with EcoRI and
         HindIII. The cDNA fragments were directionally cloned
         into the EcoRI-HindIII restriction site of the p773-Pac
         vector. The ligated cDNA fragments were transformed into
         DH10B host cells. This library was constructed by Dr.
         Randy Shoemaker."

```

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ORIGIN
Alignment Scores:
Pred. No.: 2,42e-56 Length: 635
Score: 557.00 Matches: 110
Percent Similarity: 69.19% Conservative: 36
Best Local Similarity: 52.13% Mismatches: 59
Query Match: 21.46% Indels: 6
DB: 10 Gaps: 2

US-10-014-101-4 (1-501) x BE330968 (1-635)

Qy 171 ArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThrGlyIysGlyGlu 190
      : : : : :
Db 3 CGTTATGACCTCAAAACAGCAACGTTTCATGAAATGGATGTCATCACTGGAAAGAGAG 62

Qy 191 MetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyGlyValLeuGlyIysLeu 210
      : : : : :
Db 63 TTCGTAACCTGCTCTTCACAGAGAACTTCGAGTTATTCACGCGGTTCTTGAGGCCTA 122

Qy 211 GlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHisAlaProIysArgAla 230
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Db 123 GGCCAATTTGAGTTATAGCAAGCGGCAGAAATAGCACTTGAGCCAGCCCCCAAGAGGTT 182

```

```

QY 231 LysTTPPhArgMetLeuTyrSerAspPheThrThrPheThrLysAspGlnGluArgLeu 250
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Db 183 AAGTGGTGCAGACTACTTTATAGTCACTTTTGTCTTTTACCAAGATCAGGAACGATTA 242
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QY 251 IleSerMet-----AlaAsnAspIleGlyValAspTyrLeuGluGlyGlnIlePhe 267
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Db 243 AICTCAATCAATGGAAGAAACAAAGACGATGATTTCTGGAAGGGATGCTGCTA 302
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QY 268 LeuSerAsnGlyValValAsp-----ThrSerPhePheProPheSerAspGlnSer 284
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 303 ATGACCAAGGCCCAATAAATATGAGATCCTCTTTCTCCCTATCTGACATCCC 362
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QY 285 LysValAlaAspLeuValLysGlnHisGlyIleTyrValLeuGluValAlaLysTyr 304
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 305 TyrAspAspProAsnLeuProIleIleSerLysValIleAspThrLeuThrLysThrLeu 324
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Db 423 TATGACCAACAAACCGAGATAAATGAGCAATGAAATTCAGATTTTGTCTACAGGACTA 482
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Db 483 GCTATATCCTCTGTATATATATGAGAAAAGCTGTCAATGATGAGTTCTTGATAGG 542
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 345 ValHisValGluGlnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrp 364
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QY 365 LeuAsnLeuTyrValProLysSerArgIleLeu 375
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Db 603 CTTAATATGATATACCAAGTCTCGAATCTTG 635

RESULT 15
BU084470
LOCUS
DEFINITION
    BU084470.1 Gm-c1049 Glycine max cDNA clone SOYBEAN CLONE ID:
    sar19h02.y1 similar to TR:Q9SU77 Q9SU77 CYTOKININ OXIDASE-LIKE
    PROTEIN.; mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
    ORGANISM
        Glycine max (soybean)
        Glycine max
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
        rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
        Glycine.
REFERENCE
    1 (bases 1 to 566)
    Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Corveill, V.,
    Khanna, A., Rolia, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
    Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
    Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
    Schurk, R., Ritter, S., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
    McCann, R., Waterston, R. and Wilson, R.
    Public Soybean EST Project
    Unpublished (1999)
    Contact: Shoemaker R/Public Soybean EST Project
    Public Soybean EST Project
    Washington University School of Medicine
    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
    Tel: 314 286 1800
    Fax: 314 286 1810
    Email: est@watson.wustl.edu
    This clone is available through: ResGen, Invitrogen Corp. 2130
    South Memorial Parkway Huntsville, AL 35801 For further information
    call: (800)-533-4363 or contact: cu@resgen.com web site:
    www.resgen.com
    Seq primer: -40RP from Gibco
    High quality sequence stop: 421.
    Location/Qualifiers
    1..566
    /organism="Glycine max"
FEATURES
    source

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/mol_type="mRNA"
/db_xref="taxon:3847"
/clone="SOYBEAN CLONE ID: Gm-c1049-7252"
/tissue_type="whole seedlings of greenhouse grown plants"
/dev_stage="3 week old"
/lab_host="DH10B"
/clone_lib="Gm-c1049"
/notes="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The Clark NIL was constructed and seed was provided
by Dr. J. Specht, University of Nebraska (Shoemaker and
Specht, 1995). The cDNA library was constructed from mRNA
isolated from whole seedlings of 3 week old greenhouse
grown plants. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site and a 3' anchor. EcoRI adapters were
ligated to the blunt-ended cDNA fragments followed by XhoI
digestion. The cDNA fragments were directionally cloned
into the EcoRI-XhoI restriction site of the pBluescript
vector. The ligated cDNA fragments were transformed into
DH10B host cells (GibcoBRL). The library was constructed
in cooperation with Dr. Paul Keim's laboratory at Northern
Arizona University."

```

## ORIGIN

```

Alignment Scores:
Pred. No.: 3e-56 Length: 566
Score: 555.50 Matches: 109
Percent Similarity: 72.73% Conservative: 27
Best Local Similarity: 58.29% Mismatches: 42
Query Match: 21.40% Indels: 9
DB: 13 Gaps: 3

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US-10-014-101-4 (1-501) x BU084470 (1-566)

```

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Db 4 GTCTCTAAGGACCCCTTTGATGGGTCACCTATGCGGATGTTGGAGGGGAACAACCTCGGATT 63
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QY 133 AspValLeuLysThrAlaGluLysGlyValSerProValSerThrAspTyrLeu 152
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QY 153 HisIleThrValGlyGlyThrLeuSerAsnGlyGlyIleGlyGlyGlnValPheArgAsn 172
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QY 173 GlyProLeuValSerAsnValLeuGluLeuAspValIleThrGlyLysGlyGluMetLeu 192
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QY 213 PheGlyIleIleThrArgAlaArgIleValLeuAspHisAlaProLysArgAlaLysTrp 232
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QY 233 PheArgMetLeuTyrSerAspPheThrThrPheThrLysAspGlnGluArgLeuIleSer 252
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    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 270 AsnGlyValValAsp-----ThrSerPhePheProPheSerAspGlnSerLysVal 286
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QY 287 AlaAspLeuValLysGlnHis 293
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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Search completed: April 7, 2004, 10:37:47  
Job time : 3800 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 7, 2004, 09:35:37 ; Search time 1742 Seconds  
(without alignments)  
1077.855 Million call updates/sec

Title: US-10-014-101-4  
Perfect score: 2596  
Sequence: 1 MANLEMITLITVLMTKSS.....SKRKDLFPKKLLSPGQDIF 501

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2470632 seqs, 1873875610 residues

Total number of hits satisfying chosen parameters: 4941264

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters: -DEV=xlh

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-DB=Published Applications NA -QMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -NATRIX=biosum62  
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR NORM=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US10014101.cgn2\_1\_1\_57/runat\_05042004\_154156\_8673  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq\*
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- 17: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq\*
- 18: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	2596	100.0	1506	12	US-10-311-453-26	Sequence 26, Appl
2	2596	100.0	1506	14	US-10-014-101-26	Sequence 26, Appl
3	2588	99.7	1506	14	US-10-326-184-8	Sequence 8, Appl
4	2266.5	85.6	2991	12	US-10-311-453-3	Sequence 3, Appl
5	2266.5	85.6	2991	14	US-10-014-101-3	Sequence 3, Appl
6	1822	70.2	1575	9	US-09-938-842A-2089	Sequence 2089, Ap
7	1822	70.2	1575	11	US-09-938-842A-2089	Sequence 2089, Ap
8	1822	70.2	1575	12	US-10-311-453-28	Sequence 28, Appl
9	1822	70.2	1575	14	US-10-014-101-28	Sequence 28, Appl
10	1822	70.2	1655	14	US-10-326-184-20	Sequence 20, Appl
11	1820	70.1	1575	14	US-10-326-184-10	Sequence 10, Appl
12	1539.5	59.3	2782	12	US-10-311-453-7	Sequence 7, Appl
13	1539.5	59.3	2782	14	US-10-014-101-7	Sequence 7, Appl
14	1292	49.8	1572	12	US-10-311-453-27	Sequence 27, Appl
15	1292	49.8	1572	14	US-10-014-101-27	Sequence 27, Appl
16	1292	49.8	1572	14	US-10-326-184-9	Sequence 9, Appl
17	1184	45.6	1611	12	US-10-311-453-29	Sequence 29, Appl
18	1184	45.6	1611	14	US-10-014-101-29	Sequence 29, Appl
19	1184	45.6	1620	12	US-10-311-453-34	Sequence 34, Appl
20	1184	45.6	1620	14	US-10-014-101-34	Sequence 34, Appl
21	1178	45.4	1623	14	US-10-326-184-12	Sequence 12, Appl
22	1060	40.8	1857	14	US-10-326-184-22	Sequence 22, Appl
23	1056.5	40.7	1728	12	US-10-311-453-25	Sequence 25, Appl
24	1056.5	40.7	1728	14	US-10-014-101-25	Sequence 25, Appl
25	1016	39.1	6732	14	US-10-326-184-1	Sequence 1, Appl
26	993	38.3	1515	12	US-10-311-453-30	Sequence 30, Appl
27	993	38.3	1515	14	US-10-014-101-30	Sequence 30, Appl
28	961	37.0	1575	14	US-10-326-184-11	Sequence 11, Appl
29	961	37.0	1873	14	US-10-326-184-21	Sequence 21, Appl
30	930	35.8	2235	12	US-10-424-599-78119	Sequence 78119, A
31	928.5	35.8	1318	12	US-10-424-599-9802	Sequence 9802, Ap
32	920.5	35.5	1936	12	US-10-311-453-11	Sequence 11, Appl
33	920.5	35.5	1936	14	US-10-014-101-11	Sequence 11, Appl
34	920.5	35.5	2805	12	US-10-311-453-9	Sequence 9, Appl
35	920.5	35.5	2805	14	US-10-014-101-9	Sequence 9, Appl
36	920.5	35.5	2814	12	US-10-311-453-33	Sequence 33, Appl
37	920.5	35.5	2814	14	US-10-014-101-33	Sequence 33, Appl
38	905.5	34.9	3302	12	US-10-311-453-5	Sequence 5, Appl
39	905.5	34.9	3302	14	US-10-014-101-5	Sequence 5, Appl
40	903.5	34.8	2236	12	US-10-311-453-1	Sequence 1, Appl
41	903.5	34.8	2236	14	US-10-014-101-1	Sequence 1, Appl
42	818.5	31.5	1257	12	US-10-425-114-3248	Sequence 3248, Ap
43	805.5	31.0	1384	12	US-10-425-114-8799	Sequence 8799, Ap
44	745	28.7	1141	12	US-10-425-114-10886	Sequence 10886, A
45	745	28.7	1142	12	US-10-424-599-1725	Sequence 1725, Ap

## ALIGNMENTS

RESULT 1  
US-10-311-453-26  
; Sequence 26, Application US/10311453  
; Publication No. US20040031073A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmilling, Thomas  
; APPLICANT: Werner, Tom s  
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and  
; TITLE OF INVENTION: physiology  
; FILE REFERENCE: 1226-4  
; CURRENT APPLICATION NUMBER: US/10/311,453  
; CURRENT FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: EP 00870132.8  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: US 60/258,415  
; PRIOR FILING DATE: 2000-12-27  
; PRIOR APPLICATION NUMBER: EP 01870053.4  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 1506  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana

US-10-311-453-26

Alignment Scores:

Pred. No.: 2,97e-308 Length: 1506  
Score: 2596.00 Matches: 501  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 12 Gaps: 0

US-10-014-101-4 (1-501) x US-10-311-453-26 (1-1506)

QY 1 MetAlaAsnLeuArgLeuMetIleThrLeuValLeuMetIleThrLysSerSer 20  
DB 1 ATGGCTAAATCTCGTTTAATGATCACTTAAATCAGCGTTTAAATGATCACCATAATCA 60  
QY 21 AsnGlyLysIleAspLeuProLysSerLeuAsnLeuThrLysSerThrAspProSer 40  
DB 61 AACGGTATTAAATGATTACCTAAATCCCTTAACTCACCCTCTCTACCGATCTCTCC 120  
QY 41 IleIleSerAlaAlaSerHisAspPheGlyAsnIleThrValThrProGlyVal 60  
DB 121 ATCATCTCCGACGCTCTCATGACTTCGGAACATACACCCGTCGACCCCGCGCGTA 180  
QY 61 IleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGlyLys 80  
DB 181 ATCTGCCCTCCCTCCACCGCTGATATCTCTCGTCTCTCCATPACCCCGCAACCGGAAA 240  
QY 81 SerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal 100  
DB 241 AGTACATCTCCAGTAGCGGCTCGGCCAAGGCCACTCTCTTAACCGCCAGCCCTCGTC 300  
QY 101 SerGlyGlyValIleValAsnMetThrCysIleThrAspValValValSerLysAspLys 120  
DB 301 TCCGGCGGAGTAATCGTCAACATGATGATGATGATGATGATGATGATGATGATGATG 360  
QY 121 LysTyrAlaAspValAlaAlaGlyThrLeuTyrValAspValLeuLysLysThrAlaGlu 140  
DB 361 AAGTACGCTGCGTGGCGCGCGGACGTTATGGTGGATGCTTAAGAGACGGCGGAG 420  
QY 141 LysGlyValSerProValSerThrAspTyrLeuHisIleThrValGlyGlyThrLeu 160  
DB 421 AAAGGGGTGTCGCGGTTCTTGACGCGATTATTGTCATATAACCGTCGGAGAACGTTG 480  
QY 161 SerAsnGlyGlyIleGlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeu 180  
DB 481 TCGAATGGTGAATGGTGGTCAAGTGTTCGAAACGCTCTCTTGTAGTAACTGCTT 540  
QY 181 GluLeuAspValIleThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnPro 200  
DB 541 GAAATGGACGTTATTACTGGAAAGGTGAAATGTTGACATGCTCGGCACAGCTAAACCCA 600  
QY 201 GluLeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleThrArgAlaArg 220  
DB 601 GAAATGTTCTATGAGGTGTAGGAGGTGTGGTCAATTTGGAATTAACGAGACGAGA 660  
QY 221 IleValLeuAspHisAlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPhe 240  
DB 661 ATTGTTTGGACCATGCACCTAAACGGGCCAAATGTTTCGGATGCTCTACAGTGATTC 720  
QY 241 ThrThrPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAsp 260  
DB 721 ACAACTTTTACAAAGGACCAAGACGTTGATATCAATGGCAACAGATATGGAGTCGAC 780  
QY 261 TyrLeuGluGlyGlnIlePheLeuSerAsnGlyValValAspThrSerPheProPro 280  
DB 781 TATTAGAGGTCAATATTTCTATCAACCGTGTGCTTGACACCTCTTTTCCACCT 840  
QY 281 SerAspGlnSerLysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGlu 300  
DB 841 TCAGATCAATCTAAGTCGCTGATCTAGTCAAGCAACACGCTATCATCTATGTTCTTGA 900  
QY 301 ValAlaLysTyrTyrAspAspProAsnLeuProIleIleSerLysValIleAspThrLeu 320

DB 901 GTAGCAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTTATTGACACATT 960  
QY 321 ThrLysThrLeuSerTyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAsp 340  
DB 961 ACGAAAAACATTAAAGTTACTTCCCGGTTTCATATCAATGCACGACGTGGCTACTTCGAT 1020  
QY 341 PheLeuAsnArgValHisValGluGluAsnLysLeuArgSerLeuGlyLeuTyrPheGluLeu 360  
DB 1021 TTTCTTGAACCGTGTACATGTCGAAGAAATAAACTCAGATCTTTGGGATTATGGAACTT 1080  
QY 361 ProHisProTrpLeuAsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGly 380  
DB 1081 CCTCATCTTGGCTTAACTTACCTTACGTTCTTAAATCTCGGATCTTCGATTTTCAACGGT 1140  
QY 381 ValValLysAspIleLeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrPro 400  
DB 1141 GTTCTCAAGACATTCTTCTTAAGCAAAATCAGTTTCGGGACTCGCTCTTCTATCCA 1200  
QY 401 ThrAsnArgAsnLysTrpAspAsnArgMetSerAlaValIleProGluIleAspGluAsp 420  
DB 1201 ACAAACCGGAATAATGGCAATCGTATGTCGGCGATGATACAGAGATCGATGAAGAT 1260  
QY 421 ValIleTyrIleIleGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGlu 440  
DB 1261 GTTATATATATTCGGACTACTACATCCGCTACCCCAAGGATCTTCCAGAGTGGAG 1320  
QY 441 SerValAsnGluLysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyr 460  
DB 1321 AGCGTTAACGAGAGATAAATTAGGTTTTCGAAGGATTTCAGGTATTAAGTAAAGCAATAT 1380  
QY 461 LeuMetHisTyrThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAsp 480  
DB 1381 CTATGCAATATATAGTAAAGAGATTGGATTGAGCATTTTGGATCAAAATCGGATGAT 1440  
QY 481 PheSerLysArgLysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIle 500  
DB 1441 TTTTTCGAAGAGAGAAAGATCTATTTCATCCCAAGAACTGTTATCTCCAGGCGCAAGCATC 1500  
QY 501 Phe 501  
DB 1501 TTT 1503

RESULT 2

US-10-014-101-26  
; Sequence 26, Application US/10014101  
; Publication No. US20030074698A1  
; GENERAL INFORMATION:  
; APPLICANT: Schuelling, Thomas  
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and  
; TITLE OF INVENTION: physiology  
; FILE REFERENCE: 1195-2  
; CURRENT APPLICATION NUMBER: US/10/014,101  
; CURRENT FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: PC/EP01/06833  
; PRIOR FILING DATE: 2001-06-16  
; PRIOR APPLICATION NUMBER: EP 00870132.8  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: US 60/258,415  
; PRIOR FILING DATE: 2000-12-27  
; PRIOR APPLICATION NUMBER: EP 01870053.4  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 1506  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-014-101-26

Alignment Scores: 2.97e-308 Length: 1506  
Pred. No.:

Score: 2596.00 Matches: 501  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 14 Gaps: 0

US-10-014-101-4 (1-501) x US-10-014-101-26 (1-1506)

QY 1 MetAlaAsnLeuArgLeuMetIleThrLeuIleThrValLeuMetIleThrLysSerSer 20  
DB 1 ATGGCTAATCTCGTTTAAATGATCACTTAAATCAGGGTTTAAATGATCAACCAATATCA 60  
QY 21 AsnGlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSer 40  
DB 61 AACGGTATTAAATGATTTACCTAAATCCCTTAACTCCACCTCTCTACCGATCCCTTCC 120  
QY 41 IleIleSerAlaAlaSerHisAspPheGlyAsnIleThrValThrProGlyGlyVal 60  
DB 121 ATCATCTCGGAGCCTCTCATGACTTCGGAACATAACACCGTGACCCCGCGGGCGTA 180  
QY 61 IleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnThrValAlaAlaAsnGlyLys 80  
DB 181 ATCTGCCCTCTCCACCGCTGATATCTCTCTCTCCCAATACCGCGCAAGCGGAAA 240  
QY 81 SerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal 100  
DB 241 AGTACATCTCCAAAGTAGCGGCTCGTGGCCAAAGCCACTCTCTTAAACGGCCAAAGCTCGGTC 300  
QY 101 SerGlyGlyValIleValAsnMetThrCysIleThrAspValValValSerLysAspLys 120  
DB 301 TCCGGCGGAGTAAATCGTCAACATGACGTATCACTGACGTGGTGTTCCTCAAAAGACAAAG 360  
QY 121 LysTyrAlaAspValAlaAlaGlyThrLeuTyrValAspValLeuLysIleThrAlaGlu 140  
DB 361 AAGTACGCTGAGCTGGCGCGGAGCTTATGGTGGATGTGCTTAAAGACGCGGAG 420  
QY 141 LysGlyValSerProValSerThrThrAspTyrLeuHisIleThrValGlyGlyThrLeu 160  
DB 421 AAAGGGGTGTCGCGGTTCTTGGACGGATTAATTTGCATATAACCGTCGGAGGAACGTTG 480  
QY 161 SerAsnGlyGlyIleGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeu 180  
DB 481 TCGAATGGTGGATTCGTCGAAGTGTTCGAAACGGTCCCTCTTGTAGTAACGTCCTT 540  
QY 181 GluLeuAspValIleThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnPro 200  
DB 541 GAATTGGACGTATTACTGGGAAGGTGAATGTTGACATGCTCGCGACAGCTAAACCCA 600  
QY 201 GluLeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArg 220  
DB 601 GAATTGTTCTATGAGTGTAGGAGGTTTGGGTCAATTTGGAAATTAACGAGAGCCAGA 660  
QY 221 IleValLeuAspHisAlaProLysArgAlaLysTyrPheArgMetLeuTyrSerAspPhe 240  
DB 661 ATTGTTTGGACCATGCACTAACCGGCCAAATGGTTTCGGATGCTCTACAGTGTTC 720  
QY 241 ThrThrPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAsp 260  
DB 721 ACAACTTTTACAAAGGACCAAGAACGTTTGATATCAATGCAACCAACGATATTGGAGTCGAC 780  
QY 261 TyrLeuGlyGlyGlnIlePheLeuSerAsnGlyValValAspThrSerPhePheProPro 280  
DB 781 TATTAGAAGGTCAAAATATTCTATCAACCGGTGCTGTCGACACCTCTTTTCCACCT 840  
QY 281 SerAspGlnSerLysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGlu 300  
DB 841 TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACCGGTATCATCTATGTTCTGAA 900  
QY 301 ValAlaLysTyrTyrAspAspProAsnLeuProIleSerLysValIleAspThrLeu 320  
DB 901 GTAGCCAAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTATTGACATTA 960  
QY 321 ThrLysThrLeuSerTyrLeuProGlyPheIleSerMetHisAspValAlaLysPheAsp 340

DB 961 ACGAAACAAATTAAAGTTACTTCCCGGTTCAATATCATGCAAGCGTGCCTACTTCGAT 1020  
QY 341 PheLeuAsnArgValHisValGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeu 360  
DB 1021 TTCTTGAACCGGTGATCATGTCGAAGAAAATAAATCAGATCTTTGGGATTATGGGAATT 1080  
QY 361 ProHisProTyrLeuAsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGly 380  
DB 1081 CCTCATCTCTGGCTTAACCTCTACGTTCTTAATCTCGGATTTCTCGATTTTATACAGGT 1140  
QY 381 ValValLysAspIleLeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrPro 400  
DB 1141 GTTGTCAAGACATCTCTTCTTAAGCAAAAATCAGCTTCGGGACTCGCTCTCTATCCA 1200  
QY 401 ThrAsnArgAsnLysTyrAspAsnArgMetSerAlaMetIleProGluIleAspGluAsp 420  
DB 1201 ACAAAACGGAATAAATGGGACAATCGTATGTGCGGATGATACACAGAGATCGATGAAGAT 1260  
QY 421 ValIleTyrIleIleGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGlu 440  
DB 1261 GTTATATATATATTCGCACTACTACATCCGTACCCCAAGGATCTTCCAGAGTGGAG 1320  
QY 441 SerValAsnGluLysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyr 460  
DB 1321 AGCGTTAAACGAGAAGATAAATAGGTTTTCAGAGGATTCAGGTATTAAAGATTAAAGCAATAT 1380  
QY 461 LeuMetHisTyrThrSerLysGluAspTyrIleGluHisPheGlySerLysTyrAspAsp 480  
DB 1381 CTAATGATTTATCTAGTAAGAAGATTGGATTGACATTTTGGATCAAAATCGGATGAT 1440  
QY 481 PheSerLysArgLysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIle 500  
DB 1441 TTTTCGAAGAGAAAGATCTATTTGATCCCAAGAAACTGTATCTCCAGGGCAAGACATC 1500  
QY 501 Phe 501  
DB 1501 TTT 1503  
RESULT 3  
US-10-326-184-8  
; Sequence 8, Application US/10326184  
; Publication No. US20030163847A1  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Company  
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C  
; FILE OF INVENTION: OXIDASE 1  
; FILE REFERENCE: MTC6781.1  
; CURRENT APPLICATION NUMBER: US/10/326,184  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: US 60/343,129  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 1506  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-326-184-8  
Alignment Scores:  
Pred. No.: 2,86e-307 Length: 1506  
Score: 2588.00 Matches: 500  
Percent Similarity: 99.80% Conservatives: 0  
Best Local Similarity: 99.80% Mismatches: 1  
Query Match: 99.65% Indels: 0  
DB: 14 Gaps: 0  
US-10-014-101-4 (1-501) x US-10-326-184-8 (1-1506)  
QY 1 MetAlaAsnLeuArgLeuMetIleThrLeuIleThrValLeuMetIleThrLysSerSer 20  
DB 1 ATGGCTAATCTCGTTTAAATGATCACTTAAATCAGGGTTTAAATGATCAACCAATATCA 60



Db 121 ATCATCTCCGAGCCTCTCATGCTTCGGAACAATACCAACCGTGACCCCGCGCGGTA 180  
Qy 61 lIeCysProSerThrAlaAspIleSerArgLeuLeuGlnTyraAlaAsnGlyLys 80  
Db 181 ATCTGCCCTCTCCACCGCTGATCTCTGCTCTCTCCCAATACGCGCAACGGA 240  
Qy 81 SerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal 100  
Db 241 AGTACATCTCCAGTAGCGGCTCGTGCCCAAGGCCACTCTTAAACGGCCAAAGCCTCGTC 300  
Qy 101 SerGlyGlyValIleValAsnMetThrCysIleThrAspValValSerLysAspLys 120  
Db 301 TCCGCGGAGTAATCGTCAACATGACGTGATCATCTGACGTGGTGTTCACAAAGACAAG 360  
Qy 121 LysThrAlaAspValAlaAlaGlyThrLeuThrValAspValLeuLysLysThrAlaGlu 140  
Db 361 AAGTACGCTGACGTGCGCGCGGCGGACGTATGGGTGGATGCTTAAAGAACGCGCGAG 420  
Qy 141 LysGlyValSerProValSerThrPheThrAspTyraLeuHisIleThrValGlyGlyThrLeu 160  
Db 421 AAAGGGGTGTCCCGGTTCTTGACGGATATTGTGCATATAACCGTCGGAGAACGTTG 480  
Qy 161 SerAsnGlyGlyIleGlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeu 180  
Db 481 TCGAATGGTGGAAATGGTGGTCAAGTGTTCGAAACGGTCTCTTGTGTAGTAACTGCTT 540  
Qy 181 GluLeuAspValIleThr----- 186  
Db 541 GAATGGACGTTATTACTGGTAGCGCATCTCTAAACTTTGATGTACATACAAACAACAAA 600  
Qy 186 ----- 186  
Db 601 ACTGTTTTTGTATTATAGTATTTCATTTTTTGTACCATAGGTTTTATGTTTATAGTT 660  
Qy 186 ----- 186  
Db 661 GTGCTAAACTCTTGCCACACACAGTAAGTCTTCGAAACACAAATCGGTAAACGATCTAT 720  
Qy 186 ----- 186  
Db 721 ATGTTTTTTGTACATATTGAATGTTGTTTCATGAGAAATAAGTAATTACATATACACACA 780  
Qy 186 ----- 186  
Db 781 TTTATTGCTGATACATATAATAATAATAAGACAAATTTTCAATTTGGTAGCGTGTAA 840  
Qy 186 ----- 186  
Db 841 TTTGGGATTTTGTAAATGATACATGACATGACGATGATGAGCTTTTCGGTTTCTTA 900  
Qy 186 ----- 186  
Db 901 GATTTGCTGATGATTTCAAATATATCATTTATTTCTTCGAATAAAGAGGTGATATT 960  
Qy 186 ----- 186  
Db 961 TTTAAATAGCAACATTTCCAGATTTTCTTTGAATTTACATTTTAAATTTGTTATTGT 1020  
Qy 187 -----GlyLysGlyGluMetLeuThrCysSerArgG1 197  
Db 1021 TAATATGGAATTTTGAATAAATAATTTTCAGGAAAGGTGAAATGTTGACATGCTCGGACA 1080  
Qy 197 nLeuAsnProGluLeuPheThrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleth 217  
Db 1081 GCTAAACCCAGAAATTTGTTCTATGGAGTGTAGAGGTTTTGGGTCAATTTGGAAATTATAAC 1140  
Qy 217 rArgAlaArgIleValLeuAspHisAlaProLys----- 228  
Db 1141 GAGAGCCAGAATTTGTTGGACCATGCACTTAAACGGGTACGTATCATCATATTTTACCA 1200  
Qy 228 ----- 228

Db 1201 TTTGTTTTAGTCAGCATTTCATTTTTCATTAGTAATTCGGTTTCAATTTCTAAATTTTTT 1260  
Qy 228 ----- 228  
Db 1261 AGTCAATAGAAAATGATCTTTATGTCAGAGCTTGATATTATTAGTGATTTTATTAGATA 1320  
Qy 228 ----- 228  
Db 1321 AAATAAATATAACCTAACGGAATAATTATTTTACTAATCGGATAATGCTGTGATTAATA 1380  
Qy 228 ----- 228  
Db 1381 CATTTTATGATATTACACTAAGAGAGTTAGAGCGTATGATGCATCAAAAAACATGAAGCTTT 1440  
Qy 228 ----- 228  
Db 1441 CTTAGATGTTATCCTTAAACTTAAAGTTAGGTACAAAGTTTGGAAATTTAGTCAAAATGCTTA 1500  
Qy 228 ----- 228  
Db 1501 AGTTGCATTAATTTGAACAAAATCTATGCATTTGAATAAAAAAAGATATGGATTTATTTA 1560  
Qy 228 ----- 228  
Db 1561 TAAAGTATAGTCCTTGTAAATCCTAGGACTTGTGTCTAATCTTGTCTTATGCGTCAAAAT 1620  
Qy 228 ----- 228  
Db 1621 CTTTTGATGTCAAATATAATAATCCTTGTTTTATTAGAGTCAAAGCTCTTTCATTAGTCAACT 1680  
Qy 228 ----- 228  
Db 1681 ACTCAATATACCTCAAAGTTTGAATATAGTCTTCTGACTAATTAGAATTCATTACAACCG 1740  
Qy 228 ----- 228  
Db 1741 ATAAACGTTACAATTTGGTTTATCATTTTAAAAAAACAGATTTGGTGCATATATACGATGAC 1800  
Qy 228 ----- 228  
Db 1801 GTTCTGTTTTAGTTTCATCTATTTCACAAATTTTATAATAATTATTTTCAAGAAAAATTGA 1860  
Qy 228 ----- 228  
Db 1861 AATACATACGTGTAATATGTTTCTTTATATATGTTGTATATAAATTAATGGGATTTT 1920  
Qy 229 -----ArgAlaLysThrPheArgMetLeuTyraSerAspPheThr 242  
Db 1921 TCTCTAAATGAAATTTGTGTAGGCC-AAATGGTTTCGGATGCTCTACAGTGATTTCAAC 1979  
Qy 242 rPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyraLe 262  
Db 1980 TTTTACAAAGGACCAAGAACGTTTGTATCAATGGCAACGATATTGGAGTCGACTATTT 2039  
Qy 262 uGluGlyGlnIlePheLeuSerAsnGlyValValAspThrSerPhePheProPheSerAs 282  
Db 2040 AGAAGGTCAAAATTTCTATCAACCGGTGTCGTGACACCTCTTTTCCACCTTCAGA 2099  
Qy 282 pGlnSerLysValAlaAspLeuValLysGlnHisGlyIleIleTyraValLeuGluValAl 302  
Db 2100 TCAATCTAAAGTCCTGATCTTAGTCAAGCAACACGGTATCATCTATGTTCTTGAAGTAGC 2159  
Qy 302 aLysTyraAspAspProAsnLeuProIleIleSerLys----- 315  
Db 2160 CAAGTATTATGATGATCCCAATCTCCCAATCATCAGCAAGGTACTACACATTTTACATTTT 2219  
Qy 315 ----- 315  
Db 2220 CATCATCGTTTTTATCATACCATTAAGATATTAAATGATTCATCATTTGCACCACATTAAG 2279  
Qy 315 ----- 315  
Db 2280 ATATTTCATCATCATCGTTTACATTTTCTTTTGTGATCTTTATGCTTCTCATATCTACTA 2339

QY 316 -----ValileAspThrLeuThrLysThrLeuSerTyLeuProGlyPheIleSerM 333  
 Db 2340 TTGTGTAGTTATTGACACATTAAAGAAACATTAAAGTTACTTGGCCGGTTTCATATCAA 2399  
 QY 333 exHisaspValalatyRheAspPheLeuAsnAtcValHisValGluGluAsnLysLeuA 353  
 Db 2400 TCACAGAGTGGCCCTACTTCGATTTCTTGACCCGTTGATCATGTGGAAGAAATTAACCTCA 2459  
 QY 353 iSerLeuGlyLeuTrpGluLeuProHisProTrpLeuAsnLeuTyRValProLysSerA 373  
 Db 2460 GATCTTTGGGATTATGGGAACCTCTCATCTCTGCTTAACCTCTACGCTTCTAAATCTC 2519  
 QY 373 iLeuAspPheHisAsnGlyValValLysAspIleLeuLysGlnLysSerAlas 393  
 Db 2520 GGATTCCTCGATTTTCATACCGGTGTGTGCAAGACATTTCTTTAAGCAAAATCGCTT 2579  
 QY 393 exGlyLeuAlaLeuLeuTyRProTrpAsnArgAsnLys----- 405  
 Db 2580 CGGGACTCGCTCTCTCTCTATCCAAACAAACCGGAATAA-GTACATACTTCTCTTCATTCAT 2638  
 QY 405 ----- 405  
 Db 2639 ATTATCTTCAGAACCAAGTAATAATTTCTATGAACGTGATTATGCTGTATTGTTA 2698  
 QY 406 --TriAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyRleI 425  
 Db 2699 GATGGACATCGTATGTCGGCGATGATACACAGAGATCGATGAAGATGTTATATATATTA 2758  
 QY 425 leGlyLeuGlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGluL 445  
 Db 2759 TCGGACTACTCAATCCGCTACCCCAAGGATCTTCCAGAACTGGAGACGTTAAACGAGA 2818  
 QY 445 ystIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyRLeuMetHisTyR 465  
 Db 2819 AGATAATTAGTTTCCAGAGATTCCAGGATTAGGTTAAGTTAAGCAATATCTAATGCAATTATA 2878  
 QY 465 hrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspPheSerLysArgL 485  
 Db 2879 CTAGTAAAGAAAGATTGGATTGAGCATTTTGGATCAAAATGGGATGATTTTTCGAAGAGA 2938  
 QY 485 yAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501  
 Db 2939 AAGATCTATTGATCCCAAGAACTGTTATCTCCAGGCGCAACATCTTT 2988

RESULT 5

US-10-014-101-3  
 ; Sequence 3, Application US/10014101  
 ; Publication No. US20030074698A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schmulling, Thomas  
 ; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and  
 ; FILE OF INVENTION: physiology  
 ; FILE REFERENCE: 1195-2  
 ; CURRENT APPLICATION NUMBER: US/10/014,101  
 ; PRIOR FILING DATE: 2001-12-10  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/06833  
 ; PRIOR FILING DATE: 2001-06-16  
 ; PRIOR APPLICATION NUMBER: EP 00870132.8  
 ; PRIOR FILING DATE: 2000-06-16  
 ; PRIOR APPLICATION NUMBER: US 60/258,415  
 ; PRIOR FILING DATE: 2000-12-27  
 ; PRIOR APPLICATION NUMBER: EP 01870053.4  
 ; PRIOR FILING DATE: 2001-03-16  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 2991  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 US-10-014-101-3

Alignment Scores: 2.5e-262 Length: 2991  
 Pred. No.: 2226.50 Matches: 499  
 Score: 50.00% Conservative: 0  
 Percent Similarity: 50.00% Mismatches: 2  
 Best Local Similarity: 85.77% Indels: 499  
 Query Match: 14 Gaps: 4  
 DB: 14  
 US-10-014-101-4 (1-501) x US-10-014-101-3 (1-2991)  
 QY 1 MetAlaAsnLeuArgLeuMetIleThrLeuIleThrValLeuMetIleThrLysSerSer 20  
 Db 1 ATGGCTAAATCTTCGTTTAAATGATCACTTTAAATCACGGTTTAAATGATCAACCAATCATCA 60  
 QY 21 AsnGlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSer 40  
 Db 61 AAGCGTATTAAATTAATGATTACCTAAATCCCTTAACCTCACCTCTCTACCGATCCTTTC 120  
 QY 41 IleIleSerAlaAlaSerHisAspPheGlyAsnIleThrValThrValThrProGlyGlyVal 60  
 Db 121 ATCATCTCCGACGCTCTCATGACTTCGGAACATAAACACCGGTGACCCCGCGCGCTA 180  
 QY 61 IleCysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyRAlaAlaAsnGlyLys 80  
 Db 181 ATCTGCCCTCTCTCCACCGCTGATATCTCTCGTCTCTCCATATACCGCAACACGGAATA 240  
 QY 81 SerThrPheGlnValAlaAlaArgGlyGlnGlyHisSerLeuAsnGlyGlnAlaSerVal 100  
 Db 241 AGTACATTCCAAGTAGCGGCTCGTGGCCAGGCCACTCTCTAAACGCGCAAGCCTCGTC 300  
 QY 101 SerGlyValSerProValSerThrTrpThrAspTyLeuHisIleThrValGlyGlyThrLeu 120  
 Db 301 TCCGGCGGAGTAAATCGCTCAACATGACGTGATCAGTGGTGGTGGTGGTGGTGGTGGTGG 360  
 QY 121 LysTyRAlaAspValAlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGlu 140  
 Db 361 AAGTACGCTGACGTGGCGGCGCGGACGTTATGGTGGATGTGCTTAAGAAGACGCGGAG 420  
 QY 141 LysGlyValSerProValSerThrTrpThrAspTyLeuHisIleThrValGlyGlyThrLeu 160  
 Db 421 AAAGGGGTGCGCGGGTTCCTTGACGGATTATTTGCATATAAACCCTCGGAGGAAACGTTG 480  
 QY 161 SerAsnGlyGlyIleGlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeu 180  
 Db 481 TCGAATGGTGGATTGGTGGTCAAGTGTTCGAAACGGTCTCTTGTAGTAGACGTCCTT 540  
 QY 181 GluLeuAspValIleThr----- 186  
 Db 541 GAATTGGACGTTATTACTGCTGACGATCTTCTAAACCTTGTGATGATACATACACACACAAA 600  
 QY 186 ----- 186  
 Db 601 ACTGTTTGTGTTTATAGTATTTTTCATTTTGTACCATAGGTTTATGTTTATAGTT 660  
 QY 186 ----- 186  
 Db 661 GTGCTAAACTTCTTGCACCACACGTAAGTCTTCGAAACACAAAATGGTAACGATCTAT 720  
 QY 186 ----- 186  
 Db 721 ATGTTTTTGTACATATTGAATGTTGTTTCATGAGAAATAAAGTAATACATATACACACA 780  
 QY 186 ----- 186  
 Db 781 TTTATTGTCGTACATATATAATAATAATTAAGACAAAATTTTCACAATTTGGTAGCGTGTAA 840  
 QY 186 ----- 186  
 Db 841 TTTGGGATTTTGTAAATGTACATGACGATGATGAGGACGTTTTCGGTTTTCCTTA 900  
 QY 186 ----- 186  
 Db 901 GATTTGTGTAGTATTTCAATATATATCATTTATTTTCTTCGATAAAGAGGTGTATATT 960

QY 186 ----- 186  
Db 961 TTTAAATAGCAACATTTTCAGAAATTTCTTTTGAATTTTACACTTTTAAATTTGTTATGT 1020  
QY 187 ----- GlyLysGlyGluMetLeuThrCysSerArgG1 197  
Db 1021 TAATATGGATTTGAATAAATAATTTTCAGGGAAGGTGAATGTTGACATGCTCGCGACA 1080  
QY 197 nLeuAsnProGluLeuPheTyrGlyValLeuGlyGlyLeuGlyGlnPheGlyIleIleTh 217  
Db 1081 GCTAAACCCAGAAATTTGTTCTATGGAGTGTAGGAGGTTGGGTCAATTTGGAAATTTATAAC 1140  
QY 217 rArgAlaArgIleValLeuAspHisAlaProLys ----- 228  
Db 1141 GAGAGCCAGAAATTTGTTGGACCATGCACCTAAACCGGTACGTATCATCATATTTTACCA 1200  
QY 228 ----- 228  
Db 1201 TTTGTTTGTAGTCAGCATTCATTTTTCATTAGTAATTCGGTTTCAATTTCTAAATTTT 1260  
QY 228 ----- 228  
Db 1261 AGTCAATAGAAATGATTCCTTATGTATGCAGAGCTTGATTTATTAGTCAATTTTATTAGATA 1320  
QY 228 ----- 228  
Db 1321 AAATAAAATATAACCTTAACCGAAATAATTTTACTAATCGGATAATGTCGTATTAATA 1380  
QY 228 ----- 228  
Db 1381 CATTTTATGATATTACACTAAGAGAGTTAGAGACGTATGGATCACAAAACATGAAGCTTT 1440  
QY 228 ----- 228  
Db 1441 CTTAGATGGTATCCTAAACCTAAAGTTAGGTACAAAGTTTGGAAATTTAGGTCAAAATGCTTA 1500  
QY 228 ----- 228  
Db 1501 AGTTGCATTAATTTGAACAAATCTATGCATTTGAATTAATAAAAGATATGGATTTATTTA 1560  
QY 228 ----- 228  
Db 1561 TAAAGTAGTCTCTGTATCTTAGGACTTTGTGTCTAATCTTGTCTTATGGTGCAAAAT 1620  
QY 228 ----- 228  
Db 1621 CTTTITGATGTCATATATAATCTTTGTTTATTAGAGTCAAGCTCTTTCATTAGTCAACT 1680  
QY 228 ----- 228  
Db 1681 ACTCAATATACTCCAAAGTTTAGAATATAGTCTTCTGACTAATTAGATCTTACCAACCG 1740  
QY 228 ----- 228  
Db 1741 ATAAAGTTTACAAATTTGGTTATCATTTTAAAAAACAGATTTGGTCAATAATATACGATGAC 1800  
QY 228 ----- 228  
Db 1801 GTTCTGTTTGTAGTTTCATCTATTCAAAATTTTATATAATTATTTCAGAAAAATATTGA 1860  
QY 228 ----- 228  
Db 1861 AATACTATACGTAAATATGGTTTCTTTATATATATGTGTATATAAATTTAAATGGGATTTGTTT 1920  
QY 229 ----- ArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrTh 242  
Db 1921 TCTCTAAATGAATTTGTGTAGGCC-AAATGGTTTCGGATGCTCTCAGTGATTTTCAAC 1979  
QY 242 rPheThrLysAspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLe 262  
Db 1980 TTTTACAAAGACCAAGAACGTTTGATATCAATGGCAACGATATTGGAGTCGACTATTT 2039

QY 262 uGluGlyGlnIlePheLeuSerAsnGlyValValAspThrSerPhePheProSerAs 282  
Db 2040 AGAGGTCAATATTCTATCAACCGTGTGTTGACACCTCTTTTCCACCTTCAGA 2099  
QY 282 pGlnSerLysValAlaAspLeuValysGlnHisGlyIleIleTyrValLeuGluValAl 302  
Db 2100 TCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGATATCATCTATGTTCTTGAAGTAGC 2159  
QY 302 aLysTyrTyrAspAspProAsnLeuProIleIleSerLys ----- 315  
Db 2160 CRAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTACTACACATTTFACATTTT 2219  
QY 315 ----- 315  
Db 2220 CATCATCGTTTTTATCATACCATPAAGATATTTAAATGATTCATCATTCGCCACCATTAAG 2279  
QY 315 ----- 315  
Db 2280 ATATTCAATCATCATCGTTACATTTTGTTCATCTTATGCTTCTCTATAATCTACTA 2339  
QY 316 ----- ValIleAspThrLeuThrLysThrLeuSerTyrLeuProGlyPheIleSerM 333  
Db 2340 TTGTGTAGGTTTATGACACATTAACGAAAAACATTAAGTTTACTTGGCCGGGTTTCATATCAA 2399  
QY 333 ethHisapValAlaTyrPheAspPheLeuAsnArgValHisValGluGluAsnLysLeuA 353  
Db 2400 TGCACGACGTGGCTTACTTCGATTTCTTGAAACGCTGATACATGTCGAGAAATAATACTCA 2459  
QY 353 rgSerLeuGlyLeuTrpGluLeuProHisProTrpLeuAsnLeuTyrValProLysSerA 373  
Db 2460 GATCTTTGGGATTATGGAACTTCTCATCTTGGCTTAACTCTACCTTCCCTAAATCTC 2519  
QY 373 rgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLeuLysGlnLysSerAlas 393  
Db 2520 GGATTCGATTTTCATACGGTGTGTCAAAGACATTTCTTTAAGCAAAAATCAGCTT 2579  
QY 393 ergLysLeuAlaLeuLeuTyrProThrAsnArgAsnLys ----- 405  
Db 2580 CGGGACTCGCTCTCTCTATCCAAACAAACCGGAATAA-GTACATACCTCTCTTCAATTCAT 2638  
QY 405 ----- 405  
Db 2639 ATTTATCTTCAAGAACCAAAAGTAAATAATTTCTATGAATGATTTATGCTGTTATTGTTA 2698  
QY 406 --TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleI 425  
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QY 425 leGlyLeuLeuGlnSerAlaThrProLysAspLeuProGluValGluSerValAsnGluL 445  
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QY 445 yIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyrT 465  
Db 2819 AGATAATTTAGTTTTCAGGATTCAGTATTAGATTAGCAATATCTAATGCATTATA 2878  
QY 465 hrSerLysGluAspTyrIleGluHisPheGlySerLysTrpAspAspPheSerLysArgL 485  
Db 2879 CTAGTAAAGAAGATTGGATTGAGCATTTTGATCAAAATGGGATGATTTTTCGAAGAGGA 2938  
QY 485 yAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501  
Db 2939 AAGATCTATTGATCCCAAGAACTGTATCTCCAGGCGCAAGCATCTTT 2988

RESULT 6  
US-09-938-842A-2089  
; Sequence 2089, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
 ; TITLE OF INVENTION: SAME, AND METHODS OF USE  
 ; FILE REFERENCE: SCRIPT300-3  
 ; CURRENT APPLICATION NUMBER: US/09/938,842A  
 ; CURRENT FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: US 60/227,866  
 ; PRIOR FILING DATE: 2000-08-24  
 ; PRIOR APPLICATION NUMBER: US 60/264,647  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/300,111  
 ; PRIOR FILING DATE: 2001-06-22  
 ; NUMBER OF SEQ ID NOS: 5379  
 ; SEQ ID NO 2089  
 ; LENGTH: 1575  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; US-09-938-842A-2089

Alignment Scores:  
 Pred. No.: 4.47e-213 Length: 1575  
 Score: 1822.00 Matches: 345  
 Percent Similarity: 80.08% Conservative: 69  
 Best Local Similarity: 66.73% Mismatches: 79  
 Query Match: 70.18% Indels: 24  
 DB: 5 Gaps: 5

US-10-014-101-4 (1-501) x US-09-938-842A-2089 (1-1575)

Qy	7	MetileThrLeuIleThrValLeuMet-----lleThrLysSerSerAsn	21
Db	25	CTCATCACCTAATAACGCTTTTATAAGTTTAAACCCCAACCTTAATCAATCAGATGAG	84
Qy	22	GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle	41
Db	85	GGCATTGATGTTTCTTACCCATATCACTCAACCTTACGGTCTAACCCGATCCTTCTCC	144
Qy	42	IleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyValIle	61
Db	145	ATCTCTGCCGCTTCTCAGCACTTCGGTAAACATAACCGACGAAAAATCCGGCGCGCTCCTC	204
Qy	62	CysProSerSerThrAlaAspIleSerArgLeuLeuGlnThrAlaAlaAsnGly-----	79
Db	205	TGCCCTTCCTCCACACGAGGTGGCTGCTCTCTCGTTTCGCTAACGGAGGATCTCT	264
Qy	80	-----LysSerThrPheGlnValAlaAlaArgGlyGlnGly	91
Db	265	TACAATAAAGGCTCAACCCAGCCCGCGCTACTTTCAAGTGGCTGCTCAGAGGCCAAGGC	324
Qy	92	HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle	111
Db	325	CACCTCCCTCCGTGGCAAGCCTCTGACCCCGAGGTGCTGCTGCAATGATGACGTGCTC	384
Qy	112	-----ThrAspValValValSerLysAspLysLysTyrAlaAspVal	125
Db	385	GCCATGGCGGCTAAACACCGCGCGTGTGTTATCTCGGCAGACGGGACTTACGCTGACGTG	444
Qy	126	AlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerPro	145
Db	445	GCTGCCGGAGAGTGGTGGATGTTCTGAAGCGCGGTGGATGATGAGGGGCTCTCCCGG	504
Qy	146	ValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle	165
Db	505	GTATCATGACGCGATATTATTTGTATCTACGCTCGCGGGAGCTTGTGGAACGCTGGAATC	564
Qy	166	GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle	185
Db	565	GGTGTGTACAGCTTTAGACACGGCCCTCAGATTAGTACGTTTCATGACGTTGACGTTATT	624
Qy	186	ThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGly	205
Db	625	ACCGGAAAAGGTGAATCATGACTTCTGCTCTCAAAAGTTAAACCCCTGGAATTGTTCTATGGA	684
Qy	206	ValLeuGlyGlyLeuGlnPheGlyIleThrArgAlaAlaArgIleValLeuAspHis	225

Db 685 GTTTTAGGAGGTTTGGGTCAATTCGGTATTATACAGAGGGCCAGGATTTCGGTTGGATCAT 744

Qy 226 AlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLys 245

Db 745 GCACCCACACAGGGTGAATGGTCTCGCATACTCTACAGTGACTTCTCGCTTTTAAAAAGA 804

Qy 246 AspGlnGluArgLeuLeuSerMetAlaAsnAspIleGlyValAspTyrLeuGluGln 265

Db 805 GACCAAGAGCGTTTAAATATCAATGACCAATGATCTCGGAGTTGACTTTTGGAAAGTCAA 864

Qy 266 IlePheLeuSerAsnGlyValValAspThrSerPhePheProSerAspGlnSerLys 285

Db 865 CTTATGATGTCAAATGGCTTCGTAGACACCTCTTCTTCCCACTCTCGATCAACAGA 924

Qy 286 ValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAlaLysTyrTyr 305

Db 925 GTCCGATCTCTTGTAATGACACCGGATCATCTATGTTCTCGAAGTAGCCAAAGTATTAT 984

Qy 306 AspAspProAsnLeuProIleLeuSerLysValIleAspThrLeuThrLysThrLeuSer 325

Db 985 GACAGAACACACCTCTCCCAATTATGACCAAGGTGATTTGACACGTTAGTAGAATCTTAGT 1044

Qy 326 TyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArgVal 345

Db 1045 TTCGCTCCAGGGTTTATGTTTCGTACAAAGATGTTCCGTATTTCCGATTTCTTGAAACCGTGTC 1104

Qy 346 HisValGluGlnAsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeu 365

Db 1105 CGAAACGAGAGAGAAATCAATCTCAGATCTTTAGACTATGGAGAGTTCCTCATCCATGGCTT 1164

Qy 366 AsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIle 385

Db 1165 AACATCTTTGTCGCGGGTCTCGAATCCAAAGATTTTTCATGATGGTGTATTATTAATGGCCTT 1224

Qy 386 LeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys 405

Db 1225 CTTCCTAAACCAACCTCAACTCTCGTGTTACTCTCTCTATCCCAACAAACCGAAACAAA 1284

Qy 406 TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIle 425

Db 1285 TGGAAACAACCGCATGTCAACGATGACACCG-----GACCAAGATGTTTTTATGTGATC 1338

Qy 426 GlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSerValAsnGlu 444

Db 1339 GGATTTACTGCATCAGCTGGTGGATCTCAAAATGGCAAGACTTGAAATCTCAACGAC 1398

Qy 445 LysIleLeuArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMetHisTyr 464

Db 1399 AAGGTTATTAGATTTTGTGAAAACTCGGGAATTAAGATTAAAGAAATTTTGTATGCACTAT 1458

Qy 465 ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspPheSerLysArg 484

Db 1459 ACAAGAAAAGAGATTGGGTAAACATTTTGGACCAAAATGGGATGATTTTTTAAGAAAG 1518

Qy 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyLysAspIlePhe 501

Db 1519 AAAATTATGTTGATCCCAAAAGACTATTGTTCCAGGACAAGACATATTT 1569

RESULT 7

US-09-938-842A-2089

; Sequence 2089, Application US/09938842A

; Publication No. US20040009476A9

; GENERAL INFORMATION:

; APPLICANT: Harper, Jeff

; APPLICANT: Kreps, Joel

; APPLICANT: wang, Xun

; APPLICANT: Zhu, Xong

; TITLE OF INVENTION: SPRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING SPRESS-REGULATED GENES OF PLANTS, AND METHODS OF USE

; FILE REFERENCE: SCRIP1300-3

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-08-24

RESULT 7  
US-03-938-842A-2089  
; Sequence 2089, Application US/09938842A  
; Publication No. US20040009476A9  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Krepel, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIFA300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24



; PRIOR APPLICATION NUMBER: US 60/227,866  
 ; PRIOR FILING DATE: 2000-08-24  
 ; PRIOR APPLICATION NUMBER: US 60/264,647  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/300,111  
 ; PRIOR FILING DATE: 2001-06-22  
 ; NUMBER OF SEQ ID NOS: 5379  
 ; SEQ ID NO 2089  
 ; LENGTH: 1575  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 US-09-938-842A-2089

Alignment Scores:  
 Pred. No.: 4,476-213 Length: 1575  
 Score: 1822.00 Matches: 345  
 Percent Similarity: 80.08% Conservative: 69  
 Best Local Similarity: 66.73% Mismatches: 79  
 Query Match: 70.18% Indels: 24  
 DB: 11 Gaps: 5

US-10-014-101-4 (1-501) x US-09-938-842A-2089 (1-1575)

QY 7 MetileThrLeuThrValLeuMet-----IleThrLysSerSerAsn 21  
 DB 25 CTCATCACCCCTAATACCGCTTTTATAGTTTAAACCCCAACCTTAATCAATCAGATCAG 84  
 QY 22 GlyileLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41  
 DB 85 GCGATTGATGTTTCTTACCATATACCTCAACCTTACCGTCTTAACCGATCCCTTCTCC 144  
 QY 42 IleSerAlaAspSerHisAspPheGlyAsnIleThrValThrProGlyGlyValIle 61  
 DB 145 AICTCTGCCGCTTCTCAGCACTTCGGTAACATACGACGAGAAATCCCGGCCGCTCCTC 204  
 QY 62 CysProSerSerThrAlaAspIleSerArgLeuLeuGlnThrValAlaAlaAsnGly----- 79  
 DB 205 TGCCTCTCTCCACACGAGGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 264  
 QY 80 -----LysSerThrPheGlnValAlaAlaArgGlyGlnGly 91  
 DB 265 TACAATAAGGCTCAACACGCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 324  
 QY 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle 111  
 DB 325 CACTCCCTCCGTGGCCCAAGCCCTCGACCGGAGGTGCTGCTGGAACATGACGTGCTC 384  
 QY 112 -----ThrAspValValSerLysAspLysIleThrAlaAspVal 125  
 DB 385 GCCATGCGCGCTAAACACGCGCGTGTATCTCTCGGACGCGGACTTACGCTGACGTG 444  
 QY 126 AlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGlyLysGlyValSerPro 145  
 DB 445 GCTGCCGGACGATGGGTGGATGTTCTGAAGCGCGGTGGATAGAGCGCTCTCGCG 504  
 QY 146 ValSerTrpThrAspTrpLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle 165  
 DB 505 GTTACATGACGATATTATTGTATCTCAGCGCTCGCGGACGCTTGTGCAACGCTGGAATC 564  
 QY 166 GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle 185  
 DB 565 GGTGGTACGCTTTAGACGCGCTCTCAGCTTACGATGATGATGATGATGATGATGATGAT 624  
 QY 186 ThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTrpGly 205  
 DB 625 ACCGAAAAGGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 684  
 QY 206 ValLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 225  
 DB 685 GTTTTAGAGGTTTGGTCAATTCGGTATTATTAACGAGGCCAGGATTCGTTGGATCAT 744  
 QY 226 AlaProLysArgAlaLysTrpPheArgMetLeuTrpSerAspPheThrThrPheThrLys 245

DB 745 GCACCCACAAGGGTGAATGGTCTCGCATCTCTACAGTACTTCTCGGCTTTTAAAGA 804  
 QY 246 AspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTrpLeuGluGlyGln 265  
 DB 805 GACCAAGAGCGTTAATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 864  
 QY 266 IlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLys 285  
 DB 865 CTTATGATGTCAAATGGCTTCGTAGACACCTCTTCTTCTCCCACTCTCCGATCAACA 924  
 QY 286 ValAlaAspLeuValLysGlnHisGlyIleIleTrpValLeuGluValAlaLysTrpTrp 305  
 DB 925 GTGCACTCTCTTGTGAATGACCAACCGATCATCTATGTTCTCGAAGTAGCAATATTAT 984  
 QY 306 AspAspProAsnLeuProIleLeuSerLysValIleAspThrLeuThrLysThrLeuSer 325  
 DB 985 GACAGAACCACCCCTTCCCATATTATGACCAAGGATGACACGTTAGTAGAAGCTCTAG 1044  
 QY 326 TyrLeuProGlyPheIleSerMetHisAspValAlaTrpPheAspPheLeuAsnArgVal 345  
 DB 1045 TTCCTCCAGGTTTATGTCGTACAGATGTTCCGTATTTCGATTTCCTGAACCGTGT 1104  
 QY 346 HisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeu 365  
 DB 1105 CGAAACGACAGAGATAAAGCTCAGATCTTTAGGACTATGGAAAGTTCTCATCCATGG 1164  
 QY 366 AsnLeuTrpValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIle 385  
 DB 1165 AACATCTTTGTCGGGGTCTCGAATCCAGATTTTCATGATGATGATGATGATGATGAT 1224  
 QY 386 LeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTrpProThrAsnArgAsnLys 405  
 DB 1225 CTTCTAAACCAACCTCAACTTCTGTGTACTCTCTCTATCCCAACCAACCAACCAAC 1284  
 QY 406 TrpAspAsnArgMetSerAlaMetIleProGluLeuAspGluAspValIleTrpIleIle 425  
 DB 1285 TGAACCAACCGCATGTCACGATGACACCG-----GACCAAGATGTTTATGATGATC 1338  
 QY 426 GlyLeuLeuGlnSerAla-----ThrProLysAspLeuProGluValGluSerValAsnGlu 444  
 DB 1339 GGATTACTCAATCAGCTGTGTGATCTCAAAATTTGCAAGACTTGAATAATCTCAACGAC 1398  
 QY 445 LysIleIleArgPheCysLysAspSerGlyIleIleIleLysGlnTrpLeuMetHisTrp 464  
 DB 1399 AAGTTATTAGTTTGTGAAGTCTCGGAATTAAGAAATTAAGAAATTAAGAAATTAAGAA 1458  
 QY 465 ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspPheSerLysArg 484  
 DB 1459 ACAAGAAAAGAGAGATGCGTTAAACATTTTGGACCAAAATGGGATGATTTTAAAGA 1518  
 QY 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501  
 DB 1519 AAAATTATGTTGATCCCAAGACTATTGTTCTCCAGCAAGACATATTTT 1569

RESULT 8

US-10-331-453-28  
 ; Sequence 28, Application US/10311453  
 ; Publication No. US20040031073A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schmilling, Thomas  
 ; APPLICANT: Werner, Tom s  
 ; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and  
 ; TITLE OF INVENTION: physiology  
 ; FILE REFERENCE: 1226-4  
 ; CURRENT APPLICATION NUMBER: US/10/311,453  
 ; PRIOR FILING DATE: 2002-12-16  
 ; PRIOR APPLICATION NUMBER: EP 00870132.8  
 ; PRIOR FILING DATE: 2000-06-16  
 ; PRIOR APPLICATION NUMBER: US 60/258,415  
 ; PRIOR FILING DATE: 2000-12-27  
 ; PRIOR APPLICATION NUMBER: EP 01870053.4  
 ; PRIOR FILING DATE: 2001-03-16  
 ; NUMBER OF SEQ ID NOS: 36

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-311-453-28

Alignment Scores:
  4.47e-213      Length:      1575
  1822.00        Matches:      345
  80.08%         Conservative: 61
  66.73%         Mismatches:   79
  70.18%         Indels:       24
  12             Gaps:        5

US-10-014-101-4 (1-501) x US-10-311-453-28 (1-1575)

QY 7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerSer 21
Db 25 CTCATCACCCCTAATAAGCTTTTATAAGTTTAAACCCCAACCTTAATCAATCAGATGAG 84
QY 22 GlyIleIleAspLeuProLysSerLeuAsnLeuThrAspProSerIle 41
Db 85 GGCAATTGATGTTTCTTACCCATATCCTCAACCTTACGGTCTCAACCCATCCCTTCTCC 144
QY 42 IleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyValIle 61
Db 145 ATCTCTCCGCTTCTCAGACTTCGGTAACATACCGAGCGAAATCCCGCGCGCTCC 204
QY 62 CysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly----- 79
Db 205 TGCCCTTCTCCACCGAGGTGGTCTCTCCCTCCGTTTCGCTTACCGAGGATTCCT 264
QY 80 -----LysSerThrPheGlnValAlaAlaArgGlyGlnGly 91
Db 265 TACAATAAGGCTCAACCGCCCGCTCTACTTTCAAGTGGCTGCTCGAGGCCAAGGC 324
QY 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyValIleValAsnMetThrCysIle 111
Db 325 CACTCCCTCCGTCGCAAGCTCTGCACCGGAGGTGCTCGTGACATGACGTGCTCTC 384
QY 112 -----ThrAspValValSerLysAspLysLysTyrAlaAspVal 125
Db 385 GCATGCGCGCTAAACAGCGCGGTGTTATCTCGCGACACGGGACTTACGTGACGIG 444
QY 126 AlaAlaGlyThrLeuTrpValAspValLysLysThrAlaGlyLysGlyValSerPro 145
Db 445 GCTCGCGGACGATGGGTGGATGTTCTGAAGCGCGCGGTGATAGAGCGGTCTCGCCG 504
QY 146 ValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle 165
Db 505 GTTACATGGACGGATTATTGTATCTCAGCGTGGCGGACGTTGTTCGAACCGTGAATC 564
QY 166 GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle 185
Db 565 GGTGGTCAGAGCTTTAGACACGGCCCTCAGATTAGTAACGTTTCATGAGCTTGACGTATT 624
QY 186 ThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheThrGly 205
Db 625 ACCGAAAGGTGAATGATGACTTGCTCTCAAGTTTAAACCCCTGAATTGTCTATGGA 684
QY 206 ValLeuGlyLeuGlyGlnPheGlyIleIleThrArgAlaArgIleValLeuAspHis 225
Db 685 GTTTTAGAGGTTTGGGTCAATTCCGTATTATAACGAGGCGCAGGATTGGCTGGATCAT 744
QY 226 AlaProLysArgAlaLysTyrPheArgMetLeuTyrSerAspPheThrThrLys 245
Db 745 GCACCCACAGGGTGAATGTTCTCGCATATCTACAGTGACTTCTCGGCTTTTAAAGA 804
QY 246 AspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLeuGluGlyGln 265
Db 805 GACCAAGAGCGTTTAAATATCATGACCATGATCTCGAGTTGACTTTTTCGAAGTCAA 864

RESULT 9
US-10-014-101-28
; Sequence 28, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schumling, Thomas
; APPLICANT: Werner, Tom S
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 1575
; TYPE: DNA
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ORGANISM: Arabidopsis thaliana  
US-10-014-101-28

Alignment Scores:

Pred. No.: 4,476-213 Length: 1575  
Score: 1822.00 Matches: 345  
Percent Similarity: 80.08% Conservative: 69  
Best Local Similarity: 66.73% Mismatches: 79  
Query Match: 70.18% Indels: 24  
DB: 14 Gaps: 5

US-10-014-101-4 (1-501) x US-10-014-101-28 (1-1575)

Qy 7 MettleThrLeuIleThrValLeuMet-----lleThrLysSerSerAsn 21  
Db 25 CTCATCCCTTAATAGCGTTTATAAGTTTAAACCCCAACCTTTAATCAAAATCAGATGAG 84  
Qy 22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41  
Db 85 GGCATTGATGTTTCTTACCATATCACTCAACCTTAGCGTCCTAAACCGATCCCTTCTCC 144  
Qy 42 IleSerAlaIleSerHisAspPheGlyAsnIleThrValThrProGlyGlyValIle 61  
Db 145 ATCTCTCGCGTCTCTCAGACTTCGGTAAACATAACCGACGAAATCCCGCGCGCTCC 204  
Qy 62 CysProSerThrAlaAspIleSerArgLeuLeuGlnThrValAlaIleAsnGly----- 79  
Db 205 TGCCCTTCTCCACACGAGGTGGCTCTCTCTCGTTTCGTTTCGTAACGAGGATTCCT 264  
Qy 80 -----LysSerThrPheGlnValAlaIleAsnGlyGlyGly 91  
Db 265 TACAATAAAGGCTCAACACGCGCGGTCTACTTTCAAGTGGGTCTGCTCGAGGCGCAAGGC 324  
Qy 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyValIleValAlaAsnMetThrCysIle 111  
Db 325 CACTCCCTCCGTGGCGAAGCTCTGACCCCGAGGTGTCGTCGTAACATGACGTGTC 384  
Qy 112 -----ThrAspValValSerLysLysLysLysLysLysLysLysLysLysLysLys 125  
Db 385 GCCATGGCGGTAAACACGCGCGGTGTTTATCTCGGACGCGGACTACGCTGACGTG 444  
Qy 126 AlaIleGlyThrLeuTrpValAspValLeuLysThrAlaGlyLysGlyValSerPro 145  
Db 445 GCTCCCGGACGATGGTGGTGGATGTTCTGAAGCGCGGTGGATAGAGCGCTCTCGCG 504  
Qy 146 ValSerTrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle 165  
Db 505 GTTACATGACGCGATTATTTCTATCTCAGCTCGCGGAGCTTGTGCAACGCTGGATC 564  
Qy 166 GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle 185  
Db 565 GGTGTCAGAGCTTTAGACACGCGCCCTCAGATTAGTAACGTTCTATGAGCTTGACGTTATT 624  
Qy 186 ThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrGly 205  
Db 625 ACCGAAAAGTGAAATGATGACTGCTCTCAAGTTAAACCTTGAATGTTCTATGGA 684  
Qy 206 ValLeuGlyGlyLeuGlyGlnPheGlyIleThrArgAlaIleValLeuAspHis 225  
Db 685 GTTTTAGAGGTTTGGGTCAATTCGGTATTATAACGAGGCGCAGGATTCGTTGGATCAT 744  
Qy 226 AlaProLysArgAlaIleTrpPheArgMetLeuTyrSerAspPheThrPheThrLys 245  
Db 745 GCACCAAGAGGTGAATGGTCTCGCATCTCTACAGTGACTTCTCGGCTTTAAAGA 804  
Qy 246 AspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLeuGluGlyGln 265  
Db 805 GACCAAGAGCGTTTAAATATCAATGACCAATGATCTCGGAGTTGACTTTTGAAGGTCAA 864  
Qy 266 IlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLys 285  
Db 865 CTTATGATGTCAATGGCTTCGTAGACACCTTTTCTTCCCACTCTCCGATCAACACAGA 924

Qy 286 ValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAlaLysTyrTyr 305  
Db 925 GTCGCATCTCTTGTGAATGACACCGGATCATCTATGTTCTGAAGTAGCAAGTATTAT 984  
Qy 306 AspAspProAsnLeuProIleSerLysValIleAspThrLeuThrLysThrLeuSer 325  
Db 985 GACAGAACCCCTTCCCATTTATGACCAAGGTGATGACGTTAAGTAGAAGTCTAGGT 1044  
Qy 326 TyrLeuProGlyPheIleSerMetHisAspValAlaIleTyrPheAspPheLeuAsnArgVal 345  
Db 1045 TTCGCTCCAGGGTTTATGTTTCGTACAGATGTTCCGATTTCGATTTCTTGAACCGTGC 1104  
Qy 346 HisValGluGluAsnLysLeuArgSerLeuGlyLeuTyrGluLeuProHisProTrpLeu 365  
Db 1105 CGAAGCAAGAGATAAATCTCAGATCTTTAGACTATGGAGTTCCTCATCATGGCTT 1164  
Qy 366 AsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIle 385  
Db 1165 AACATCTTTGTCGCGGTCTCGAATCAAGATTTTCATGATGGTGTATTATTAATGGCCTT 1224  
Qy 386 LeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys 405  
Db 1225 CTTCTAAACCAACCTCAACTTCTGTTTACTCTCTTCTATCCCAACCGAAACAAA 1284  
Qy 406 TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIle 425  
Db 1285 TGAACACCGCATGTCACGATGACACG-----GACGAGATGTTTATGATGATC 1338  
Qy 426 GlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSerValAsnGlu 444  
Db 1339 GGATTAATCAATCACTGCTGGTGTCTCAAAATTTGGCAAGACTTGAATAATCTCAACGAC 1398  
Qy 445 LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrLeuMethIstYr 464  
Db 1399 AAGTTATTGATTTGTGAAACCTCGGGAATTAAGATAAGGAATATTGATGACTAT 1458  
Qy 465 ThrSerLysGluAspTrpIleGluHisPheGlySerLysTyrAspAspPheSerLysArg 484  
Db 1459 ACAAGAAAAGAGATGGGTAAACATTTTGACCAAAATGGGATGATTTTAAAGAAAG 1518  
Qy 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501  
Db 1519 AAATATTGTTTGTATCCCAAGAGACTTTGCTCCAGACACAGACATATTT 1569

RESULT 10

US-10-326-184-20

; Sequence 20, Application US/10326184

; Publication No. US20030163847A1

; GENERAL INFORMATION:

; APPLICANT: Monsanto Company

; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C

; TITLE OF INVENTION: OXIDASE 1

; FILE REFERENCE: MTC6781.1

; CURRENT APPLICATION NUMBER: US/10/326,184

; PRIOR FILING DATE: 2002-12-20

; PRIOR APPLICATION NUMBER: US 60/343,129

; PRIOR FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 20

; LENGTH: 1655

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-10-326-184-20

Alignment Scores:

Pred. No.: 4,866-213 Length: 1655  
Score: 1822.00 Matches: 345  
Percent Similarity: 80.08% Conservative: 69  
Best Local Similarity: 66.73% Mismatches: 79  
Query Match: 70.18% Indels: 24  
DB: 14 Gaps: 5

US-10-014-101-4 (1-501) x US-10-326-184-20 (1-1655)

QY	7	MetIleThrLeuIleThrValLeuWet-----lIethrlysserSerAsn	21
Dd	:	:::	:
Dd	25	CfTcATCACCCCTAAATAACCGCTTTTAAAGTTTAACCCCAACCTTAATCAAAATCAGATGAG	84
QY	22	GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerile	41
Dd	:	:::	:
Dd	85	GGCATTTGATGTTTTCTTACCATATCACTCAACTAGCGTCCTAACCGATTCCCCTTCCTCC	144
QY	42	IleSerAlaIleAsenHisAspPheGlyAsnIleThrThrValThrProGlyGlyValille	61
Dd	:	:::	:
Dd	145	AfTCTGTGGCGTCTTCACGATTCGGTAACAATAACGAGAAAATCCCGCGCGCTCTCCTC	204
QY	62	CysProSerSerThrAlaAspIleSerArgLeuLeuGlnTrAlaAlaAsnGly-----	79
Dd	:	:::	:
Dd	205	TGCCTCTCTCCACCACGAGGTCGCTCGTCTCTCGTTTCGTAAACGGAGGATTCCTCT	264
QY	80	-----LysSerThrPheGlnValAlaAlaArgGlyGlnGly	91
Dd	:	:::	:
Dd	265	TAcAATAAAGGCTCAACACGCGCGGTCTACTTTCAAAGTGCGTCTCGAGGCCCAAGGC	324
QY	92	HissErLeuAsnGlyGlnAlaSerValserGlyGlyValilleValAsnMetThrCysile	111
Dd	:	:::	:
Dd	325	CACCTCCCTCGTGGCCAAAGCCTCTGCACCCGGAGGTGTCGTGAACATGACGNGTCTC	384
QY	112	-----ThrAspValvalValserlysAspIlyslsyrAlaaspVal	125
Dd	:	:::	:
Dd	385	GCATGTGGCGGCTAAACGACGCGCGGTGTATCTCGCAGACGGGACTTACCGCTGACGTG	444
QY	126	AlaAlaGlyThrLeuTrpValAspValLeuLyssylsThrAlaGluLyssglyValserPro	145
Dd	:	:::	:
Dd	445	GCTCGCGGACGATGTGGTGCATGTTCTGAAGCGCGGTGTGATAGAGAGCGCTCTCGCG	504
QY	146	ValserTrpThrAspTyrrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyile	165
Dd	:	:::	:
Dd	505	GTTATCATGACGGATTATTGTGTATCTCAGCGTCGGCGGACGTTGTCGAACGCTCGAATC	564
QY	166	GlyGlyGlnValPheArgAsnGlyProLeuValserAsnValLeuGluLeuAspValille	185
Dd	:	:::	:
Dd	565	GGTGTCTCAGACGTTTAGACACGCGCCTCAGATTAGTAACGTTTCATGAGCTTGACGTATT	624
QY	186	ThrGlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTyrcly	205
Dd	:	:::	:
Dd	625	ACCGAALAAGGTGAATGATGACTGTCTCTCAAAGTTAAACCTGAATGTCTTATCGA	684
QY	206	ValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaArgileValLeuAsphis	225
Dd	:	:::	:
Dd	685	GTTTTAGGAGGTTTGGGTCAATTCCGTTATTATAACGAGGCCAGGATTCGTTGCATCAT	744
QY	226	AlaProLysArgAlaLysTrpPheArgMetLeuTyrrSerAspPheThrThrPheThrlys	245
Dd	:	:::	:
Dd	745	GCACCCACACAGGTGAATGTCTCGCATCTCTACAGTCACCTTCGCGCTTTTAAAAAGA	804
QY	246	AspGlnGluArgLeuIleSerMetAlaAsnAspiledyValAspTyrrLeuGluGlygln	265
Dd	:	:::	:
Dd	805	GACCAAGAGCGTTTAAATCAATCAATGACCAATGATCTCGAGTTTGACTTTTTGAAGGTCAA	864
QY	266	IlePheLeuSerAsnGlyValvalAspThrSerPhePheProProSerAspGlnSerlys	285
Dd	:	:::	:
Dd	865	CTTATGATGTCAAAATGGTTCGTAGACACCTCTTTCTCCACTCTCCGATCAAAACAAGA	924
QY	286	ValAlaAspLeuValLysGlnHisGlyIleIleTyrrValLeuGluValAlalysTyrryr	305
Dd	:	:::	:
Dd	925	GTFCGATCTCTTGTGAATGACCAACCGCATCATCTATGTTCTCGAGTAGCCAAAGTATTAT	984
QY	306	AspAspProAsnLeuProIleIleSerLysValIleAspThrLeuThrIlysthreusSer	325
Dd	:	:::	:
Dd	985	GACGAACACCCCTTCCCATTTATTACACAGGTGATTGACACGTAAAGTAGAACTCTAGGT	1044
QY	326	TyrLeuProGlyPheIleSerMetHisAspValalatyrrPheAspPheLeuAsnArgVal	345
Dd	:	:::	:
Dd	1045	TTTCGTCCAGGGTTATTGCTGTACAAAGATGTTCCGTTATTTCATTTCTTGACCGCTGC	1104

Qy	346	HsValGluGlnAsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProTrpLeu	365
Db	1105	CGAAACGAAGAAGAAATAACTCAGATCTTTAGGACTATGGGAAGTTCTCTCATCATGGCTT	1164
Qy	366	AsnLeuTyValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIle	385
Db	1165	AACATCTTGTCTCCGGGTCTCGAATCCAAGATTTTCATGATGGTGTTATTATATGGCCTT	1224
Qy	386	LeuLeuLysGlnLysSerIleAspGlyLeuAlaLeuLeuTyTrpProThrAsnArgAsnLys	405
Db	1225	CTTCTTAACCAACCAACCTCAACTCTCTGTGTATTACTCTTCTATCCCAACCAACCGAAACAA	1284
Qy	406	TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyIleIle	425
Db	1285	TGCAACAAACCGCATGTCACGATGACACCG-----GACGAACATGTTTTTTATGTGATC	1338
Qy	426	GlyLeuLeuGlnSerIle---ThrProLysAspLeuProGluValGluSerValasnGlu	444
Db	1339	GGATTACTCGAATCAGCTGGTGGATCTCAAAATTTGCCAAGAACTTGAATAATCTCAACGAC	1398
Qy	445	LysIleIleArgPheCysLysAspSerGlyIleLysIleLysGlnTyTrpLeuMetHisTyTr	464
Db	1399	AAGTTATTACGTTTGTGAAAACTCGGGAATTAAGATTAAAGAAATATTGTATGCACTAT	1458
Qy	465	ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspAspPheSerLysArg	484
Db	1459	ACAAGAAAAGAAATTGGGTAAACATTTTGGACCAAAATGGGATGATTTTTTAAGAAAG	1518
Qy	485	LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe	501
Db	1519	AAATATGTTTTCATCCAAAGAACTATTGCTCTCAGGACCAACACATATTT	1569
RESULT 11			
US-10-326-184-10			
; Sequence 10, Application US/10326184			
; Publication No. US20030163847A1			
; GENERAL INFORMATION:			
; APPLICANT: Monsanto Company			
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRES			
; TITLE OF INVENTION: OXIDASE 1			
; FILE REFERENCE: MTC6781.1			
; CURRENT APPLICATION NUMBER: US/10/326,184			
; CURRENT FILING DATE: 2002-12-20			
; PRIOR APPLICATION NUMBER: US 60/343,129			
; PRIOR FILING DATE: 2001-12-20			
; NUMBER OF SEQ ID NOS: 24			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 10			
; LENGTH: 1575			
; TYPE: DNA			
; ORGANISM: Arabidopsis thaliana			
US-10-326-184-10			
Alignment Scores:			
Pred. No.: 7,88e-213 Length: 1575			
Score: 1820.00 Matches: 345			
Percent Similarity: 79.88% Conservatives: 68			
Best Local Similarity: 66.73% Mismatches: 80			
Query Match: 70.11% Indels: 24			
DB: 14 Gaps: 5			

US-10-014-101-4 (1-501) x US-10-326-184-10 (1-1575)

Alignment Scores:			
Pred. No.:	7.88e-213	Length:	1575
Score:	1820.00	Matches:	345
Percent Similarity:	79.98%	Conservative:	68
Best Local Similarity:	66.73%	Mismatches:	80
Query Match:	70.11%	Indels:	24
DB:	14	Gaps:	5

Db 145 ATCTCTGCGGCTTCTCAGGACTTCGGTAACATAACCGAGCAAAATCCCGCGCGTCTCTC 204  
 QY 62 CysProSerSerThraAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly----- 79  
 Db 205 TGCCCTTCTCTCCACCGAGGTGCTCTCTCCCTGTTTCGGTAAACGGAGATTCTCT 264  
 QY 80 -----LysSerThrPheGlnValAlaAlaAargGlyGlnGly 91  
 Db 265 TACAATAAAGGCTCAACAGCCCGCGCTACTTTCAAAGTGGCTGCTCGAGCCCAAGC 324  
 QY 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle 111  
 Db 325 CACTCCCTCCGCGGCAAGCCTCTCAGCCGAGGTGCTCGTGAACATGACGCTGCTC 384  
 QY 112 -----ThrAspValValSerLysAspLysValSerLysValSerVal 125  
 Db 385 GCCATGGCGGCTAAACAGCGCGGTGTATCTCGGCAGCGGCACTTACGCTGACGTG 444  
 QY 126 AlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerPro 145  
 Db 445 GCTGCGGAGCATGTGGGTGGATGTTCTGAAGGCGGCGGTGATAGAGAGCGCTCTCGCG 504  
 QY 146 ValSerTrpThrAspTrpLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIle 165  
 Db 505 GITACATGACGGATTTATTTGTATCTCAGCGTCGCGGAGCGTGTGACCGCTGGAATC 564  
 QY 166 GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle 185  
 Db 565 GGTGGTCAGACGTTAGACCGGCTCAGATTAGTAGTAACGTTTCATGAGCTTGACGTTAT 624  
 QY 186 ThrGlyGlyGlyGluMetLeuThrCysSerArgGlnLeuAsnProGluLeuPheTrpGly 205  
 Db 625 ACCGGAAGAGGTGAATGATGACTTCTCTCAAGTGAACCCCTGAATGTTCTATGGA 684  
 QY 206 ValLeuGlyGlyLeuGlyGlnPheGlyIleIleThrArgAlaAargIleValLeuAspHis 225  
 Db 685 GTTTTAGGAGGTTTGGTCAATTCGGTAATATAACGAGGCGCAGGATTGCGTGCATCAT 744  
 QY 226 AlaProLysArgAlaLysTrpPheArgMetLeuTyrSerAspPheThrThrPheThrLys 245  
 Db 745 GCACCCACAAGGTGAATGGTCTCGCATCTCTCAGTACTCTCAGTACTCTCGGCTTTTAAAGA 804  
 QY 246 AspGlnGluArgLeuIleSerMetAlaAsnAspIleGlyValAspTyrLeuGluGlyGln 265  
 Db 805 GACCAAGAGCGTTTATATCAATGACCAATGATCTCGGAGTTGACTTTTGGAGGTCAA 864  
 QY 266 IlePheLeuSerAsnGlyValValAspThrSerPhePheProProSerAspGlnSerLys 285  
 Db 865 CTATATGATGTCAATGGCTTCGTAGACACCTCTTCTCCCACTCTCCGATCAAAACAAGA 924  
 QY 286 ValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAlaLysTrpTyr 305  
 Db 925 GTCGCATCTCTGTGAATGACCAACCGGATCATCTATGTTCTCGAGTAGCCCAAGTATTAT 984  
 QY 306 AspAspProAsnLeuProIleLeuSerLysValIleAspThrLeuThrLysThrLeuSer 325  
 Db 985 GACAGAACCAACCTCCCATTAATGACCAAGGTGATTGACACGTTAAGTAGAACTCTAGGT 1044  
 QY 326 TyrLeuProGlyPheIleSerMetHisAspValAlaTyrPheAspPheLeuAsnArgVal 345  
 Db 1045 TTCGTCACAGGTTATGTTGTCGACAGAGTTCCGTTATTTGATTTCTTGAAACCGTGTTC 1104  
 QY 346 HisValGluGluAsnLysLeuArgSerLeuGlyLeuTrpGluLeuProHisProtrpLeu 365  
 Db 1105 CGAAACGAAGAATAAACTCAGATCTTTAGGACTATGGGAAGTTCCTCATCCATGGCTT 1164  
 QY 366 AsnLeuTyrValProLysSerArgIleLeuAspPheHisAsnGlyValValLysAspIle 385  
 Db 1165 AACATCTTTCGCGGGGCTCGAATCCCAAGATTTTCATGATGGTGTATTATATGGCCTT 1224  
 QY 386 LeuLeuLysGlnLysSerAlaSerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys 405

Db 1225 CTTCTAAACCAACCTCAAACTTCTGGTGTACTCTCTCTATCCCAACCAACAAACAAA 1284  
 QY 406 TrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIleIle 425  
 Db 1285 TGAACAACACCGCATGTCAACGATGACACCG-----GACGAGATGTTTTTATGTGATC 1338  
 QY 426 GlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSerValAsnGlu 444  
 Db 1339 GGATTACTCAATCAGTCTGGTGGATCTCAAAATTTGGCAAGAACTTGAAAATCTCAACGAC 1398  
 QY 445 LysIleIleArgPheCysLysAspSerGlyIleLeuValIleLysGlnTyrLeuMetHisTyr 464  
 Db 1399 AAGTTATTACGTTTGTGAAAACCTCGGAATTAAGATTAAGGAATATTATGATGACTAT 1458  
 QY 465 ThrSerLysGluAspTrpIleGluHisPheGlySerLysTrpAspPheSerLysArg 484  
 Db 1459 ACAAGAAAGAGAGATGGGTAAACATTTTGGACCAAAATGGGATGATTTTAAAGAAAG 1518  
 QY 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501  
 Db 1519 AAAATTATGTTTATCCCAAGAACTATTGTCTCCAGGACAAGACATATTT 1569  
 RESULT 12  
 US-10-311-453-7  
 ; Sequence 7, Application US/10311453  
 ; Publication NO. US20040031073A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schmilling, Thomas  
 ; APPLICANT: Werner, Tom s  
 ; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and  
 ; TITLE OF INVENTION: physiology  
 ; FILE REFERENCE: 1226-4  
 ; CURRENT APPLICATION NUMBER: US/10/311,453  
 ; PRIOR FILING DATE: 2002-12-16  
 ; PRIOR APPLICATION NUMBER: EP 00870132.8  
 ; PRIOR FILING DATE: 2000-06-16  
 ; PRIOR APPLICATION NUMBER: US 60/258,415  
 ; PRIOR FILING DATE: 2000-12-27  
 ; PRIOR APPLICATION NUMBER: EP 01870053.4  
 ; PRIOR FILING DATE: 2001-03-16  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: Patent In Ver. 2.1  
 ; SEQ ID NO 7  
 ; LENGTH: 2782  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 US-10-311-453-7  
 Alignment Scores:  
 Pred. No.: 6,25e-178 Length: 2782  
 Score: 1539.50 Matches: 344  
 Percent Similarity: 44.89% Conservative: 69  
 Best Local Similarity: 37.39% Mismatches: 80  
 Query Match: 59.30% Indels: 429  
 DB: 12 Gaps: 9  
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 QY 7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21  
 Db 25 CTCATCACCTTAATAAGCTTTTATAAGTTAAACCCCAACCTTATCAATCAGATGAG 84  
 QY 22 GlyIleLysIleAspLeuProLysSerLeuAsnLeuThrLeuSerThrAspProSerIle 41  
 Db 85 GGCATTGATGTTTTCTTACCCTATATCACTCAACCTTACGCTTAAACCGATCCCTTCTCC 144  
 QY 42 IleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyValIle 61  
 Db 145 ATCTCTGCGGCTTCTCAGCTTCGGTAAACATAACCGACGAAATCCCGCGCGTCTC 204  
 QY 62 CysProSerSerThraAlaAspIleSerArgLeuLeuGlnTyrAlaAlaAsnGly----- 79  
 Db 205 TGCCCTTCTCTCCACCGAGGTGCTCTCTCTCGTCTCTCGTAAACGAGGAGTATCTCT 264

QY	80	-----LysSerThrPheGlnValAlaAlaAargGlyGlnGly	91
DB	265	TACAATAAGGCTCAACACGCCCGCTACTTTCAAAGTGGCTGCTCGAGGCCAAGGC	324
QY	92	HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysAlle	111
DB	325	CACCTCCCTCCGTGGCAAGCCCTCTGCACCCGGAGGTGTCGCTGGTAACATCACGTGCTC	384
QY	112	-----ThrAspValValSerLysAspLysLysTyzAlaAspVal	125
DB	385	GCCATGGCGGCTAAACACGCCGCGGTGTATCTCGCAGACGGGACTTACGCTGACGTG	444
QY	126	AlaAlaGlyThrLeuTrpValAspValLeuLysLysThrAlaGluLysGlyValSerPro	145
DB	445	GCTGCGGACGATGTGGGTGATGTCTTGAAGCGCGGTGGATAGAGGGCTCTCGCGC	504
QY	146	ValSerTrpThrAspTyrLeuHisIleThrValGlyThrLeuSerAsnGlyGlyIle	165
DB	505	GTTCATGACGCGATTATTGTATCTCACGCTCGCGGACGTTGTGAAACGCTGGAAATC	564
QY	166	GlyGlyGlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIle	185
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QY	186	Thr-----	186
DB	625	AC-CGGTACGTAAATACCAAACTTCCTAAATCTCGTTACAATTTTTTAATTTTTTGGTA	683
QY	186	-----	186
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QY	186	-----	186
DB	744	GATGCTCTTTTTTGTCTGCAAGCTTTAATTGTAGTAACATCAGCGATATATATACAA	803
QY	186	-----	186
DB	804	TGCATGTGATTAATTGATGATAATATAATGTTTTTAGTTACAAATTTGATTCTCAAGT	863
QY	186	-----	186
DB	864	AAAACTCACACGCCATAACCCAGTATAAACTCCAAAAATCACGTTTGGTCAGAAATACA	923
QY	186	-----	186
DB	924	TATCCTTCATAACAGTAGTATGCTAATAATTTGTGATTATAAATAAATCTCCGAGTTGT	983
QY	187	-----GlyLysGlyGluMetLeuThrCysSerArgGlnLeuAsnPro	200
DB	984	TCACAAATACATAATTTTCAGGAAAAGGTGAATGATGACTTGCTCTCCAAAGTTAAACCCCT	1043
QY	201	GluLeuPheTyrGlyValLeuGlyGlyLeuGlnPheGlyIleIleThrArgAlaAsp	220
DB	1044	GAATGTGTTCTATGGAGTTTGGAGGTTTGGGTCAATTCGGTATTATAACGAGGGCCAGG	1103
QY	221	IleValLeuAspHisAlaProLys-----	228
DB	1104	ATTGGTTGGATCATGACCCACCAAGGGTATGATCATGTCATCTATAGTGAATCAATTT	1163
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QY	229	-----	231
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QY	232	TTPheAqMetLeuTyr-SerAspPheThrThrPheThrLysAspGlnGluArgLeuIle	251
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QY	252	SerMetAlaAsnAspIleGlyValAspTyrLeuGluGlyGlnIlePheLeuSerAsnGly	271
Db	1703	TCAATGACCAATGATCTCGAGTTCACCTTTTGAAGGTCAACTATGATCTCAATGGC	1762
QY	272	ValValAspThrSerPhePheProSerAspGlnSerLysValAlaAspLeuValLys	291
Db	1763	TTCGTAGACACTCTTTCTCCACTCTCCGATCAACCAAGAGTCGCATCTCTTGTAAT	1822
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QY	315	-----	315
Db	1943	ATCACCAAATTACCATCATCATTGTCATATATGATCCAAAGTAATATATACATGATAT	2002
QY	315	-----	315
Db	2003	AAATAAATCGTTCAAATCTTTTTTTTTTAAAGAAATAAAGAAATCATTTTCAAGCATTACTC	2062
QY	315	-----	315
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QY	316	-----	332
Db	2123	TGTTTGTAGGTGATTGACACGTTTAAGTAGAACTCTAGGTTTCGCTCCAGGGTTATGTTTC	2182
QY	333	MethIleAspValAlaTyrPheAspPheLeuAsnAcqValHisValGluGluAsnLysLeu	352
Db	2183	GTCACAAATGTTCCGATATTTTCGATTTCTTGAACCGTGTCGGAACCGAAGAGATAACTC	2242
QY	353	ArgSerLeuGlyLeuTyrGluLeuProHisProTyrPheAsnLeuTyrValProLysSer	372
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QY	373	ArgIleLeuAspPheHisAsnGlyValValLysAspIleLeuLysGlnLysSerAla	392
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QY	393	SerGlyLeuAlaLeuLeuTyrProThrAsnArgAsnLys-----	405
Db	2363	TCTGGTGTACTCTCTCTATCCACAAACCGGAACAAAGTAATAATATTACTTTTGATT	2422
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 Qy 423 TyrllelleGlyLeuLeuGlnSerAla---ThrProLysAspLeuProGluValGluSer 441  
 Db 2537 TATGTGATCGGATTAATCAATCACTAGCTGGATCTCAAAATTTGGCAAGAACITTGAAAT 2596  
 Qy 442 ValAsnGluLysIlelleArgPheCysLysAspSerGlyIleLysIleLysGlnTyrlleu 461  
 Db 2597 CTCACGACAGAGTTATTCAGTTTGTGAAACCTCGGAATTAAGATTAAGATATTTG 2656  
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RESULT 13  
 US-10-014-101-7  
 ; Sequence 7, Application US/10014101  
 ; Publication No. US20030074698A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schmulling, Thomas  
 ; APPLICANT: Werner, Tom s  
 ; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and  
 ; FILE REFERENCE: 1195-2  
 ; CURRENT APPLICATION NUMBER: US/10/014,101  
 ; PRIOR FILING DATE: 2001-12-10  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/06833  
 ; PRIOR FILING DATE: 2001-06-16  
 ; PRIOR APPLICATION NUMBER: EP 00870132.8  
 ; PRIOR FILING DATE: 2000-06-16  
 ; PRIOR APPLICATION NUMBER: US 60/258,415  
 ; PRIOR FILING DATE: 2000-12-27  
 ; PRIOR APPLICATION NUMBER: EP 01870053.4  
 ; PRIOR FILING DATE: 2001-03-16  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 7  
 ; TYPE: DNA  
 ; LENGTH: 2782  
 ; ORGANISM: Arabidopsis thaliana  
 US-10-014-101-7

Alignment Scores:  
 Pred. No.: 6,25e-178 Length: 2782  
 Score: 1539.50 Matches: 344  
 Percent Similarity: 44.89% Conservative: 69  
 Best Local Similarity: 37.39% Mismatches: 80  
 Query Match: 59.30% Indels: 429  
 DB: 14 Gaps: 9

US-10-014-101-4 (1-501) x US-10-014-101-7 (1-2782)  
 Qy 7 MetIleThrLeuIleThrValLeuMet-----IleThrLysSerSerAsn 21  
 Db 25 CTCATCACCTTATTAACGGTTTATTATAGTTTAAACCCCAACCTTAATCAATCAGATGAG 84  
 Qy 22 GlyIleLysIleAspLeuProLysSerLysLeuLeuThrLeuSerThrAspProSerIle 41  
 Db 85 GGCATTGATGTTTCTTACCCATATCACTCAACCTTACGGTCTCAACCGATCCCTTCTCC 144  
 Qy 42 IleSerAlaAlaSerHisAspPheGlyAsnIleThrThrValThrProGlyGlyValile 61  
 Db 145 AUCTGCGCTTCTCAGCAGCTTCGGTAACTAACCCGAGAAATCCCGGCGCCCTCTC 204

Qy 62 CysProSerSerThrAlaAspIleSerArgLeuLeuGlnTyrlAlaAlaAsnGly----- 79  
 Db 205 TGCCCTTCTCCACACGAGGTGCTGCTCTCCCTCCGTTTCGCTAACGGAGATCTCTCT 264  
 Qy 80 -----LysSerThrPheGlnValAlaAlaArgGlyGlnGly 91  
 Db 265 TACAATAAAGGCTCAACACGAGCCCGCTCTACTTTCAAAGTGGCTGCTCGAGGCCAAGC 324  
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 Db 325 CACTCCCTCGTGGCGCAAGCCTCTGCACCCGAGGTGCTGCTGTAACATGACGTGCTC 384  
 Qy 112 -----ThrAspValValSerLysAspLysLysAspLysTyrlAlaAspVal 125  
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 Db 1381 GAAATACTGAAGTTTGTGAGGATGCTAATATGGGGTTTATACAAATATCTTCTTATCAT 1440  
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 QY 485 LysAspLeuPheAspProLysLysLeuLeuSerProGlyGlnAspIlePhe 501  
 Db 1501 AATATATAATATGATCCCAAAATGATATTATCACCAGGACAAAATATATT 1551

Search completed: April 7, 2004, 12:30:47  
 Job time : 1781 secs

QY 72 LeuLeuGlnTyrAlaAlaAsnGlyLysSerThrPheGlnValAlaAlaArgGlyGlnGly 91  
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 QY 92 HisSerLeuAsnGlyGlnAlaSerValSerGlyGlyValIleValAsnMetThrCysIle 111  
 Db 313 CACAGCCACCGTGGCCACGCTCGCTAAGACGGAGTTGGTCAACATCGGTCCATG 372  
 QY 112 ThrAsp-----ValValValSerLysAspLysLysTyrAlaAspValAlaAla 127  
 Db 373 GTAACCGGATCGAGGTATCAAGTGTCTAGGACCTGTTTATATGTTGACGTGACGCT 432  
 QY 128 GlyThrLeuTyrValAspValLeuLysThrAlaGluLysGlyValSerProValSer 147  
 Db 433 GCGTGCTATGATTGAGGTGTGAATAAACTTTGGAGTTAGGTTAAGCGCGGTTCCT 492  
 QY 148 TrpThrAspTyrLeuHisIleThrValGlyGlyThrLeuSerAsnGlyGlyIleGly 167  
 Db 493 TGGACGGATATTGTATTAACTGCTCGGTGGAGCTTATCAACGGCGGAATTAGTGA 552  
 QY 168 GlnValPheArgAsnGlyProLeuValSerAsnValLeuGluLeuAspValIleThrGly 187  
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 QY 285 LysValAlaAspLeuValLysGlnHisGlyIleIleTyrValLeuGluValAlaLysTyr 304  
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 QY 405 LysTrpAspAsnArgMetSerAlaMetIleProGluIleAspGluAspValIleTyrIle 424  
 Db 1267 AAGTGGATGATCGGATGCTGCGCTATACCCGAG-----GAAGATGATTTTATGCG 1320

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: April 6, 2004, 20:38:20 ; Search time 6045 Seconds  
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10798.116 Million cell updates/sec

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hgt.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
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- 15: em\_ba.\*
- 16: em\_fun.\*
- 17: em\_hum.\*
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- 22: em\_ov.\*
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- 24: em\_ph.\*
- 25: em\_pl.\*
- 26: em\_ro.\*
- 27: em\_sts.\*
- 28: em\_un.\*
- 29: em\_vi.\*
- 30: em\_htg\_hum.\*
- 31: em\_htg\_inv.\*
- 32: em\_htg\_other.\*
- 33: em\_htg\_mus.\*
- 34: em\_htg\_pln.\*
- 35: em\_htg\_rtd.\*
- 36: em\_htg\_mam.\*
- 37: em\_htg\_vrt.\*
- 38: em\_sy.\*
- 39: em\_htgo\_hum.\*
- 40: em\_htgo\_mus.\*
- 41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

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44	200.8	13.3	1330	8	AK101022	Oryza sat
45	188.4	12.5	1776	8	ZMY18377	Zea mays mr

ALIGNMENTS

RESULT 1	AX339729	AX339729	1506 bp	DNA	linear	PAT 10-JAN-2002
LOCUS	Sequence 26 from Patent WO0196580.					
DEFINITION	AX339729					
ACCESSION	AX339729					
VERSION	AX339729.1	GI:18135722				
KEYWORDS	Arabidopsis thaliana (thale cress)					
SOURCE	Arabidopsis thaliana					
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;					
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;					
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi					
REFERENCE	Schmueling, T. and Werner, T.					
AUTHORS	Method for modifying plant morphology, biochemistry and physiology					
TITLE						

JOURNAL Patent: WO 0196580-A 26 20-DEC-2001;  
Schmullling, Thomas (DE); Werner, Tomas (DE)  
FEATURES  
source  
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LOCUS Sequence 26 from Patent WO03050287.  
DEFINITION AX785077  
ACCESSION AX785077.1 GI:32952908  
VERSION  
KEYWORDS  
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ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
REFERENCE  
AUTHORS Schmullling, T. and Werner, T.  
TITLE Method for modifying plant morphology, biochemistry and physiology  
JOURNAL Patent: WO 03050287-A 26 19-JUN-2003;  
Schmullling, Thomas (DE); Werner, Tomas (DE)  
FEATURES  
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Query Match 100.0%; Score 1506; DB 6; Length 1506;  
Best Local Similarity 100.0%; Pred. No. 0;  
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QY 1 ATGGCTAATCTTCGTTTAATGATCACTTAAATCAGCGTTTAAATGATCAACCAATCATCA 60  
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DEFINITION  
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Arabidopsis thaliana clone U20989 putative cytokinin oxidase  
(At2g19500) mRNA, complete cds.

ACCESSION  
BT005653  
VERSION  
BT005653.1  
KEYWORDS  
FLU\_CDNA.  
SOURCE  
Arabidopsis thaliana (thale cress)  
ORGANISM  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE  
AUTHORS  
1 (bases 1 to 1537)  
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M.,  
Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C.,  
Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y.,  
Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M.,  
Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P.,  
Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W.,  
Ecker, J.R. and Theologis, A.  
Arabidopsis Open Reading Frame (ORF) Clones  
Unpublished

TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
2 (bases 1 to 1537)  
Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M.,  
Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C.,  
Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y.,  
Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M.,  
Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P.,  
Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W.,  
Ecker, J.R. and Theologis, A.  
Direct Submission

TITLE  
JOURNAL  
COMMENT  
Submitted (15-MAR-2003) Plant Gene Expression Center, 800 Buchanan  
Street, Albany, CA 94710, USA  
The RIKEN Genomic Sciences Center (GSC) members carried out the  
collection and clustering of RAPL cDNAs (RAPL cDNA: RIKEN  
Arabidopsis Full-length cDNA): Seki, M., Narusaka, M., Ishida, J.,  
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,  
Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGECC (SSP) Consortium members constructed and

sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.B., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A.

Yamada, K. (SGP/PSEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PSEC) contributed equally to this work as PIs.

Annotation based on July 2002 version of the Arabidopsis genome submitted to Genbank.

# FEATURES

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## 3' UTR

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RESULT 4

BT004107

LOCUS

DEFINITION Arabidopsis thaliana clone RAFL15-29-H04 (R20989) putative cytochrome oxidase (At2g19500) mRNA, complete cds.

ACCESSION BT004107

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 1687)

Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

Arabidopsis Full Length cDNA Clones

Unpublished

2 (bases 1 to 1687)

Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Kawai, J., Kim, C.J., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.

Direct Submission

Submitted (14-FEB-2003) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Chan, M.M., Chang, C.H., Dale, J.M., Hsuan, V.W., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yu, G., Yuan, S., Carninci, P., Chen, H., Cheuk, R., Jones, T., Kim, C.J., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tripp, M.G., Wu, T., Davis, R.W., Ecker, J.R. and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation based on July 2002 version of the Arabidopsis genome submitted to Genbank.

Location/Qualifiers

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 VERSION AF303978.1 GI:1120507  
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 SOURCE Arabidopsis thaliana  
 ORGANISM Arabidopsis thaliana  
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 1 (bases 1 to 1506)  
 BILYEU, K.D., LASKEY, J.G., RIEKHOF, W.R., VANVICKLE, S. and  
 MORRIS, R.O.

A family of cytokinin oxidases from Arabidopsis thaliana  
 Unpublished  
 2 (bases 1 to 1506)  
 Bilyeu, K.D., Laskey, J.G., Riekhof, W.R., VanVickle, S. and  
 Morris, R.O.  
 Direct Submission  
 Submitted (11-SEP-2000) University of Missouri, 210 Waters Hall,  
 Columbia, MO 65211, USA

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DEFINITION Sequence 28 from Patent WO0196580.  
ACCESSION AX339731  
VERSION AX339731.1 GI:18135724  
KEYWORDS Arabidopsis thaliana (thale cress)  
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ORGANISM Arabidopsis thaliana  
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Schmulling, T. and Werner, T.  
Method for modifying plant morphology, biochemistry and physiology  
Patent: WO 0196580-A 28 20-DEC-2001;  
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VERSION	AX507394.1	GI:23388631			
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1 Harper, J.F., Kreps, J., Wang, X. and Zhu, T.  
Stress-regulated genes of plants, transgenic plants containing  
same, and methods of use  
Patent: WO 0216655-A 2089 28-FEB-2002;  
The Scripps Research Institute (US) ; Syngenta Participations AG  
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 Schumling, T. and Werner, T.  
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 Bilyeu,K.D., Laskey,J.G., Riekhof,W.R., VanVickle,S. and Morris,R.O.  
 A family of cytochrome oxidases from Arabidopsis thaliana  
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 Bilyeu,K.D., Laskey,J.G., Riekhof,W.R., VanVickle,S. and Morris,R.O.  
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 Columbia, MO 65211, USA  
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AUTHORS

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ORIGIN

Query Match

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Arabidopsis thaliana (thale cress)

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Southwick, A., Karlin-Neumann, G., Nguyen, M., Lam, B., Miranda, M.,  
Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H.,  
Cheuk, R., Chung, M.K., Hayashizaki, Y., Ishida, J., Kamiya, A.,  
Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K.,  
Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K.,  
Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.

Direct Submission

Submitted (28-AUG-2001) DNA Sequencing and Technology Center,  
Stanford University, 855 California Avenue, Palo Alto, CA 94304,  
USA

e-mail for correspondence: arab@sequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the  
collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN  
Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J.,  
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,  
Hayashizaki, Y. and Shinozaki, K.

The Saik, Stanford, PGEC (SSP) Consortium members carried out the  
sequencing and annotation of the RAFL cDNAs: Nguyen, M.,  
Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C.J.,  
Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M.K.,  
Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P.,  
Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.

Southwick, A., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed  
equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.W.  
(SSP/Stanford) contributed equally to this work as PIs.

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LOCUS		
DEFINITION	AC005917 92822 bp DNA linear PLN 27-FEB-2002	
	Arabidopsis thaliana chromosome 2 clone F3P11 map C1C06E08,	
	complete sequence.	
ACCESSION	AC005917	
VERSION	AC005917.3	GI:20197478
KEYWORDS	HTG.	
SOURCE	Arabidopsis thaliana (thale cress)	
ORGANISM	Arabidopsis thaliana	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;	
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.	
REFERENCE	1 (bases 1 to 92822)	
AUTHORS	Lin,X., Kaul,S., Shea,T.P., Fujii,C.Y., Shen,M., VanAken,S.E.,	
	Barnstead,M.E., Mason,T.M., Bowman,C.L., Ronning,C.M.,	
	Benito,M.-I., Carrera,A.J., Creasy,T.H., Buell,C.R., Town,C.D.,	
	Nierman,W.C., Fraser,C.M. and Venter,J.C.	
	Unpublished	
JOURNAL	2 (bases 1 to 92822)	
REFERENCE	Lin,X.	
AUTHORS	Lin,X.	
TITLE	Direct Submission	
JOURNAL	Submitted (09-MAR-2000) The Institute for Genomic Research, 9712	
	Medical Center Dr., Rockville, MD 20850, USA	
REFERENCE	3 (bases 1 to 92822)	
AUTHORS	Town,C.D. and Kaul,S.	
TITLE	Direct Submission	
JOURNAL	Submitted (27-FEB-2002) The Institute for Genomic Research, 9712	
	Medical Center Dr., Rockville, MD 20850, USA, cdtown@tigr.org	
COMMENT	On Apr 18, 2002 this sequence version replaced gi:6598497.	
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Query Match 38.3%; Score 577; DB 8; Length 92822;  
Best Local Similarity 75.9%; Pred. No. 1.5e-152;  
Matches 852; Conservative 0; Mismatches 40; Indels 231; Gaps 2;  
QY 615 AGTGTAGGAGGTTGGGTCAATTTGGAAATTAACGAGAGCCAGAATTTGGACCA 674  
Db 40172 ACTGTAATATGGTTCTTTATATATATGTTGTAATAAATTAATGGGATGTTTCTCTAAA 40113  
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QY 944 ----- 943  
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Search completed: April 7, 2004, 04:38:06  
Job time : 6061 secs

OM nucleic - nucleic search, using sw model

Run on: April 6, 2004, 20:36:10 ; Search time 691 Seconds  
(without alignments)  
9258.736 Million cell updates/sec

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Perfect score: 1506  
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Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0  
Searched: 3373863 seqs, 2124099041 residues  
Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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8: geneseqn2003bs:.\*  
9: geneseqn2003cs:.\*  
10: geneseqn2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1506	100.0	1506	6	ABK28625 CDNA enco
2	1506	100.0	1506	8	ACC85294 Arabidops
3	1454	96.5	1548	3	AAC43214 Arabidops
4	778.2	51.7	1575	3	ACC42383 Arabidops
5	778.2	51.7	1575	6	ABZ14284 Arabidops
6	778.2	51.7	1575	6	ABK28627 CDNA enco
7	778.2	51.7	1575	7	ADA68648 Arabidops
8	778.2	51.7	1575	8	ACC85296 Arabidops
9	577	38.3	2991	6	ABK28607 DNA enco
10	577	38.3	2991	8	ACC85276 Arabidops
11	470	31.2	1572	6	ABK28626 CDNA enco
12	461.2	30.6	1572	8	ACC85295 Arabidops
13	318.6	21.2	1602	3	AAC36788 Arabidops
14	306.2	20.3	1611	6	ABK28628 CDNA enco
15	306.2	20.3	1611	8	ACC85297 Arabidops
16	306.2	20.3	1620	6	ABK28632 CDNA enco
17	306.2	20.3	1620	8	ACC85301 Arabidops
18	248.8	16.5	1728	6	ABK28624 CDNA enco
19	248.8	16.5	1728	8	ACC85293 Arabidops
20	238.2	15.8	1566	7	ADA71115 Rice gene
21	238.2	15.8	1566	7	ADA69574 Rice gene
22	232	15.4	1587	7	ADA69574 Rice gene
23	225.8	15.0	2782	6	ABK28609 DNA enco

24	225.8	15.0	2782	8	ACC85278 Arabidops
25	209	13.9	1590	7	ADA69773 Rice gene
26	185.2	12.3	1605	2	AAO2914 Z. mays c
27	183.4	12.2	1593	7	ADA69430 Rice gene
28	181	12.0	1608	3	ACC8501 DNA enco
29	172	11.4	3302	6	ABK28608 Arabidops
30	172	11.4	3302	8	ACC85277 Arabidops
31	171	11.4	1515	6	ABK28629 CDNA enco
32	171	11.4	1515	8	ACC85298 Arabidops
33	144.4	9.6	1677	7	ADA70177 Rice gene
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36	123.8	8.2	2814	6	ABK28631 DNA enco
37	123.8	8.2	2814	8	ACC85300 Arabidops
38	108.2	7.2	6733	2	AAO2913 Z. mays c
39	84	5.6	84	6	ABK28630 A. thalia
40	84	5.6	84	8	ACC85299 Arabidops
41	73.8	4.9	1936	6	ABK28611 DNA enco
42	73.8	4.9	1936	8	ACC85280 Arabidops
43	73.2	4.9	2236	6	ABK28606 DNA enco
44	73.2	4.9	2236	8	ACC85275 Arabidops
45	53.6	3.6	1464	7	ABT32136 Benzodiaz

ALIGNMENTS

RESULT 1  
ABK28625  
ID ABK28625 standard; cDNA; 1506 BP.  
XX  
AC ABK28625;  
XX  
DT 09-APR-2002 (first entry)  
XX  
DE cDNA encoding A. thaliana cytokinin oxidase AtCKX2.  
XX  
KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;  
KW root growth; lateral root; adventitious root; root geotropism; herbicide;  
KW root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
FN WC200196580-A2.  
XX  
PD 20-DEC-2001.  
XX  
PF 18-JUN-2001; 2001WO-EP006833.  
XX  
PR 16-JUN-2000; 2000EP-00870132.  
PR 27-DEC-2000; 2000US-0258415P.  
PR 16-MAR-2001; 2001EP-00870053.  
PA (SCHM/) SCHMULLING T.  
PA (WERN/) WERNER T.  
XX  
PI Schmulling T, Werner T;  
XX  
DR WPI; 2002-130736/17.  
XX  
PT Polynucleotide encoding novel plant protein having cytokinin oxidase  
PT activity and the protein useful for stimulating root growth, enhancing  
PT the formation of lateral or adventitious roots, altering root geotropism.  
XX  
PS Claim 2; Page 146-147; 154pp; English.  
XX  
CC The invention relates to an isolated polynucleotide (I) encoding a novel  
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for  
CC production of transgenic plants, plant cells or tissues; for production  
CC of altered plants, plant cell or tissues; and for effecting the  
CC expression of (II) where (I) is operably linked to one or more control  
CC sequences. The methods further comprises regenerating a plant from the  
CC plant cell. (I) and (II) are useful for stimulating root growth;



XX (SCHM/) SCHMULLING T.  
PA (WERN/) WERNER T.  
XX  
XX Schumulling T, Werner T;  
XX  
XX WPI; 2003-541577/51.  
XX  
XX Stimulating root growth, enhancing lateral or adventitious root formation  
PT or altering root geotropism comprises increasing plant cytokinin oxidase  
PT levels or other protein or nucleic acid that reduces active cytokinins in  
PT a plant.  
XX  
XX Claim 3; Page 167-168; 177pp; English.  
XX  
XX The present invention relates to a method for stimulating root growth or  
CC enhancing the formation of lateral or adventitious roots or altering root  
CC geotropism, which comprises increasing in a plant or plant part the level  
CC of a plant cytokinin oxidase or other protein that reduces the level of  
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and  
CC coding sequences from Arabidopsis thaliana are also provided. The method  
CC is useful in modifying plant morphological, biochemical and physiological  
CC properties, such as in modifying the initiation, stimulation or  
CC enhancement of root growth, adventitious root formation, lateral root  
CC formation, root geotropism, shoot growth, apical dominance, branching,  
CC timing of senescence, timing of flowering, flower formation, seed  
CC development and/or seed yield. The present sequence is a coding sequence  
CC shown in the invention  
XX  
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XX  
XX Query Match 100.0%; Score 1506; DB 8; Length 1506;  
XX Best Local Similarity 100.0%; Pred. No. 0;  
XX Matches 1506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 ATGGCTAATCTCGTTTAAATGATCACTTAAATCAAGGTTTAAATGATCAACCAATATCA 60  
XX  
XX 61 AACGGTATTAATGATTTACCTAAATCCCTTAACTCAAGGTTTAAATGATCAACCAATATCA 120  
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DB 121 ATCATCTCGGAGCTCTCATGCTCGGAAACATAACCAAGGTTTAAATGATCAACCAATATCA 180  
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XX 241 AGTACATTCAGTAGCGGCTGTGGCCAGGCACTCTCTAAACGGCCAAAGCTCGGTC 300  
DB 241 AGTACATTCAGTAGCGGCTGTGGCCAGGCACTCTCTAAACGGCCAAAGCTCGGTC 300  
XX  
XX 301 TCCGGCGGAGTAAATCGTCAACATGACGCTGATCACTGACGCTGTTTCAAAAGACAAG 360  
DB 301 TCCGGCGGAGTAAATCGTCAACATGACGCTGATCACTGACGCTGTTTCAAAAGACAAG 360  
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XX 361 AAGTAGCTGACGTGGCGCGGAGCGTTATGGTGGATGCTTAAAGAGACGCGGAG 420  
DB 361 AAGTAGCTGACGTGGCGCGGAGCGTTATGGTGGATGCTTAAAGAGACGCGGAG 420  
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XX 421 AAAGGGGTGTGGCGGCTTCTTGGAGCGGATTAATTCATATACCGCTCGGAGAACGTTG 480  
DB 421 AAAGGGGTGTGGCGGCTTCTTGGAGCGGATTAATTCATATACCGCTCGGAGAACGTTG 480  
XX  
XX 481 TCGAATGGTGAATTTGGTGGTCAAGTGTTCGAAACGGTCTCTTGTAGTAAACGTCCTT 540  
DB 481 TCGAATGGTGAATTTGGTGGTCAAGTGTTCGAAACGGTCTCTTGTAGTAAACGTCCTT 540  
XX  
XX 541 GAATTTGACGCTTAACTCGGAAAGTGAATGTTGACATGCTCGCGACAGCTAAACCCA 600

DB 541 GAAATTTGGACGTTATTACTGGGAAAGGTGAAATGTTGACATGCTCGCGACAGCTAAACCCA 600  
QY 601 GAAATTTGTTCTTATGGAGTGTTAGGAGTTTGGGTCAAATTTGGAATTTATAACGAGAGCCAGA 660  
DB 601 GAAATTTGTTCTTATGGAGTGTTAGGAGTTTGGGTCAAATTTGGAATTTATAACGAGAGCCAGA 660  
QY 661 ATTGTTTGGACCATGCACTTAAACGGGCGCAAAATGGTTTGGATGCTCTACAGTATTTTC 720  
DB 661 ATTGTTTGGACCATGCACTTAAACGGGCGCAAAATGGTTTGGATGCTCTACAGTATTTTC 720  
QY 721 ACAACCTTTTACAAAGGACCAAGAACGTTTGTATATCAATGGGCAAAAGATATTTGGAGTCGAC 780  
DB 721 ACAACCTTTTACAAAGGACCAAGAACGTTTGTATATCAATGGGCAAAAGATATTTGGAGTCGAC 780  
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DB 781 TATTAGAGAGTCAAAATATTTCTATCAAAACGGGTGCTGTGACACCTCTTTTTCACACT 840  
QY 841 TCAGATCAATCTAAAGTCTGCTGATCTAGTCAAGCAACAGGTATCATCTATGTTCTTGA 900  
DB 841 TCAGATCAATCTAAAGTCTGCTGATCTAGTCAAGCAACAGGTATCATCTATGTTCTTGA 900  
QY 901 GTAGCCAACTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTTATTGACACATTA 960  
DB 901 GTAGCCAACTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTTATTGACACATTA 960  
QY 961 ACAGAAACATTAAGTTACTTTCGCGGTTTCTATCAATGACAGAGTGGCTTCTTTCGAT 1020  
DB 961 ACAGAAACATTAAGTTACTTTCGCGGTTTCTATCAATGACAGAGTGGCTTCTTTCGAT 1020  
QY 1021 TTCTTGAACCGTGTACATGTCGAAAGAAAAATAAATCAGATCTTTGGGATTTATGGGAAC 1080  
DB 1021 TTCTTGAACCGTGTACATGTCGAAAGAAAAATAAATCAGATCTTTGGGATTTATGGGAAC 1080  
QY 1081 CCTCATCTTGGGTTAACTTACCTTACGTTTCTTAATCTCGGATTCGATTTTCAATACGGT 1140  
DB 1081 CCTCATCTTGGGTTAACTTACCTTACGTTTCTTAATCTCGGATTCGATTTTCAATACGGT 1140  
QY 1141 GTTGTCAAGACATCTTCTTAAGCAAAATCAGCTTTCGGGACTCGCTCTCTCTATCCA 1200  
DB 1141 GTTGTCAAGACATCTTCTTAAGCAAAATCAGCTTTCGGGACTCGCTCTCTCTATCCA 1200  
QY 1201 ACAAAACGGGAAATTAATGGGACAAATCGTATGTGCGGATGATACAGAGATCGATGAAGAT 1260  
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DB 1321 AGCGTTAACGAGAGATAAATAGGTTTGGATTTGAGCATTTTGGATTAAGATTAAGCAATAT 1380  
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DB 1381 CTAAATGATTTACTAGTAAAGAGATTGGATTGAGCATTTTGGATTAAGATTAAGCAATAT 1440  
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QY 1501 TTTTGA 1506  
DB 1501 TTTTGA 1506

RESULT 3  
AAC43214  
ID AAC43214 standard; DNA; 1548 BP.  
XX  
AC  
AC AAC43214;  
XX

DT	17-OCT-2000	(first entry)
XX	DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 38443.
XX	DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 38443.
KW	XX	Hybridisation assay; genetic mapping; gene expression control;
KW	XX	protein identification; signal transduction pathway; metabolic pathway;
KW	XX	promoter; termination sequence; ss.
OS	XX	Arabidopsis thaliana.
PN	XX	EP1033405-A2.
PD	XX	06-SEP-2000.
PF	XX	25-FEB-2000; 2000EP-00301439.
PR	XX	25-FEB-1999; 99US-0121825P.
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PR	27-AUG-1999;	99US-0151066P.	PR	241	AGTACATTCCAAGTAGCGGCTCGTGGCCAAAGCCACTCTTAACGGCCAAAGCCTCGGTC	300
PR	27-AUG-1999;	99US-0151080P.	QY	301	TCGGCGGAGTAATCGTCAACATGCGTGTATCATGACGTGGTGGTTTCAAAAGACAAG	360
PR	30-AUG-1999;	99US-0151030P.	Db	301	TCGGCGGAGTAATCGTCAACATGCGTGTATCATGACGTGGTGGTTTCAAAAGACAAG	360
PR	01-SEP-1999;	99US-0151930P.	QY	361	AAATACGCTGACGTGGCGGCGGACGTTATGGGTGGATGTCTTAAGAAAGACGGCGGAG	420
PR	07-SEP-1999;	99US-0152233P.	Db	361	AAATACGCTGACGTGGCGGCGGACGTTATGGGTGGATGTCTTAAGAAAGACGGCGGAG	420
PR	10-SEP-1999;	99US-0153070P.	QY	421	AAAGGGGTGTCCCGGTTTCTTGGACGATTTATTTGCAATATAAACCGTGGAGGAACGTTG	480
PR	13-SEP-1999;	99US-0153758P.	Db	421	AAAGGGGTGTCCCGGTTTCTTGGACGATTTATTTGCAATATAAACCGTGGAGGAACGTTG	480
PR	15-SEP-1999;	99US-0154018P.	QY	481	TCGAATGGTGAATTTGGTCAAGTGTTCGAAACGGTCTCTTGTGTAGTAACGTCCTT	540
PR	20-SEP-1999;	99US-0154779P.	Db	481	TCGAATGGTGAATTTGGTCAAGTGTTCGAAACGGTCTCTTGTGTAGTAACGTCCTT	540
PR	22-SEP-1999;	99US-0155113P.	QY	541	GAATTGGACGTTATTAATCTGGGAAAGGTGAATGTTGACATGCTCGGACAGCTAAACCCA	600
PR	23-SEP-1999;	99US-0155486P.	Db	541	GAATTGGACGTTATTAATCTGGGAAAGGTGAATGTTGACATGCTCGGACAGCTAAACCCA	600
PR	24-SEP-1999;	99US-0155659P.	QY	601	GAATTGGTCTATGGAGTTAGGAGTTTGGTCAATTTGGAAATATAACGAGACCCAGA	660
PR	28-SEP-1999;	99US-0156458P.	Db	601	GAATTGGTCTATGGAGTTTAGGAGTTTGGTCAATTTGGAAATATAACGAGACCCAGA	660
PR	29-SEP-1999;	99US-0156596P.	QY	661	ATTGTTTTGGACCATGCACTTAACCGGCCAAATGGTTTCGGATGCTCTACAGTGATTC	720
PR	04-OCT-1999;	99US-0157117P.	Db	661	ATTGTTTTGGACCATGCACTTAACCGGCCAAATGGTTTCGGATGCTCTACAGTGATTC	720
PR	06-OCT-1999;	99US-0157753P.	QY	721	ACAACTTTTACAAGGACCAAGACGTTTGAATCAATGGGCAAGATATGAGATGCGAC	780
PR	07-OCT-1999;	99US-0158039P.	Db	721	ACAACTTTTACAAGGACCAAGACGTTTGAATCAATGGGCAAGATATGAGATGCGAC	780
PR	08-OCT-1999;	99US-0158232P.	QY	781	TATTTAGAGGTCAAAATATTTCTATCAACGGTGTCTGTGACACCTCTTTTTTCCACCT	840
PR	12-OCT-1999;	99US-0158365P.	Db	781	TATTTAGAGGTCAAAATATTTCTATCAACGGTGTCTGTGACACCTCTTTTTTCCACCT	840
PR	13-OCT-1999;	99US-0159293P.	QY	841	TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTGAA	900
PR	13-OCT-1999;	99US-0159294P.	Db	841	TCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTGAA	900
PR	13-OCT-1999;	99US-0159295P.	QY	901	GTAGCCCAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTTATTGACACATTA	960
PR	14-OCT-1999;	99US-0160741P.	Db	901	GTAGCCCAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTTATTGACACATTA	960
PR	21-OCT-1999;	99US-0160767P.	QY	961	ACGAAAACATTAAGTTACTTTGCGCGGTTTCAATCAATGACGACGCTGCGCTACTTCGAT	1020
PR	21-OCT-1999;	99US-0160768P.	Db	961	ACGAAAACATTAAGTTACTTTGCGCGGTTTCAATCAATGACGACGCTGCGCTACTTCGAT	1020
PR	21-OCT-1999;	99US-0160770P.	QY	1021	TTCTTGAACCGGTACATGTCGAAAGAAATAAATCAATCTTTGGGATTTATGGGAACCTT	1080
PR	21-OCT-1999;	99US-0160814P.	Db	1021	TTCTTGAACCGGTACATGTCGAAAGAAATAAATCAATCTTTGGGATTTATGGGAACCTT	1080
PR	22-OCT-1999;	99US-0160815P.	QY	1081	CCTCATCTTGGCTTAACCTCTACGTTCTGATTTCTGAAATCTCGGATTTCTCGATTTTCAATACGCT	1140
PR	22-OCT-1999;	99US-0160980P.	Db	1081	CCTCATCTTGGCTTAACCTCTACGTTCTGATTTCTGAAATCTCGGATTTCTCGATTTTCAATACGCT	1140
PR	22-OCT-1999;	99US-0160981P.	QY	1141	GTGTCAAGACATCTTCTTAAAGCAAAATCAGCTTCGAGCTTCGCTCTCTCTATCCA	1200
PR	22-OCT-1999;	99US-0161361P.	Db	1141	GTGTCAAGACATCTTCTTAAAGCAAAATCAGCTTCGAGCTTCGCTCTCTCTATCCA	1200
PR	28-OCT-1999;	99US-0161920P.	QY	1201	ACAAACCGGAAT-----AAATGG	1218
PR	28-OCT-1999;	99US-0161933P.	Db	1201	ACAAACCGGAAT-----AAATGG	1218
PR	29-OCT-1999;	99US-0162142P.	QY	1219	GACAACTGATGTCGGGATGATACAGAGATCGATGAAGATGTTATATATATATCGGA	1278
PR	29-OCT-1999;	99US-0162142P.	Db	1261	GACAACTGATGTCGGGATGATACAGAGATCGATGAAGATGTTATATATATATCGGA	1320
PR	29-OCT-1999;	99US-0162142P.	QY	1279	CTACTCAATCCCGTACCCCAAGAGTCTTCCAGAAAGTGGAGAGCGTTAACGAGAAGATA	1338
PR	29-OCT-1999;	99US-0162142P.	Db	1321	CTACTCAATCCCGTACCCCAAGAGTCTTCCAGAAAGTGGAGAGCGTTAACGAGAAGATA	1380

Query Match 96.5%; Score 1454; DB 3; Length 1548;  
 Best Local Similarity 97.3%; Pred. No. 0;  
 Matches 1506; Conservative 0; Mismatches 0; Indels 42; Gaps 1;

QY	1	ATGGCTAATCTCGTTTAAATGATCACTTTAATCAACGGTTTAAATGATCAACCAATCATCA	60
Db	1	ATGGCTAATCTCGTTTAAATGATCACTTTAATCAACGGTTTAAATGATCAACCAATCATCA	60
QY	61	AAAGGTATTAAATTAATTAATCACTAAATCCCTTAAACCTCACCTCTCTACCGATCCTTCC	120
Db	61	AAAGGTATTAAATTAATTAATCACTAAATCCCTTAAACCTCACCTCTCTACCGATCCTTCC	120
QY	121	ATCATCTCGGAGCCTCTCATGACTCGGAAACATACCAACCGTACCCCGGCGGCTA	180
Db	121	ATCATCTCGGAGCCTCTCATGACTCGGAAACATACCAACCGTACCCCGGCGGCTA	180
QY	181	ATCTGCCCTCTCCACCGCTGATATCTCTCGTCTCTCCCAATACGCGGCAAAACGAAAA	240
Db	181	ATCTGCCCTCTCCACCGCTGATATCTCTCGTCTCTCCCAATACGCGGCAAAACGAAAA	240
QY	241	AGTACATTCCAAGTAGCGGCTCGTGGCCAAAGCCACTCTTAACGGCCAAAGCCTCGGTC	300
Db	241	AGTACATTCCAAGTAGCGGCTCGTGGCCAAAGCCACTCTTAACGGCCAAAGCCTCGGTC	300





	Matches	1093;	Conservative	0;	Mismatches	363;	Indels	57;	Gaps	4;
PR	06-AUG-1999;	99US-0147303P.								
PR	06-AUG-1999;	99US-0147416P.								
PR	09-AUG-1999;	99US-0147493P.								
PR	09-AUG-1999;	99US-0147935P.								
PR	10-AUG-1999;	99US-0148171P.								
PR	11-AUG-1999;	99US-0148319P.								
PR	12-AUG-1999;	99US-0148341P.								
PR	13-AUG-1999;	99US-0148565P.								
PR	13-AUG-1999;	99US-0148684P.								
PR	16-AUG-1999;	99US-0149368P.								
PR	17-AUG-1999;	99US-0149175P.								
PR	18-AUG-1999;	99US-0149436P.								
PR	20-AUG-1999;	99US-0149722P.								
PR	20-AUG-1999;	99US-0149929P.								
PR	23-AUG-1999;	99US-0149902P.								
PR	23-AUG-1999;	99US-0149930P.								
PR	25-AUG-1999;	99US-0150566P.								
PR	26-AUG-1999;	99US-0150884P.								
PR	27-AUG-1999;	99US-0151065P.								
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PR	27-AUG-1999;	99US-0151080P.								
PR	30-AUG-1999;	99US-0151303P.								
PR	31-AUG-1999;	99US-0151438P.								
PR	01-SEP-1999;	99US-0151930P.								
PR	07-SEP-1999;	99US-0152363P.								
PR	10-SEP-1999;	99US-0153070P.								
PR	13-SEP-1999;	99US-0153758P.								
PR	15-SEP-1999;	99US-0154018P.								
PR	16-SEP-1999;	99US-0154039P.								
PR	20-SEP-1999;	99US-0154779P.								
PR	23-SEP-1999;	99US-0155139P.								
PR	23-SEP-1999;	99US-0155488P.								
PR	24-SEP-1999;	99US-0155659P.								
PR	28-SEP-1999;	99US-0156458P.								
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PR	04-OCT-1999;	99US-0157117P.								
PR	05-OCT-1999;	99US-0157753P.								
PR	08-OCT-1999;	99US-0157865P.								
PR	08-OCT-1999;	99US-0158029P.								
PR	08-OCT-1999;	99US-0158232P.								
PR	12-OCT-1999;	99US-0158369P.								
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PR	14-OCT-1999;	99US-0159638P.								
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PR	21-OCT-1999;	99US-0160770P.								
PR	21-OCT-1999;	99US-0160814P.								

Query Match 51.7%; Score 778.2; DB 3; Length 1575;  
Best Local Similarity 72.2%; Pred. No. 1.9e-228;  
Best Local Similarity 72.2%; Pred. No. 1.9e-228;

CC array or probes representative of the plant cell genome; and (b)  
CC detecting a profile of expressed polynucleotides in the plant cell  
CC characteristic of a stress response. The method is useful in the  
CC production of transgenic plants, cells and seeds and in producing plants  
CC with increased tolerance to abiotic stresses. The present sequence is that  
CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used  
CC in methods of the invention. Note: The sequence data for this patent is  
CC not represented in the printed specification but is based on sequence  
CC information supplied to Derwent by the European Patent Office  
XX  
SQ Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;

Query Match 51.7%; Score 778.2; DB 6; Length 1575;  
Best Local Similarity 72.2%; Pred. No. 1.9e-228;  
Matches 1093; Conservative 0; Mismatches 363; Indels 57; Gaps 4;

QY 42 AATGATCACAATCATCAACGGTATTAAATGATTACCTAAATCCCTTAACCTCAAC 101  
DB 63 AACCTTAATCAATCAGATGAGGGCATTTGATGTTTCTTACCCTATCACTCAACCTTAC 122  
QY 102 CTTCTCTACCGATCTCTCCATCATCTCCGACCTCTCATGACTTCGGAACATAACCAAC 161  
DB 123 GGTCTTAACCGATCCCTTCTCCATCTCTCCGCTTCTCAGACTTCGGTAACATAACCGA 182  
QY 162 CTTGACCCCGGGGGGTAATCTGCCCTCTCCACCGCTGATATCTCTGCTCTCTCC 220  
DB 183 CGAAATCCCGGGCGCTCTCTGCCCTTCTCCACCGAGGCTGCTGCTCTCTCCG 242  
QY 221 -----AATACGCGCGCAACCGGTAATGCTTACATAAAGCTCAACAGCCCGCTACTTCAA 251  
DB 243 TTTTCGTAACGGAGGATTTCTTTACATAAAGCTCAACAGCCCGCTACTTCAA 302  
QY 252 AGTAGCGGCTCTGGCGAAGGCGCTCTTAACCGCGAAGCTCGTCTCGGGGAGT 311  
DB 303 AGTGGCTGCTCGAGGCGCAAGGCGCTCTCCGCTCGGCGAGTGTGGTGTGAGGCGGC 362  
QY 312 AATCGTCAACATGACGTGTATC-----ACTGACGTGGTGGTTTCAAA 353  
DB 363 CGTCGTGAACATGACGTGTCTGCCATGCGGCTAAACCGCGGCTGTTTATCTCGGC 422  
QY 354 AGACAAGATGCTGACGTGCGCGCGGAGCGTTATCGGTGGATGCTCTTAAGAGAC 413  
DB 423 AGACGGACTTACGCTGACGTGCTCGCGGAGTGTGGTGGATGCTCTGAAGCGGC 482  
QY 414 GCGGGAAGAGGGGTGTGCGCGGTTTCTTGACCGGATTTTGCATATAACCGCTCGGAG 473  
DB 483 GGTGGATAGAGCGTCTCGCGGTTACATGGACGGATTTTGTATCTCAGCGTGGCGG 542  
QY 474 AACGTTGCGAATGGTGGAAATCGGTGTCGAAGTGTTCGAACCGGCTCTCTTGTAGTAA 533  
DB 543 GACGTTGCGAAGCTGGAATCGGTGTCAGACGTTTAGACACGCGCTCAGATTAGTAA 602  
QY 534 CGTCTTGAATTCGACGTTTACTGGAAGGTGAAATGTTGACATGCTCGCGACAGCT 593  
DB 603 GGTTCATGAGCTTGACGTTTATTCGGAAGAGTGAATGATGACTTGTCTCCAAAGT 662  
QY 594 AAACCCAGAATTGTTCTATCGAGTGTAGAGGTTGGGTCAATTTGGAATTAACGAG 653  
DB 663 AAACCTGAAATTGTTCTATGAGGTTTGGGTCAATTCGGTATTATAACGAG 722  
QY 654 AGCCAGAAATGTTTGGACCATGACCTAAACCGGCGCAATGTTTCGGATGCTCTACAG 713  
DB 723 GCCCAGGATTCGTTGGATCATGACCCCAAGGTCGAATGCTCTCGATCTCTACAG 782  
QY 714 TGATTTCAACACTTTTCAAGGACCAAGAACGTTTGATATCAATGCGCAACGATATGG 773  
DB 783 TGACTTCTCGCTTTTAAAGAGACCAAGAGCGTTTAAATATCAATGACCAATGATCTCG 842  
QY 774 AGTCGACTTTTAGAGGTCGAATTTCTTCAACGGTGTGCTTGACACCTCTTTTT 833  
DB 843 AGTTGACTTTTGAAGGTCGAATTTATGATGTCGAATGGCTTGTGACACCTCTTTCT 902  
QY 834 CCCACCTTCAGATCAATCTAAAGTCGCTGATGTAGTCAAGCAACCGGTATCATGT 893

QY 1074 GGAATCTCTCATCTTGCGTTAACTTACCTCTAGCTTCTTAATCTCGGATTTCTCGATTTC 1133  
DB 1143 GGAATCTCTCATCTTGCGTTAACTTACCTTCTGCTCCGGGCTCTCGAATCCAAGATTTTC 1202  
QY 1134 TAAAGGTTGTTGCAAGACATTTCTTAAAGCAAAATCACTTCGGGACTCGCTCTTCT 1193  
DB 1203 TGATGGTGTATTATGAGCTTCTTCTTAACCAACCTCACTTCTGTTACTCTTCT 1262  
QY 1194 CTATCCAAACAAACCGGAATAAATGGCAATCGATGATGTCGCGGATGATACAGAGATCGA 1253  
DB 1263 CTATCCCAACAAACCGGAATAAATGGCAATCGATGATGTCACAGATGACACC-----GGA 1316  
QY 1254 TGAAGTGTATATATATATGCGACTACTACATCCGC---TACCCCAAGGATCTTCC 1310  
DB 1317 CGAAGATGTTTATGATGCGGATTTACTGCAATCAGCTGCTGATCTCAAAATTCGCA 1376  
QY 1311 AGAAGTGGAGCGGTTAACGAGAAGATAATTAGTTTTCGAAGATTCAGTATTAAGAT 1370  
DB 1377 AGAAGTGAATCTCAACGACAGGTTATTCAAGTTTGTGAAACTCGGGAATTAAGAT 1436  
QY 1371 TAAGCAATATCTAATGCAATTAAGTAAGAGAGATTTGAGCAATTTTGGATCAAA 1430  
DB 1437 TAAGGAATTTTGTGCACTATACAGAAAGAGATTTGGGTTAAACATTTTGGACCAA 1496  
QY 1431 ATGGGATGATTTTTCGAAGAGAAAGATCTATTTGATCCCAAGAACTGTTATCTCCAGG 1490  
DB 1497 ATGGGATGATTTTAAAGAAAGAAATTTATGTTGATCCCAAGAGATTTATGCTCCAGG 1556  
QY 1491 GCAAGACATCTTT 1503  
DB 1557 ACAAGACATATTT 1569

RESULT 5

ID AB214284  
AC AB214284;  
XX  
XX  
DT 21-JAN-2003 (first entry)  
XX  
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2089.  
XX  
XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.  
XX Arabidopsis thaliana.  
XX  
XX  
PN WO200216655-A2.  
XX  
PD 28-FEB-2002.  
XX  
XX 24-AUG-2001; 2001WO-US026685.  
XX  
XX 24-AUG-2000; 2000US-0227866P.  
PR 26-JAN-2001; 2001US-0264647P.  
PR 22-JUN-2001; 2001US-0300111P.  
XX  
XX (SCRI ) SCRIPPS RES INST.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
XX Harper JF, Kreps J, Wang X, Zhu T;  
XX WPI; 2002-304127/34.  
XX  
XX  
PT Identifying a stress condition to which a plant cell has been exposed and  
PT producing plants with increased tolerance to these abiotic stresses.  
XX  
XX Claim 144; SEQ ID NO 2089; 577pp + Sequence Listing; English.  
PS  
XX  
XX The invention relates to identifying a stress condition to which a plant  
CC cell has been exposed, comprising: (a) contacting nucleic acid  
CC representative of expressed polynucleotides in the plant cell with an

Db	903	CCCACTCTCCGATCAACAGAGTCGATCTCTTGTGAATGACACCGGATCATCTATGT	962
Qy	894	TCTTGAAGTAGCAAGATTAATGATGATCCCAATCTCCCATCATCAGCAAGGTATTGA	953
Db	963	TCTCGAAGTAGCAAGTATTATGACAGAACACCCCTCCCATTTACACAGGTGATTGA	1022
Qy	954	CACATTACGAAACATTAAGTTACTTGGCCGGTTCATATCAATGACACGCGGGCTTA	1013
Db	1023	CACGTTAAGTAGAATCTAGGTTTCGCTCCAGGGTTATGTTGTCGACAGATGTCGGTA	1082
Qy	1014	CTTCGATTTCTTGAACCGTGTACATGTCGAAGAAATAAATCACTAGATCTTTGGGATTATG	1073
Db	1083	TTTCGATTTCTTGAACCGTGTCCGAACGAAGAAATAAATCACTAGATCTTTAGGACTATG	1142
Qy	1074	GGAATCTCTCATCTCTGGCTTAACCTCTACGTTCTTAAATCTCGGATCTCGATTTTCA	1133
Db	1143	GGAATCTCTCATCTCTGGCTTAACCTCTTGTCCGGGTCTCGAATCCAGATTTTCA	1202
Qy	1134	TAAAGGTTGTTCGAAGACATTTCTTTAAGCAAAATTCAGCTTCGGGACFTCGTCTTCT	1193
Db	1203	TGATGGTGTATTAAATGGCTTCTTAAACCAACCTCAACTTCTGTGTACTCTCTT	1262
Qy	1194	CTATCCACCAACCGGATTAATGGCAATCGTATGTCGGGATGATACAGAGATCGA	1253
Db	1263	CTATCCCAACCAACCGGATTAATGGCAATCGTATGTCGGGATGATACAGATGACAC	1316
Qy	1254	TGAAGATGTTATATATTATTCGGACTACTACAATCCGC---TACCCCAAGGATCTTCC	1310
Db	1317	CGAAGATGTTTATGATGCGGATTAATGATGATGATGATGATGATGATGATGATGATG	1376
Qy	1311	AGAGTGGAGCGGTTCAGAGAGATTAATGATGATGATGATGATGATGATGATGATGATG	1370
Db	1377	AGAACTTGAAATCTCAACGCAAGGTTATTCAGTTTGTGAAACTCGGGAATTAAGT	1436
Qy	1371	TAAAGCAATCTTAATGCAATTATCTAGTAAAGAGATGATGATGATGATGATGATGATGATG	1430
Db	1437	TAAAGCAATCTTAATGCAATTATCTAGTAAAGAGATGATGATGATGATGATGATGATGATG	1496
Qy	1431	ATGGATGATTTTTCAGAGAGAGATCTATTGATCCGAGAACTGTTATCTCCAGG	1490
Db	1497	ATGGATGATTTTTCAGAGAGAGATCTATTGATCCGAGAACTGTTATCTCCAGG	1556
Qy	1491	GCAAGACATCTTT	1503
Db	1557	ACAGACATATT	1569
RESULT 6			
ID	ABK28627	standard; cDNA; 1575 Bp.	
XX	AC	ABK28627;	
XX	DT	09-APR-2002 (first entry)	
DE	DE	cDNA encoding A. thaliana cytokinin oxidase AtCKX4.	
XX	KW	Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;	
KW	KW	root growth; lateral root; adventitious root; root geotropism; herbicide;	
KW	KW	root meristem; shoot meristem; leaf senescence; parthenocary; gene; ss.	
XX	OS	Arabidopsis thaliana.	
XX	PN	WO200196580-A2.	
XX	PD	20-DEC-2001.	
XX	PF	18-JUN-2001; 2001WO-BP006833.	
XX	PR	16-JUN-2000; 2000BP-00870132.	
PR	PR	27-DEC-2000; 2000US-0258415P.	
PR	PR	16-MAR-2001; 2001BP-00870053.	

XX	(SCHM/) SCHMULLING T.		
PA	(WERN/) WERNER T.		
XX	Schmullling T, Werner T;		
PI	WPI; 2002-130736/17.		
XX	Polynucleotide encoding novel plant protein having cytokinin oxidase		
XX	activity and the protein useful for stimulating root growth, enhancing		
PT	the formation of lateral or adventitious roots, altering root geotropism.		
PT	Claim 2; Page 147-148; 154pp; English.		
PS	The invention relates to an isolated polynucleotide (I) encoding a novel		
CC	plant protein (II) having cytokinin oxidase activity. (I) is useful for		
CC	production of transgenic plants, plant cells or tissues; for production		
CC	of altered plants, plant cell or tissues; and for effecting the		
CC	expression of (II) where (I) is operably linked to one or more control		
CC	sequences. The methods further comprises regenerating a plant from the		
CC	plant cell. (I) and (II) are useful for stimulating root growth;		
CC	enhancing the formation of lateral or adventitious roots; altering root		
CC	geotropism, leading to an increase in yield; and for screening growth		
CC	promoting chemical of herbicides. (I) is useful for increasing the size		
CC	of the root meristem; increasing root size; increasing leaf senescence;		
CC	shoot meristem; delaying leaf senescence and altering leaf senescence;		
CC	increasing leaf thickness; reducing or increasing the vessel size;		
CC	inducing parthenocary; improving standability of the seedlings;		
CC	increasing branching and for improving lodging resistance. Antibody (III)		
CC	to (II) is useful for identifying and obtaining proteins interacting with		
CC	(II) comprising a screening assay, preferably a two-hybrid screening		
CC	assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase		
CC	coding sequences and PCR primers of the invention		
XX	Sequence 1575 Bp; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;		
SQ	Query Match 51.7%; Score 778.2; DB 6; Length 1575;		
	Best Local Similarity 72.2%; Pred. No. 1.9e-228;		
	Matches 1093; Conservative 0; Mismatches 363; Indels 57; Gaps 4;		
Qy	42	AATGATCACCAATCATCAACGGTATTAAATTTACCTTAATCCCTTAACCTCAC	101
Db	63	AACCTTAATCAATCAGATGAGGGCAATTGATGTTTCTTACCATATCACTACCTTAC	122
Qy	102	CCTCTTACCGATCCTTCCATCATCTCCGAGCCTCTCATGCTTCGAAACATAACAC	161
Db	123	GGTCTTAACCGATCCTTCTCCATCTCTCGCGCTTCTCAGACTTCGGTAACATAACCGA	182
Qy	162	CGTACCCCGCGGGGTAAATCTGCCCTCTCCACCGCTGATATCTCTGCTCTCTCC	220
Db	183	CGAAATCCCGCGCGCTCTCTGCTCTCTCCACCGAGGTGGCTGCTCTCTCCG	242
Qy	221	-----AATACGCGCAACGAAACGAAAGTACATTTCCA	251
Db	243	TTTCGCTAACGAGGATCTCTTACAATAAGGCTCAACCGCCCGCTACTTTCAA	302
Qy	252	AGTAGCGGTCTGGCGCAAGCCACTCTTAAACGGCCAGCCTCGTCTCCGGCGAGT	311
Db	303	AGTGGTGTCTCGAGGCCAAGGCCACTCTCTCCGTCGCAAGCCTCTGCAACCGGAGTGT	362
Qy	312	AATCGTCAACATGACGTGATC-----ACTGAGGTGGTGGTTTCAA	353
Db	363	CGTCTGAAACATGACGTCTCTCCCATGGCGGTAAACACGCGCGGTTTATCTCGGC	422
Qy	354	AGACAAGATGACTGACCTGACCTGGCGCGGAGCGTTATGGGTGGATGCTGTTAAGAGAC	413
Db	423	AGACGGACTTACGCTGACGTGGCTGCGCGGACAGATGTTGGGTGGATGTTCTGAAGCGGC	482
Qy	414	GGCGGAGAAAGGGGTGTCGCCGGTTTCTTGGACGGATTATTTCATATAACCGTCCGAGG	473
Db	483	GGTGATAGAGGGCTCTCGCCGGTTATGACGACGGATTATTGTTAICTACGCTCGCGCG	542
Qy	474	AACGTTTCTGAATGGTGAATTTGGTGGTCAAGTGTCTTTCGAAACCGTCTCTTGTAGTAA	533

543 GACGTTGTCGACGCGTGAATCGGTGTCAGACGTTTACGACGCGCCCTCAGATTAGTAA 602  
 534 CGTCTTGAATGACGCTTATCTACGGAAGGTGAAATCTTGACATGCTCGGACAGCT 593  
 603 CGTTCATGAGCTTGACGCTTATCTACGGAAGGTGAAATCTTGACATGCTCGGACAGCT 662  
 594 AAACCCGAAATGTTCTATGAGGTGTTAGGAGGTTTGGGTCAATTTGGGAATATACAG 653  
 663 AAACCCGAAATGTTCTATGAGGTGTTAGGAGGTTTGGGTCAATTTGGGAATATACAG 722  
 654 AGCCAGAAATGTTTGGACCATGACCTAAACCGGCGCAATGTTTGGGTCAATTTGGGAATATACAG 713  
 723 GGCAGGATTCGTTGGATCATGACCCACCAAGGTTGAAATGCTTCGATCTCTACAG 782  
 714 TGATTTCAACTTTTACAGAGGACCAAGACGTTTGCATATCAATGCAAGATATG 773  
 783 TGACTTCTCGGCTTTTAAAGAGACCAAGACGTTTGCATATCAATGCAAGATATG 842  
 774 AGTCAGATTTTGAAGGTCAAAATTTCTTATCAACCGGTGCTGTTGACACCTCTTTT 833  
 843 AGTTGACTTTTGGAAAGGTCAACTATGATGTCAAATGGCTTCGTAGACACCTCTTTT 902  
 834 CCCACCTTCAGATCAATCTAAGTCGCTGATCTAGTCAAGCAACACGCTATCATCT 893  
 903 CCCACTCTCCGATCAACAGAGTCGATCTCTTGTGAATGACACCGGATCATCTAT 962  
 894 TCTTGAAGTACCGAAGTATTAATGATGCCAATCTCCCATCATCAGCAAGTTATGA 953  
 963 TCTGAAGTACCGAAGTATTAATGATGCCAATCTCCCATCATCAGCAAGTTATGA 1022  
 954 CACATTAACGAAACATTAAGTACTTCCCGGCTTCATATCAATGACAGACGTCGCTA 1013  
 1023 CAGCTTATGATAGACTCTAGTTTCCGCTCCAGGTTTATGTTGATCAAGATGTTCCGTA 1082  
 1014 CTTCGATTTCTGAACCGGTGATATGTCGAAGAAATAAATCAATCATGATCTTTGGGATATG 1073  
 1083 TTTGATTTCTGAACCGGTGATATGTCGAAGAAATAAATCAATCATGATCTTTGGGATATG 1142  
 1074 GAACTTCTCATCTTGGCTTAACTCTAGCTTCTTAAATCTCGGATCTCGATTTTCA 1133  
 1143 GGAAGTCTCTCATCTTGGCTTAACTCTAGCTTCTTAAATCTCGGATCTCGATTTTCA 1202  
 1134 TAACGCTGTTTGAAGACATCTTCTTAAGCAAAATCAATGCTTGGGATCTGCTTCT 1193  
 1203 TGATGCTGTTTGAAGACATCTTCTTAAGCAAAATCAATGCTTGGGATCTGCTTCT 1262  
 1194 CTATCCAAACACCGGATTAATGGAAGATATGATGTCGCGATGATACAGATGCA 1253  
 1263 CTATCCCAACACCGGATTAATGGAAGATATGATGTCGCGATGATACAGATGCA 1316  
 1254 TGAAGATGTTTATATATTTATGCGACTACTACAAATCCGCTTACCCCAAGGATCTTCC 1310  
 1317 CGAAGATGTTTATGATGCGATTAATGCAATCAAGCTGCTGATCTCAAAATGGCA 1376  
 1311 AGAAGTGGAGAGCGTTAAGCAAGATATGATGTTTGAAGATTCAGGTATTAAGAT 1370  
 1377 AGAAGTGGAGAGCGTTAAGCAAGATATGATGTTTGAAGATTCAGGTATTAAGAT 1436  
 1371 TAAGCAATATCTAATGCAATTAATGATTAAGAGATGATGATGATGATGATGATGATGAT 1430  
 1437 TAAGCAATATCTAATGCAATTAATGATTAAGAGATGATGATGATGATGATGATGATGAT 1496  
 1431 ATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1490  
 1497 ATGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1556  
 1491 GCAAGACATCTTT 1503  
 1557 ACAAGACATATTT 1569

RESULT 7

ADA8648  
 ID ADA8648 standard; DNA; 1575 BP.  
 AC ADA8648;  
 XX 20-NOV-2003 (first entry)  
 XX Arabidopsis thaliana gene, SEQ ID 428.  
 XX Plant; bacterial infection; fungal infection; viral infection; ds.  
 XX Arabidopsis thaliana.  
 XX WO2003000898-A1.  
 PD 03-JAN-2003.  
 XX 22-JUN-2001; 2001WO-IB001105.  
 XX 22-JUN-2001; 2001WO-IB001105.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
 PI Xatagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
 XX WPI; 2003-175290/17.  
 XX Identifying at least one gene involved in plant resistance or response to  
 PT pathogenic infection for conferring resistance or tolerance to a plant to  
 PT bacterial, fungal or viral infection by determining or detecting plant  
 PT gene expression.  
 XX Claim 6; SEQ ID NO 428; 899pp; English.  
 CC The present invention relates to a method (M1) for identifying genes  
 CC involved in plant resistance or response to pathogenic infection. M1  
 CC comprises identifying a gene whose expression is significantly altered in  
 CC the incompatible interaction of plant gene expression relative to  
 CC expression of the gene in an uninfected plant, in a mutant plant that  
 CC does not express a gene associated with response to pathogenic infection,  
 CC or in a corresponding incompatible or compatible interaction. (M1) is  
 CC useful for conferring resistance to resistance or tolerance to a plant to  
 CC bacterial, fungal or viral infection. The present sequence was used to  
 CC illustrate the invention.  
 XX SQ Sequence 1575 BP; 418 A; 368 C; 349 G; 440 T; 0 U; 0 Other;  
 Query Match 51.7%; Score 778.2; DB 7; Length 1575;  
 Best Local Similarity 72.2%; Pred. No. 1.9e-228; Indels 57; Gaps 4;  
 Matches 1093; Conservative 0; Mismatches 363;  
 QY 42 AATGATCAACCAATCAATAAAGGTATTAATAATGATTTTACCTTAATCCCTTAACCTCAC 101  
 DB 63 AACCTTAATCAATCAATGAGGCAATGATTTTCTTACCCATATCACTCAACCTTAC 122  
 QY 102 CCTCTCTACCGATCCTTCCATCATCTCCGACGCTCTCATGACTTCGGAACATACACAC 161  
 DB 123 GGTCTTAACCGATCTCTTCCATCTCTCCGCTCTCAGACTTCGGTAACATACACCA 182  
 QY 162 CGTGACCCCGCGCGGTAAATCTGCCCTCTCCACCGCTGATATCTCTGCTCTCTCC- 220  
 DB 183 CGAAATTCGCGCGCTCTCTGCCCTCTCCACCGAGGTGCTGCTCTCTCCG 242  
 QY 221 -----AATACGCGCAACAGGAAAGATACATTCA 251  
 DB 243 TTTGCTTAACGAGGATTTCTTACATTAAGGCTCAACCGCCCGGCTCTACTTTCAA 302  
 QY 252 AGTAGCGGTCTGCGCAAGGCACTCTTAAACCGCAAGCTCTGCTCTCGGCGGAGT 311  
 DB 303 AGTGGGTCTGCGAGGCAAGGCACTCTCTCGGTCGCGCAAGCTCTGACCCCGGAGGT 362  
 QY 312 AATCGTCAACATCACTGTATC-----ACTGAGTGGTGTTCATAA 353





CC plant cell. (I) and (II) are useful for stimulating root growth;  
CC enhancing the formation of lateral or adventitious roots; altering root  
CC geotropism, leading to an increase in yield; and for screening growth  
CC promoting chemical of herbicides. (I) is useful for increasing the size  
CC of the root meristem; increasing root size; increasing the size of the  
CC shoot meristem; delaying leaf senescence and altering leaf senescence;  
CC increasing leaf thickness; reducing or increasing the vessel size;  
CC inducing parthenocary; improving standability of the seedlings;  
CC increasing branching and for improving lodging resistance. Antibody (III)  
CC to (II) is useful for identifying and obtaining proteins interacting with  
CC (II) comprising a screening assay, preferably a two-hybrid screening  
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase  
CC coding sequences and PCR primers of the invention  
XX  
SQ Sequence 2991 BP; 920 A; 522 C; 521 G; 1028 T; 0 U; 0 Other;  
  
Query Match 38.3%; Score 577; DB 6; Length 2991;  
Best Local Similarity 75.9%; Pred. No. 2.5e-166;  
Matches 852; Conservative 0; Mismatches 40; Indels 231; Gaps 2;  
  
QY 615 AGTGTAGAGGTTGGGTCATTTGGAATTAAACGAGAGCCAGAAATGTTTGGACCA 674  
DB 1869 ACTGTAATATGTTTCTTATATATGTTGATATAAATTAATGAGGATGTTTCTCTAAA 1928  
  
QY 675 TGCACCTAAACGGCGCAAAATGGTTTCGGATGCTCTACAGTGTTCACAACTTTTACAAA 734  
DB 1929 TGAATTTGTAGGCCAAATGGTTTCGGATGCTCTACAGTGAITTCACAACTTTTACAAA 1988  
  
QY 735 GGACCAAGACGTTTGATATCAATGCGCAACGATATGAGTGCAGTATTTAGAAAGTCA 794  
DB 1989 GGACCAAGACGTTTGATATCAATGCGCAACGATATGAGTGCAGTATTTAGAAAGTCA 2048  
  
QY 795 AATATTTCTATCAACGGTGTGTTGACACTCTTTTCCACCTTCAGATCAATCTAA 854  
DB 2049 AATATTTCTATCAACGGTGTGTTGACACTCTTTTCCACCTTCAGATCAATCTAA 2108  
  
QY 855 AGTCGTGATCTAGTCAAGCAACGATATCTATGTTCTTGAAGTAGCCAAAGTATTA 914  
DB 2109 AGTCGTGATCTAGTCAAGCAACGATATCTATGTTCTTGAAGTAGCCAAAGTATTA 2168  
  
QY 915 TGATGATCCGATCTCCGATCATCAGA----- 943  
DB 2169 TGATGATCCGATCTCCGATCATCAGAAGTACTACACATTTACATTTTCATCATCGT 2228  
  
QY 944 ----- 943  
DB 2229 TTTTATCATACCAAGATATTTAAATGATTCATCATTTGCACCACATTAAGATATTCATC 2288  
  
QY 944 -----AGG 946  
DB 2289 ATCATCATCGTTACATTTTTTTTTTGCACTTATGCTTCTCATATCTACTATTTGTGTAGG 2348  
  
QY 947 TTATTGACACATTAAACGAAACATTAAGTTACTTGCCTGGGTTTCATATCAATGACGACG 1006  
DB 2349 TTATTGACACATTAAACGAAACATTAAGTTACTTGCCTGGGTTTCATATCAATGACGACG 2408  
  
QY 1007 TGGCTACTTCGATTTCTTGAACCGTGTACATGTCGAGAAATAAATACTCAGATCTTTGG 1066  
DB 2409 TGGCTACTTCGATTTCTTGAACCGTGTACATGTCGAGAAATAAATACTCAGATCTTTGG 2468  
  
QY 1067 GATTATGGAACTTCTCATCTCTTGGCTTAACTCTACCTCTACCTTCTTAAATCTCGGATCTCG 1126  
DB 2469 GATTATGGAACTTCTCATCTCTTGGCTTAACTCTACCTCTACCTTCTTAAATCTCGGATCTCG 2528  
  
QY 1127 ATTTCATAACGGTGTGTCGAAAGACATCTTCTTAAGCAAAAATAGCTTCGGGACTCG 1186  
DB 2529 ATTTCATAACGGTGTGTCGAAAGACATCTTCTTAAGCAAAAATAGCTTCGGGACTCG 2588  
  
QY 1187 CTCCTCTCTATCCAAACCGGATATA----- 1214  
DB 2589 CTCCTCTCTATCCAAACCGGATATAAGTACATACCTCTCTTCATTCATATTTATCTTC 2648  
  
QY 1215 -----ATGGGCAAA 1223

Db 2649 AAGAACCAAGTAATAATTTCTATGAACCTGATTGCTGTTATTGTTAGATGGGACAA 2708  
QY 1224 TCGTATTCGCGGATGATACACGAGATCGATGAAGATGTTATATATATATATTCGGACTACT 1283  
Db 2709 TCGTATTCGCGGATGATACACGAGATCGATGAAGATGTTATATATATATATTCGGACTACT 2768  
QY 1284 ACATCCGCTACCCCAAGGATCTTCCAGAGTGGAGAGCGTTAAACGAGAAAGATAATTAG 1343  
Db 2769 ACATCCGCTACCCCAAGGATCTTCCAGAGTGGAGAGCGTTAAACGAGAAAGATAATTAG 2828  
QY 1344 GTTTTGAAGGATTCAGGTATTAAAGATTAAGCAATATCTAATGCATTATATCTAGTAAAGA 1403  
Db 2829 GTTTTGAAGGATTCAGGTATTAAAGATTAAGCAATATCTAATGCATTATATCTAGTAAAGA 2888  
QY 1404 AGATGAGATTGAGCATTTTGGATCAAAATGGATGATTTTTCGAGAGGAAAGATCTTATT 1463  
Db 2889 AGATGAGATTGAGCATTTTGGATCAAAATGGATGATTTTTCGAGAGGAAAGATCTTATT 2948  
QY 1464 TGATCCCAAGAAACTGTTATCTCCAGGCGCAAGACATCTTTGA 1506  
Db 2949 TGATCCCAAGAAACTGTTATCTCCAGGCGCAAGACATCTTTGA 2991  
  
RESULT 10  
ACC85276  
ID ACC85276 standard; DNA; 2991 BP.  
XX  
AC ACC85276;  
XX DT 18-SEP-2003 (first entry)  
XX Arabidopsis cytokinin oxidase-like protein 2 gene.  
XX Maize; root growth; root geotropism; cytokinin oxidase; seed size;  
KW embryo size; cotyledon size; transgenic plant; herbicide; gene; ds.  
XX Arabidopsis thaliana.  
XX WC2003050287-A2.  
XX 19-JUN-2003.  
XX 10-DEC-2002; 2002WO-EP013990.  
XX 10-DEC-2001; 2001US-00014101.  
XX (SCHM/) SCHMULLING T.  
XX (WERN/) WERNER T.  
XX Schmulling T, Werner T;  
XX WPI; 2003-541577/51.  
XX P-PSDB; ABR63569.  
XX Stimulating root growth, enhancing lateral or adventitious root formation  
PT or altering root geotropism comprises increasing plant cytokinin oxidase  
PT levels or other protein or nucleic acid that reduces active cytokinins in  
PT a plant.  
XX Claim 3; Page 145-146; 177pp; English.  
XX The present invention relates to a method for stimulating root growth or  
CC enhancing the formation of lateral or adventitious roots or altering root  
CC geotropism, which comprises increasing in a plant or plant part the level  
CC of a plant cytokinin oxidase or other protein that reduces the level of  
CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and  
CC coding sequences from Arabidopsis thaliana are also provided. The method  
CC is useful in modifying plant morphological, biochemical and physiological  
CC properties, such as in modifying the initiation, stimulation or  
CC enhancement of root growth, adventitious root formation, lateral root  
CC formation, root geotropism, shoot growth, apical dominance, branching,  
CC timing of senescence, timing of flowering, flower formation, seed

CC development and/or seed yield. The present sequence is a coding sequence  
XX shown in the invention  
SQ Sequence 2991 BP; 920 A; 522 C; 521 G; 1028 T; 0 U; 0 Other;  
Query Match 38.3%; Score 577; DB 8; Length 2991;  
Best Local Similarity 75.9%; Pred. No. 2.5e-166;  
Matches 852; Conservative 0; Mismatches 40; Indels 231; Gaps 2;  
QY 615 AGTGTAGAGGTTGGTCAATTTGGAAATTAACGAGAGCAGAAATGTTTGGACCA 674  
Db |||||  
QY 1869 ACTGTAATATGTTCTTTATATATGTTGTATATAATTAATGGAATGTTTCTCTAAA 1928  
Db |||||  
QY 675 TGCACCTAAACGGGCCAAATGGTTTTCGGATGCTCTACAGTGAATTCACAACTTTTACAAA 734  
Db |||||  
QY 1929 TGAATTTGTGTAGGCCAAATGGTTTTCGGATGCTCTACAGTGAATTCACAACTTTTACAAA 1988  
Db |||||  
QY 735 GGACCAAGAGCGTTTGATATCAATGGCAACGATATTTGGAGTCGACTATTTAGAGGTCA 794  
Db |||||  
QY 1989 GGACCAAGAGCGTTTGATATCAATGGCAACGATATTTGGAGTCGACTATTTAGAGGTCA 2048  
Db |||||  
QY 795 AATATTTCTATCAAAACGGTGTGTTGACAGCTCTTTTTCGCCACCTTCAGATCAATCTAA 854  
Db |||||  
QY 2049 AATATTTCTATCAAAACGGTGTGTTGACAGCTCTTTTTCGCCACCTTCAGATCAATCTAA 2108  
Db |||||  
QY 855 AGTGGCTGATAGTCAAGCAACGATATCAATGTTCTTGAAGTAGCCAGATATTA 914  
Db |||||  
QY 2109 AGTGGCTGATAGTCAAGCAACGATATCAATGTTCTTGAAGTAGCCAGATATTA 2168  
Db |||||  
QY 915 TGATGATCCCAATCTCCCAATCATCAGCA----- 943  
Db |||||  
QY 2169 TGATGATCCCAATCTCCCAATCATCAGCAAGGTACTACATTTTATCATCTCT 2228  
Db |||||  
QY 944 ----- 943  
Db |||||  
QY 2229 TTTTATCATACATAAGATATTTAAATGATCATCATGTCACCAATTAAGATATTCATC 2288  
Db |||||  
QY 944 -----AGG 946  
Db |||||  
QY 2289 ATCATCATCGTTACATTTTGTGATCTTATGCTTCTCATATCTACTATTTGTGTAGG 2348  
Db |||||  
QY 947 TTTTATGACATTAACGAAACATTAAGTTACTTGCCTGGTTCATATCAATGACGAGC 1006  
Db |||||  
QY 2349 TTTTATGACATTAACGAAACATTAAGTTACTTGCCTGGTTCATATCAATGACGAGC 2408  
Db |||||  
QY 1007 TGGCTTACTTGGATTTCTTGAACGCTGTACATGTCGAAGAAATAAATCAGATCTTTGG 1066  
Db |||||  
QY 2409 TGGCTTACTTGGATTTCTTGAACGCTGTACATGTCGAAGAAATAAATCAGATCTTTGG 2468  
Db |||||  
QY 1067 GATTATGGGAATCTTCTGCTTGGCTTAACTCTACGTTCCCTAAATCTCGGATCTCG 1126  
Db |||||  
QY 2469 GATTATGGGAATCTTCTGCTTGGCTTAACTCTACGTTCCCTAAATCTCGGATCTCG 2528  
Db |||||  
QY 1127 ATTTTTCATAACGGTGTGTCGAAGACATTTCTTGAAGCAAAATCAGCTTCGGACTCG 1186  
Db |||||  
QY 2529 ATTTTTCATAACGGTGTGTCGAAGACATTTCTTGAAGCAAAATCAGCTTCGGACTCG 2588  
Db |||||  
QY 1187 CTCCTTCTCTATCCAAACCGGATTA----- 1214  
Db |||||  
QY 2589 CTCCTTCTCTATCCAAACCGGATTAAGTACATCTTCTCTCATCATATTTATCTTC 2648  
Db |||||  
QY 1215 -----ATGGGACAA 1223  
Db |||||  
QY 2649 AAGAACCAAGTAAATTTCTATGAACGTATTATGCTGTTATTGTTAGATGGACAA 2708  
Db |||||  
QY 1224 TCGTATGTCGGGATGATACCAAGATCGATGAGATGTTATATATTTATTCGGACTCT 1283  
Db |||||  
QY 2709 TCGTATGTCGGGATGATACCAAGATCGATGAGATGTTATATATTTATTCGGACTCT 2768  
Db |||||  
QY 1284 ACAATCCGCTACCCCAAGGATCTTCCAGAGTGGAGAGCGTTTAAACGAGAAGATATTA 1343  
Db |||||  
QY 2769 ACAATCCGCTACCCCAAGGATCTTCCAGAGTGGAGAGCGTTTAAACGAGAAGATATTA 2828  
Db |||||

QY 1344 GTTTTGCAGGATTCAGGTATTAAAGNTAAAGCAATATCTAATGCATTAATCTAGTAAAGA 1403  
Db |||||  
QY 2829 GTTTTGCAGGATTCAGGTATTAAAGNTAAAGCAATATCTAATGCATTAATCTAGTAAAGA 2888  
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QY 1404 AGATTGGATTGAGCAATTTTGGATCAAAATGGGATGATTTTTCGAAGAGGAAAGATCTATT 1463  
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QY 2889 AGATTGGATTGAGCAATTTTGGATCAAAATGGGATGATTTTTCGAAGAGGAAAGATCTATT 2948  
Db |||||  
QY 1464 TGATCCCAAGAACTGTTATCTCCAGGCGCAAGACATCTTTTGA 1506  
Db |||||  
QY 2949 TGATCCCAAGAACTGTTATCTCCAGGCGCAAGACATCTTTTGA 2991  
Db |||||  
RESULT 11  
ABK28626  
ID ABK28626 standard; cDNA; 1572 BP.  
XX  
AC ABK28626;  
XX  
DT 09-APR-2002 (first entry)  
XX  
XX cDNA encoding A. thaliana cytokinin oxidase AtCKX3.  
XX  
DE Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;  
XX  
KW root growth; lateral root; adventitious root; root geotropism; herbicide;  
KW root meristem; shoot meristem; leaf senescence; parthenocarpy; Gene; ss.  
XX  
OS Arabidopsis thaliana.  
XX  
PN WO200196580-A2.  
XX  
PD 20-DEC-2001.  
XX  
PF 18-JUN-2001; 2001WO-BP006833.  
XX  
PR 16-JUN-2000; 2000EP-00870132.  
PR 27-DEC-2000; 2000US-0258415P.  
PR 16-MAR-2001; 2001EP-00870053.  
XX  
XX (SCHM/) SCHMULLING T.  
XX (WERN/) WERNER T.  
XX  
XX Schmulling T, Werner T;  
XX WPI; 2002-130736/17.  
XX  
XX Polynucleotide encoding novel plant protein having cytokinin oxidase  
PT activity and the protein useful for stimulating root growth, enhancing  
PT the formation of lateral or adventitious roots, altering root geotropism.  
XX  
XX Claim 3; Page 147; 154pp; English.  
XX  
XX The invention relates to an isolated polynucleotide (I) encoding a novel  
CC plant protein (II) having cytokinin oxidase activity. (I) is useful for  
CC production of transgenic plants, plant cells or tissues; for production  
CC of altered plants, plant cell or tissues; and for effecting the  
CC expression of (II) where (I) is operably linked to one or more control  
CC sequences. The methods further comprises regenerating a plant from the  
CC plant cell. (I) and (II) are useful for stimulating root growth;  
CC enhancing the formation of lateral or adventitious roots; altering root  
CC geotropism, leading to an increase in yield; and for screening growth  
CC promoting chemical of herbicides. (I) is useful for increasing the size  
CC of the root meristem; increasing root size; increasing the size of the  
CC shoot meristem; delaying leaf senescence and altering leaf senescence;  
CC increasing leaf thickness; reducing or increasing the vessel size;  
CC inducing parthenocarpy; improving standability of the seedlings;  
CC increasing branching and for improving lodging resistance. Antibody (III)  
CC to (II) is useful for identifying and obtaining proteins interacting with  
CC (II) comprising a screening assay, preferably a two-hybrid screening  
CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase  
CC coding sequences and PCR primers of the invention  
XX  
XX Sequence 1572 BP; 461 A; 327 C; 348 G; 436 T; 0 U; 0 Other;



Qy 1022 TCTTGAACCGGTGTACATGTGCGAAGAAAATAAATCTCAGATCTTTGGGATTTATGGAACTTC 1081  
Db 1076 TCCTAAACCGAGTTCGAAACCGGAGAGCTAAACCTGAAATCCAAAGGCGCAATGGGATGTTT 1135  
Qy 1082 CTCATCTCTGGCTTAAACCTCTACGTTTCTAAATCTCGGATTTCTGATTTTCATAACCGTG 1141  
Db 1136 CACATCAATGGCTTAACTCTCTGTCACAAATACTCAAATCTCCAAATTTGATGATGGTG 1195  
Qy 1142 TTGTCAAAGACATTTCTTTTAAGCAAAAATCAGCTTCGGGACTCGCTCTTCTCTATCAA 1201  
Db 1196 TTTTAAAGGTATTATCTCTAAGAAATAACATCACTAGCGGTCTCTGTTCTTTTATCCTA 1255  
Qy 1202 CAAACCGGAATAAATGGGACAATCGATGTCGGGATGATACCAAGAGATCGATGAAGATG 1261  
Db 1256 TGAATCGCAACAGTGGAAATGATCGGATGTCGCGCTATACCCGAG-----GAAATG 1309  
Qy 1262 TTATATATATTATCGGACTACTACAATCCGCTACCCCAAGGATTTTCCAGAAATGGAGA 1321  
Db 1310 TATTTATGCGGTAGGTTTTTAAAGATCCGCGGTTTTGACAATTTGGAGGCTTTTGATC 1369  
Qy 1322 GGGTTAAAGCAAGATAATTAGGTTTTGCAAGGATTCAGGTATTAAAGATTAAAGCAATATC 1381  
Db 1370 AAGAAACATGGAATACTGAAGTTTTGTGAGGATGCTAAATATGGGGTTATACAAATATC 1429  
Qy 1382 TAAATCAATATATAGTAAAGAAAGATTGGATTGAGCATTTTTGGATCAAAAATGGGATGATT 1441  
Db 1430 TTCCTTATCATTCATCAACAAGAGATGGGTTAGACATTTTTGGTCCGAGGTGGAATATTT 1499  
Qy 1442 TTTCGAAGCAAGATCTATTGATCCCAAGAAATCTGTTATCTCCAGGCGCAAGACATCT 1501  
Db 1490 TCGTAGAGAGAAATATAAATATGATCCCAAAATGATATTATCACCGGCAAAATATAT 1549  
Qy 1502 TT 1503  
Db 1550 TT 1551

RESULT 12

ACC85295  
ID ACC85295 standard; cDNA; 1572 BP.

XX ACC85295;

XX 18-SEP-2003 (first entry)

XX Arabidopsis cytokinin oxidase-like protein 3 cDNA.

XX Maize; root growth; root geotropism; cytokinin oxidase; seed size;  
XX embryo size; cotyledon size; transgenic plant; herbicide; gene; ss.

XX Arabidopsis thaliana.

XX W02003050287-A2.

XX 19-JUN-2003.

XX 10-DEC-2002; 2002WO-BP013990.

XX 10-DEC-2001; 2001US-00014101.

XX (SCHM/) SCHMULLING T.

XX (WERN/) WERNER T.

XX Schmullling T, Werner T;

XX WPI; 2003-541577/51.

XX Stimulating root growth, enhancing lateral or adventitious root formation  
XX or altering root geotropism comprises increasing plant cytokinin oxidase  
XX levels or other protein or nucleic acid that reduces active cytokinins in  
XX a plant.

PS Claim 3; Page 168-169; 177pp; English.

Query Match 31.2%; Score 470; DB 6; Length 1572;  
Best Local Similarity 58.7%; Pred. No. 1.6e-133;  
Matches 881; Conservative 0; Mismatches 600; Indels 21; Gaps 3;  
Qy 17 TAATGATCACTTTAATCAACGGTTTTAATGATCAACAAATCAATCAACGGTATTAAATG 76  
Db 56 TCATCAATTAATCTCTCAACTCCGATCAACACCAACATCAACCAACCAATGATATATCC 115  
Qy 77 ATTACTTAATCCCTTAACTCACTCACTCTCTCTACCGATCCCTCCATCATCTCCGAGCCT 136  
Db 116 TTTTCAACAAGATTCGCCGGAATACTCACTCTCTCTCTCTCTCGTTCGATCAGCG 175  
Qy 137 CTCATGATCTCGGAAACATTAACACCGTGACCCCGCGGCGTAATCTGCGCCCTCTCCA 196  
Db 176 CCACAGATTTCCGCCACGTCAACCAAAATCTCTCCGCGCTTAAATCCCTTCTCTCG 235  
Qy 197 CCGTGATATCTCTGCTCTCTCAATACGCCGCAAAAGGAAAGTACATTTCCAAAGTAG 256  
Db 236 TTGAAGCATCAAGATCTCATAAACTCTTTTGAATCTCACTCTCTTTCTTTAG 295  
Qy 257 CCGCTCGTGCCCAAGGCACTCTCTTAAACCGGCAAGCTCGCTCTCCGCGGAGTAATCG 316  
Db 296 CCGCTCGTGTCAGGACACAGCCAGCCGTCGCAAGCTCGCTTAAAGACGGAAGTTGTG 355  
Qy 317 TCAACATGAGCTGTATCACTGAGTGG-----TGGTTTCAAAAGACAAGAGT 364  
Db 356 TCAACATGCGGTTCATGGTAAACCGGATCGAGGTATCAAGGTCTAAGACCTGTTAT 415  
Qy 365 ACGCTGACGTGGCGGCGGACGTTATGGGTGATGCTTAAAGACAGCGCGGAGAAAG 424  
Db 416 ATGTTGACGTGAGCGCTGCGTGGCTATGATGAGGTGTTGAATAAACTTTGGAGTTAG 475  
Qy 425 GGGTGTCCCGGTTTCTTGACGATTTATTTGATATAACCGTCCGAGGAACTCTCGA 484  
Db 476 GGTAAACGCGGTTTCTTGACGATTTATTTGATTTAAACAGTCCGTTGGAGCTTATCAA 535  
Qy 485 ATGTTGAATTTGGTGTCAAGTGTTCGAAACCGTCTCTTTGTAGTAAACGTCCTTGAAT 544  
Db 536 ACGCGGAATTAGTGGACAAACGTTTCGGTACGCTCCACAGATCACTAATGTTCTAGAGA 595  
Qy 545 TGGACGTTATTAATGGAAGAGTGAATGTTGATCTCGGACACTAAACCCAGAT 604  
Db 596 TGGATGTTATTAATGGAAGAGAGATGCAACTTTTCCAAGGACATGAATCGGATC 655  
Qy 605 TGTCTATGAGTGTAGGAGTTTGGTCAATTTGGAATTTAATCAAGAGGAGGAGGATG 664  
Db 656 TTTTCTTCGCGGTGTAGGAGTTTGGTCAATTCGCAATTTAACAAGAGGAGGAGATTA 715  
Qy 665 TTTTGGACCATGCACTAAACCGGCCAAATGTTTTCGGATGCTCTACAGTGAATTCACAA 724  
Db 716 AACTTGAAGTAGTCCGAAAGGGCCAAAGTGGTTAAGGTTTCTATACATAGATTTCTCCG 775  
Qy 725 CTTTTCACAAAGGACCAAGACGTTTGATATCAATGCGCAACGATATTGGAGTC--GACT 781  
Db 776 AATTCAAGAGATCAAGACGATGATATCGAAACCGGAGGTGTAGATTTCTTAGAAG 835  
Qy 782 ATTTAGAAGGTCAAATATTTCTATCAACCGTGTGTTGACACCTCTTTTTCACCTT 841  
Db 836 GTTCCATTATGGTGGACCATGGCCACCGGATACTGGAGATCCACGATATTATCCACCGT 895  
Qy 842 CAGATCAATTAAGTCTGATCTAGTCAAGCAACAGGATCATCTATGTTCTTGAAG 901  
Db 896 CCGATCACTTGAAGATCCCTCAATGGTCAACAGACATCGGTGTCATCTCTGCTTGAAG 955  
Qy 902 TAGCCAAGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTTATTGACACATTAA 961  
Db 956 TCGTCAAGTATTACAGCAAACTTCTCAATACACAGTCAACAGGAAATGGAGGAGTTAA 1015  
Qy 962 CGAAACATTAAGTTACTTTCGCGGTTTCAATCAATGACAGAGTGGCCTACTTCGATT 1021  
Db 1016 GCGATAGTTTAAACCATGAAGAGGTTTATGTACGAGAAAGATGTGACGPTATGATGATT 1075



PF	25-FEB-2000;	2000EP-00301439.	
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PR	25-FEB-1999;	99US-0121825P.	99US-0142920P.
PR	03-MAR-1999;	99US-0123180P.	99US-0142977P.
PR	09-MAR-1999;	99US-0123348P.	99US-0143542P.
PR	23-MAR-1999;	99US-0125788P.	99US-0143624P.
PR	25-MAR-1999;	99US-0126264P.	99US-0144005P.
PR	29-MAR-1999;	99US-0126785P.	99US-0144085P.
PR	01-APR-1999;	99US-0127462P.	99US-0144086P.
PR	08-APR-1999;	99US-0128234P.	99US-0144325P.
PR	16-APR-1999;	99US-0128714P.	99US-0144331P.
PR	19-APR-1999;	99US-0129845P.	99US-0144332P.
PR	21-APR-1999;	99US-0130077P.	99US-0144333P.
PR	23-APR-1999;	99US-0130449P.	99US-0144334P.
PR	28-APR-1999;	99US-0130891P.	99US-0144335P.
PR	30-APR-1999;	99US-0131449P.	99US-0144352P.
PR	30-APR-1999;	99US-0132048P.	99US-0144632P.
PR	30-APR-1999;	99US-0132407P.	99US-0144844P.
PR	04-MAY-1999;	99US-0132484P.	99US-0144844P.
PR	05-MAY-1999;	99US-0132485P.	99US-0145086P.
PR	06-MAY-1999;	99US-0132486P.	99US-0145086P.
PR	07-MAY-1999;	99US-0132487P.	99US-0145088P.
PR	11-MAY-1999;	99US-0132863P.	99US-0145088P.
PR	14-MAY-1999;	99US-0134218P.	99US-0145089P.
PR	14-MAY-1999;	99US-0134219P.	99US-0145192P.
PR	14-MAY-1999;	99US-0134221P.	99US-0145145P.
PR	14-MAY-1999;	99US-0134370P.	99US-0145218P.
PR	18-MAY-1999;	99US-0134768P.	99US-0145224P.
PR	19-MAY-1999;	99US-0134941P.	99US-0145276P.
PR	20-MAY-1999;	99US-0135112P.	99US-0145913P.
PR	21-MAY-1999;	99US-0135333P.	99US-0145918P.
PR	24-MAY-1999;	99US-0135629P.	99US-0145919P.
PR	25-MAY-1999;	99US-0136021P.	99US-0145951P.
PR	28-MAY-1999;	99US-0136392P.	99US-0146388P.
PR	01-JUN-1999;	99US-0137282P.	99US-0146389P.
PR	03-JUN-1999;	99US-0137528P.	99US-0147038P.
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28-SEP-1999; 99US-0156458P.  
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10-OCT-1999; 99US-0159331P.  
11-OCT-1999; 99US-0159637P.  
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14-OCT-1999; 99US-0160741P.  
15-OCT-1999; 99US-0160767P.  
16-OCT-1999; 99US-0160768P.  
17-OCT-1999; 99US-0160770P.  
18-OCT-1999; 99US-0160814P.  
19-OCT-1999; 99US-0160815P.  
20-OCT-1999; 99US-0160980P.  
21-OCT-1999; 99US-0160981P.  
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23-OCT-1999; 99US-0160983P.  
24-OCT-1999; 99US-0161404P.  
25-OCT-1999; 99US-0161405P.  
26-OCT-1999; 99US-0161406P.  
27-OCT-1999; 99US-0161359P.  
28-OCT-1999; 99US-0161360P.  
29-OCT-1999; 99US-0161361P.  
30-OCT-1999; 99US-0161920P.  
31-OCT-1999; 99US-0161992P.  
01-NOV-1999; 99US-0161993P.  
02-NOV-1999; 99US-0162142P.

Query Match 30.6%; Score 461.2; DB 3; Length 503;  
Best Local Similarity 99.2%; Pred. No. 4,3e-131;  
Matches 482; Conservative 2; Mismatches 0; Indels 2; Gaps 2;

QY 559 GGAAGAGTGAATGTGATGCTCGGACAGCTAAACCCAGAGTTGTTCTATGAGTG 618  
DB 18 GGGAAAGTGAATGTGATGCTCGGACAG-ATAACCCAGAGTTGTTCTATGAGTG 76  
QY 619 TTAGGAGGTTGGTCAATTTGGAATTATAACGAGAGCCAGAGTTGTTGACCATGCA 678  
DB 77 TTAGGAGGTTGGTCAATTTGGAATTATAACGAGAGCCAGAGTTGTTGACCATGCA 136  
QY 679 CCTAAACGGGCGCAATGGTTGGATGCTCTACAGTGATTCACAACTTTTCAAGGAC 738  
DB 137 CCTAAACGGGCGCAATGGTTGGATGCTCTACAGTGATTCACAACTTTTCAAGGAC 196  
QY 739 CAAGACGTTTGATATCAATGGCAACGATATTGGAGTGCATATTAGAGGTCAATA 798  
DB 197 CAAGACGTTTGATATCAATGGCAACGATATTGGAGTGCATATTAGAGGTCAATA 256  
QY 799 TTTCTATCAACGGTGTGCTGACCTCTTTTCCACCTTTCCACCTTTCAATCTAAAGTC 858  
DB 257 TTTCTATCAACGGTGTGCTGACCTCTTTTCCACCTTTCCACCTTTCAATCTAAAGTC 316  
QY 859 GCTGATCTAGTCAAGCAGAGTATCATCTATGTTCTTGAAGTACCGAGTATTAT-GA 917  
DB 317 GCTGATCTAGTCAAGCAGAGTATCATCTATGTTCTTGAAGTACCGAGTATTATGA 376  
QY 918 TGATCCCAATCTCCCATCATCAGCAGGTTATTGACATTAACGAAACATTAAAGTTA 977  
DB 377 TGATCCCAATCTCCCATCATCAGCAGGTTATTGACATTAACGAAACATTAAAGTTA 436  
QY 978 CTTGCCGGGTTTATCAATGACGAGCGTGGCTACTTCGATTTCTTGACCGGTGACA 1037  
DB 437 CTTGCCGGGTTTATCAATGACGAGCGTGGCTACTTCGATTTCTTGACCGGTGACA 496

QY 1038 TGTGCA 1043  
DB 497 TGTGCA 502  
RESULT 14  
AA02919  
ID AAX02919 standard; DNA; 1602 BP.  
XX AC AAX02919;  
XX 20-MAY-1999 (first entry)  
XX Z. mays ckl1 degenerate DNA.  
XX Cytokinin oxidase; ckl1; transgenic plant; altered growth behaviour;  
XX cytokinin-associated pathogenesis; resistance; fungi; nematode; assay;  
XX grain yield; secondary growth; metabolism; senescence; ss.  
XX Zea mays.  
XX WO9906571-A1.  
XX 11-FEB-1999.  
XX 30-JUL-1998; 98WO-US015844.  
XX 30-JUL-1997; 97US-0054268P.  
XX 29-JUL-1998; 98US-00124541.  
XX (UMOR ) UNIV MISSOURI.  
XX Morris RO;  
XX WPI; 1999-153800/13.  
XX New cytokinin oxidase from maize - used to generate transgenic plants  
XX with, e.g. better disease resistance and growth characteristics.  
XX Claim 7c; Page 130-131; 140pp; English.  
XX This sequence encodes a Zea mays cytokinin oxidase, ckl1. This gene is  
XX used to generate transgenic plants in which cytokinin-associated  
XX pathogenesis or growth behaviour is altered. Particularly applications  
XX include generation of plants with increased resistance to fungi and  
XX nematodes, increased grain yield and superior secondary growth  
XX properties. Host cells are used for production of recombinant ckl1  
XX nucleic acid which is useful in an assay for determining cytokinin  
XX concentrations, and for its studying effects on plant growth and  
XX metabolism, including senescence  
XX SQ Sequence 1602 BP; 211 A; 179 C; 336 G; 205 T; 0 U; 671 Other;  
Query Match 21.2%; Score 318.6; DB 2; Length 1602;  
Best Local Similarity 36.7%; Pred. No. 6.8e-87;  
Matches 543; Conservative 230; Mismatches 636; Indels 72; Gaps 8;  
QY 89 CCCTTACCTCACCTCTCTACGATCCTTCCATCATCTCCGAGCCTCTCATGACTCG 148  
DB 125 CNYTNGAYGNMAYRTMNGACNGAYWSNAYGNCACNGCNGCNGNACNGAYTTG 184  
QY 149 GAAACATAACCAACCGTGACCCCGCGGCGTAATCTCCCTCTCCCTCCCGTGTATCT 208  
DB 185 GNAAYATHACNWSNGCNVTCNGCNGCNGTNTAYCCNWSNWSNACNGAYTTNG 244  
QY 209 CTGCTCTCTCAATAGC---CGCAACGGAAGATACATTCGAAGTAGCGCTCGT 265  
DB 245 TNGCNYTNYTWSNCGNCAAYWSNACNCCNGNGTGGCNTAYACNATGCTTYMNG 304  
QY 266 GCCAAGGCGACTCTTAAACGGCCAAAGCCTCGGTCTCCGGCGGAGTAACTGTCACATGA 325  
DB 305 GNMGNNGNCAWSNYTNATGCGNCARGCNTTYGCNCCNGGNGGNGTNGTNAAYATGG 364

326 CGTGATCACTGACGTGGTG-----GTTTCAAAAGACAAGAGTAGC 367  
 365 CWSNNTYNGNGAYGNGCNGCNCNMGNAATHAAYGTINWNGCNGAYGNGMNTAYG 424  
 368 CTGACGTGGCGCGGACGCTTATGGGTGATGTCTTAAGAGACGGCGAGAAAGGGG 427  
 425 TNGAYGNGGNGGNGARCARGTNTGGATGAYGTNTMGNGCNGNNTYNGCNGMGNGG 484  
 428 TGTGCGCGGTTCTTGACCGATTTATTTGATATTAACCGTCGGAGGAACTTCTGCAATG 487  
 485 TNGCNCNMGNSNTGGAAYGAYTAYTNTAYTACNGTNGGNGGNGACNYTWSNAYG 544  
 488 GTGGAATTTGGTGAAGTCTTGAAGACGGTCTCTTTGTAGTAACGTCCTTGAATTTG 547  
 545 CNGGNATHWSNGCNGCARGCCTTNGCAYGNGCNCARATHWSNAYGTNTYNGARATGG 604  
 548 ACGTTATTAAGTGGAAAGGTGATGTTGACATGCTCGACACAGCTAAACCCAGAAATGT 607  
 605 AYTGNATHACNGNCAYGNGGATGATGATGATGATGATGATGATGATGATGATGAT 664  
 608 TCTATGAGGTGTTAGGAGGTGTTGGTCAATTTGGAATTTAAGACAGAGCCAGAAATGTTT 667  
 665 TYGAYGNGTNTYNGGNGTNGGNCARITTYGGNGTNTAHCNMGNGCNGNATHSCNG 724  
 668 TGGACCATGACCTAAAGCGGCAATGTTTGGATGCTCTACAGTGAATTCACAACTT 727  
 725 TNGARCCNGCNCNGCNGCNGCNGTGGTNGTNTYGTNTAYACNGAYTTTGCNCNT 784  
 728 TTACAAAGACCAAGACGTTTGTATCAATGGAACGATTTGGAGTGGACTATTATAG 787  
 785 TYWSNGNGAYCARGARMYTNACNGCNCNGCNGGNGGNGGNGCNGWSNTTYG 844  
 788 AA-----GGTCAATATTCTATCAACGCTGCTG 817  
 845 GNCNATONSNTAYTNGARNGNSNGTNTYGTNAAAYCARWSNTYNGCNGACNGAYTNG 904  
 818 TTGACACCTCTTTTCCACCTTCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAAC 877  
 905 CNAAYACNGNTTYYACNGAYGNGAYGNGCNGNATHGNTNGCNYTNGCNGGNGARM 964  
 878 ACGGT-----ATCATCTATGTTCTTGAAGTAGCAAGTATATGATGATCCCATCTCC 931  
 965 GNAAYGCNACNACNGTNTAYNSNATHGAGCNGACNTTAAATAYGAYAAAYCNCNGCNG 1024  
 932 CCATCA-----TCAGCAAGGTTATTGACACATTAAACGAAACATTAAAGTTACTTGC 985  
 1025 CNGCNGCNGCNGTNGAYCARGARYTNGCNGWSNGTNTYNGNACNYTWSNATYGTNGARG 1084  
 986 GGTTCATATCAATGACGACGCTGCTCTTCCGATCTTCCGATCTTCCGATCTTCCGAT 1045  
 1085 GNTTYGNTTYCARMGNGAYTNGCNGTAYGNGCNGTNTYTTNGAYMNGTNCAYGNGARG 1144  
 1045 AAAATAAATCAAGTCTTGGATTTATGGAATCTTCCATCTTGGCTTAACTCTACG 1105  
 1145 ARGTNGCNTNAAAYRYTNGGNTYNGGNGTNGCNGCNGCNGCNGCNGCNGCNGCNG 1204  
 1106 TTCTAAATCTCGGATCTCGATTTTCAATGCGGTGTTGTCAGAGACATCTTCTTAAGC 1165  
 1205 TNCNMGNSNMGNAATHGNCNGAYTAYGNGGNGTNTTAAAGGNAATHYTNC---ARG 1261  
 1166 AAAATACAGTCTCGGACCTCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1225  
 1262 GNAACNGAYATHGNGCNGCNGTNTYNGTNTYNGTNTYNGTNTYNGTNTYNGTNTYNG 1321  
 1226 GTATGTCGGCGATGATACAGAGATCGATGAAGATGTTATATATATATATATATATAT 1285  
 1322 GNATGNSGNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNG 1378  
 1286 AATCCGCTACCCAAAGGATCTTCCAGAGTGGAGCGCTTACAGAGAGATAATAGT 1345  
 1379 SNWSNGTNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNGCNG 1438  
 1346 TTTGCAAGGATTCAGGTATTAGATTAAGCAATATCTAATGCTATTAAGTAAAGAG 1405

Db 1439 TYTGAYTNGCNGGNAHCARTAYAAACNTAYTNGCNGMNCAYACNGAYMNGNSG 1498  
 Qy 1406 ATTGATTGACATTTTGGAT---CAAAATGGGATGATTTTTCGAAGAGGAAAGATCTAT 1462  
 Db 1499 AYTGGTNGNCATTTGNGCNGCNAARTGGAAYMGTNTYGTNGARATGAARAYART 1558  
 Qy 1463 TTGATCCCAAGAACTGTTATCTCCAGGCGAAGACATCTTT 1503  
 Db 1559 AYGAYCCNAARMGNTYNTWSNCCNGCNGCARGAYATHITY 1599

RESULT 15  
 ABK28628  
 ID ABK28628 standard; cDNA; 1611 BP.  
 XX  
 AC ABK28628;  
 XX  
 DT 09-APR-2002 (first entry)  
 XX  
 DE cDNA encoding A. thaliana cytokinin oxidase AtCKX5.  
 XX  
 KW Arabidopsis thaliana; plant; cytokinin oxidase; transgenic plant;  
 KW root growth; lateral root; adventitious root; root geotropism; herbicide;  
 KW root meristem; shoot meristem; leaf senescence; parthenocarp; gene; ss.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 XX WO200196580-A2.  
 XX  
 XX 20-DEC-2001.  
 XX  
 XX 18-JUN-2001; 2001WO-EP006833.  
 XX  
 XX 16-JUN-2000; 2000EP-00870132.  
 XX  
 XX 27-DEC-2000; 2000US-0258415P.  
 XX  
 XX 16-MAR-2001; 2001EP-00870053.  
 XX  
 XX (SCHM/) SCHMULLING T.  
 XX (WERN/) WERNER T.  
 XX  
 XX Schmulling T, Werner T;  
 XX  
 XX WPI; 2002-130736/17.  
 XX  
 XX Polynucleotide encoding novel plant protein having cytokinin oxidase  
 PT activity and the protein useful for stimulating root growth, enhancing  
 PT the formation of lateral or adventitious roots, altering root geotropism.  
 XX  
 XX Claim 3; Page 148-149; 154pp; English.  
 XX  
 XX The invention relates to an isolated polynucleotide (I) encoding a novel  
 CC plant protein (II) having cytokinin oxidase activity. (I) is useful for  
 CC production of transgenic plants, plant cells or tissues; for production  
 CC of altered plants, plant cell or tissues; and for effecting the  
 CC expression of (II) where (I) is operably linked to one or more control  
 CC sequences. The methods further comprises regenerating a plant from the  
 CC plant cell. (I) and (II) are useful for stimulating root growth;  
 CC enhancing the formation of lateral or adventitious roots; altering root  
 CC geotropism, leading to an increase in yield; and for screening growth  
 CC promoting chemical of herbicides. (I) is useful for increasing the size of the  
 CC of the root meristem; increasing root size; increasing leaf senescence;  
 CC shoot meristem; delaying leaf senescence and altering the vessel size;  
 CC increasing leaf thickness; reducing or increasing the vessel size;  
 CC inducing parthenocarp; improving standability of the seedlings;  
 CC increasing branching and for improving lodging resistance. Antibody (III)  
 CC to (II) is useful for identifying and obtaining proteins interacting with  
 CC (II) comprising a screening assay, preferably a two-hybrid screening  
 CC assay. ABK28606-ABK28633 represent Arabidopsis thaliana cytokinin oxidase  
 CC coding sequences and PCR primers of the invention  
 XX  
 XX Sequence 1611 BP; 416 A; 379 C; 409 G; 407 T; 0 U; 0 Other;  
 SQ

Query Match 20.3%; Score 306.2; DB 6; Length 1611;  
Best Local Similarity 53.6%; Pred. No. 4.5e-83;  
Matches 775; Conservative 0; Mismatches 628; Indels 42; Gaps 5;

QY 95 ACCTCACCTCTTACCGATCTTCCATCATCTCGGAGCTCTCTCATGACTTCGGAACA 154  
DB 110 AGGCCACTTACCGCTCACCGCTTCCGACTTAGCTCTCGTCTCTCAGACTTCGATGC 169  
QY 155 TAA---CCACCGTACCCCGCGCGGTAATCTGCCCCCTCTCCACCGCTGATATCTCTC 211  
DB 170 TGAAGTCACTGAAGAGCCATTGGCCGCTTCATCCATCATCGCCGGAAGCGTGCAC 229  
QY 212 GTCTCTCAATACGCCCAACGGAAGTAATCCAAAGTAGCGGCTCGTGGCCCAAG 271  
DB 230 GACTCGTCAGAACAGCTTACCGTTACCGTTCAGCCAGCGGCTTCCCGTCTCAGCCCGAGGCCACG 289  
QY 272 GCCACTCTTAAACGGCCAAAGCTCG-----GTCTCCGCGGAGTAATCG 316  
DB 290 GCCATTCCATAAACGGAACGCGCGGGGAGGAACGGTGTGGTGTGAAATGAACC 349  
QY 317 TCACAATGACGCTGATCACTGACGTGGTGGTTTCAAAGACAAGAGTACGCTCAGCTGG 376  
DB 350 ACGGGTAAACCGGGACGCGCAAGCCACTCGTCCGACCGGATGAAATGTATGTGATGTAT 409  
QY 377 CGGCCGGGACGTTATGGGTGGATGTCTTAAAGACGCGGAGAAAGGGGTGTCCGCGG 436  
DB 410 GGGGTGGAGATTATGGGTGATGTCTTCAAGAAACGTTGGAGCATGGCTTAGCACCA 469  
QY 437 TTTCTTGGACGATTATTTCATATAAACCGTCGGAGGAACGTTGTCGAATGGTGGAAATG 496  
DB 470 AATCATGACGATTACTTGTATCTAAACGTTGGAGTACACTCTCCAATCAGGAATCA 529  
QY 497 GTGGTCAAGTGTTCGAACGCTCTCTTGTAGTAACGTCCTGAAATGGACGTTATTA 556  
DB 530 GTGGTCAAGCTTTTACCATTGGTCTCAATTTAGTAACGTCCTTGGAGTCCAGCTTGTAA 589  
QY 557 CTGGAAAGGTGAAATGTTGACATGCTCGCACAGCTAAACCCAGAAATGTTCTATGGAG 616  
DB 590 CTGGAAAGGAGAGGTGATGAGATGCTCAGAAGAGAGAAACAAAGGCTATTTCCATGGAG 649  
QY 617 TGTAGGAGTTGGTCTCAATTTGNAATTAACGAGAGCCAGATTTGTTGGACCATG 676  
DB 650 TTCTTGGTGGATGAGTCAATTTGGGATCATCCTGAGCAGAAATCTCTCTCGAACCA 709  
QY 677 CACTTAAACGGGCAATGTTTGGATGCTCTACAGTGAATTCACAACTTTTACAAAGG 736  
DB 710 CTCCCCAAGGTTGAGATGAGTACGGGTATTTGATTCGAGCTTCAAAGTGTTCAGGAGG 769  
QY 737 ACCAAGAACGTTTGATATCAATGGCAACGATATTTGGAGTCGACTATTTAGAGGTCAAA 796  
DB 770 ACCAAGAGTACTTAATCTCAATGTCATGTCATTAAGTTTGAATACGTTGAAGGTTTG 829  
QY 797 TATTTCTATCAACCGGTGTCTTGACA-----CCTCTTTTTTCCACCTTCAGATC 847  
DB 830 TGATTGGAGAGAGGACTCGTCAACAATTTGGAGATCTTCTTCTCTCCACGTAACC 889  
QY 848 AATCTTAAAGTCGTGATCTAGTCAAGCAACGATATCTATGTTCTTGAAGTAGCCA 907  
DB 890 CCGTCAAGATCTCCTCTGTAGTTTCCAAACGGCTCTGTTTGTATTCCTTGAATCACCA 949  
QY 908 AGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTTATTGACACATTAACGAAAA 967  
DB 950 AGAATACCAAGACTCCGACTCCGAATCGTTGATCAGGAGTTGAGATTCATGAAGA 1009  
QY 968 CATTAAGTTACTTCCCGGTTTCAATCAATGCAAGCGTGGCTTACTTCGATTTCTTGA 1027  
DB 1010 AATTGAATTTTCAACCGACATCGTCTTTTCAACCGGATTTTACAATATGTGGACTTTCTCG 1069  
QY 1028 ACCGTGTACATGTCGAAGAAATAAATCTAGATCTTTGGGATTTATGGAACTTCCTCATC 1087  
DB 1070 ACCGGGTACAAGCGCGGAATTAAGCTCCGGTCCCAAGAAATTTATGGAGTTCCACACC 1129  
QY 1088 CTTGGCTTAACCTCTACGTTCTCTAAATCTCGGATTTCTCGATTTTTCATAACCGGTTGTCA 1147

DB 1130 CATGGCTCAACCTCTTTCGTGCGCAAAATCAAGAAATCTCTGACTTCGATAAAGCGTTTCA 1189  
QY 1148 AAGACATTTCTTAAAGCAAAAATCAGCTTCGGGACTCGCTCTTCTCTATCCAAACACC 1207  
DB 1190 AGGGCAATTTTGGGAAATAAAACA-----GTGGCCCTATTCTTATCTACCCCATGAACA 1243  
QY 1208 GGAATAAATGGACAAATCGTATGTCGGCGATGATACC-----AGAGATCGATGAAG 1258  
DB 1244 AAGACAAATGGGACGAGAGAGGACTCAGCCGTGACCGCGGATGAGGAAGTTTCTATCTGG 1303  
QY 1259 ATGTTATATATATTATTCGGACTACTACAATCCGCTACCCCAAAGGATCTTCCAGAAGTGG 1318  
DB 1304 TGGCTCTATTGAGATCAGCTTTAAACGGACGTTGAAGAGACACAGAAGCTTAGAGTATCTGA 1363  
QY 1319 AGAGCGTTAAACGAGAAGATAATTAGGTTTTCGAAGGATTCAGGTATTAAAGATTAAGCAAT 1378  
DB 1364 AAGATCAGAACCGTCGGATCTTTGGAGTCTCTGTAAACAAGCCAAAGATCAATGTGAAGCAGT 1423  
QY 1379 ATCTAATGCATTAATACTAGTAAAGAAAGATTGGATTGAGCAATTTTGGATCAAAAATGGATG 1438  
DB 1424 ATCTTCTCACCACGCAACACAGGAAGAGTGGTGGCTCATTTTGGGACAAAGTGGGATC 1483  
QY 1439 ATTTTTCGAAGAGGAAGATCTATTGATCCCAAGAACTGTTATCTCCAGGGCAAGACA 1498  
DB 1484 GGTTCAGAAGCTTAAAGGCTGAGTTTGTATCCCGCACACATACTCGCTACTGTCAGAGAA 1543  
QY 1499 TCTTT 1503  
DB 1544 TCTTT 1548

Search completed: April 7, 2004, 02:57:01  
Job time : 705 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run On: April 6, 2004, 20:47:22 ; Search time 4231 Seconds

(without alignments)  
10629.271 Million cell updates/sec

Title: US-10-014-101-26

Perfect score: 1506  
Sequence: 1 atgctaatcttcgttaaat.....cagggaagacatcttttga 1506

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- EST:\*
- 1: em\_estba:\*
  - 2: em\_esthum:\*
  - 3: em\_estin:\*
  - 4: em\_estmu:\*
  - 5: em\_estov:\*
  - 6: em\_estpl:\*
  - 7: em\_estro:\*
  - 8: em\_htc:\*
  - 9: gb\_est1:\*
  - 10: gb\_est2:\*
  - 11: gb\_htc:\*
  - 12: gb\_est3:\*
  - 13: gb\_est4:\*
  - 14: gb\_est5:\*
  - 15: em\_estfun:\*
  - 16: em\_estom:\*
  - 17: em\_gss\_hum:\*
  - 18: em\_gss\_inv:\*
  - 19: em\_gss\_pln:\*
  - 20: em\_gss\_vrt:\*
  - 21: em\_gss\_fun:\*
  - 22: em\_gss\_mam:\*
  - 23: em\_gss\_mus:\*
  - 24: em\_gss\_pro:\*
  - 25: em\_gss\_rod:\*
  - 26: em\_gss\_pug:\*
  - 27: em\_gss\_vri:\*
  - 28: gb\_gss1:\*
  - 29: gb\_gss2:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	480	31.9	561	9	AU236872
2	368.8	24.5	689	14	CD813279
3	350.6	23.3	688	28	BZ006516
4	324.4	21.5	838	28	BH575041

C	5	290.2	19.3	436	9	AU227876
C	6	288.6	19.2	792	28	BZ078445
C	7	207.4	13.5	679	28	BZ030054
C	8	203.6	13.5	626	14	CB922686
C	9	200.8	13.3	683	28	BZ006156
C	10	195.2	13.0	776	28	BZ500353
C	11	188.8	12.5	553	10	AW623777
C	12	188.6	12.5	510	14	CF607152
C	13	186.8	12.4	601	13	BU025625
C	14	185.2	12.3	451	13	BQ588342
C	15	180.6	12.0	707	14	CD843876
C	16	176.6	11.7	488	10	AW428072
C	17	174.2	11.6	401	9	AV810994
C	18	171.4	11.4	566	13	BU084470
C	19	169.8	11.3	635	10	BZ330968
C	20	168.4	11.2	811	14	CF439478
C	21	168.2	11.2	582	12	BM143498
C	22	162.8	10.8	550	29	CNS000MU
C	23	161.6	10.7	641	28	BH007926
C	24	160.4	10.7	779	28	BH513855
C	25	150	10.0	560	29	CC958884
C	26	147.6	9.8	1016	28	BZ435515
C	27	147.4	9.8	481	9	AV536711
C	28	143.2	9.5	552	12	BM528151
C	29	138.8	9.2	642	12	BI203744
C	30	138.8	9.2	715	12	BI204708
C	31	135.8	9.0	545	28	BH007927
C	32	133.2	8.8	1776	11	AY112108
C	33	130.8	8.7	407	13	BQ968442
C	34	130.8	8.7	699	28	BZ340096
C	35	129.6	8.6	665	10	AW573644
C	36	129	8.6	677	12	BI931101
C	37	128.8	8.6	528	12	BG154047
C	38	128.8	8.6	617	13	BQ871609
C	39	127.4	8.5	769	12	BG582720
C	40	125	8.3	809	14	CF209921
C	41	124.8	8.3	525	12	BI498566
C	42	124.2	8.2	505	12	BI927011
C	43	123.2	8.2	631	9	AV835311
C	44	123	8.2	312	13	BQ916347
C	45	123	8.2	854	28	BH722055

## ALIGNMENTS

RESULT 1  
AU236872  
LOCUS AU236872 561 bp mRNA linear EST 01-APR-2002  
DEFINITION AU236872 RAFL15 Arabidopsis thaliana cDNA clone RAFL15-29-H04 5', mRNA sequence.  
ACCESSION AU236872 GI:19876041  
VERSION AU236872.1  
KEYWORDS EST.  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 561)  
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,O., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.  
Large scale analysis of Arabidopsis full-length cDNA

Unpublished (2002)  
Contact: Motoaki Seki  
Plant Functional Genomics Research Group  
RIKEN Genomic Sciences Center  
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
Tel: 81-298-36-4359  
Fax: 81-298-36-9060  
Email: msekietc@cc.riken.go.jp

An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site ([http://www.gsc.riken.go.jp/e/plant/index\\_e.html](http://www.gsc.riken.go.jp/e/plant/index_e.html)) for further details.

#### FEATURES

Location/Qualifiers  
 1..561  
 /organism="Arabidopsis thaliana"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3702"  
 /clone="RAF15-29-H04"  
 /tissue\_type="mixture of silique and flower"  
 /lab\_host="DH10B"  
 /clone\_lib="RAF15"  
 /note="Site\_1: BamHI; Site\_2: SalI"

#### ORIGIN

Query Match 31.9%; Score 480; DB 9; Length 561;  
 Best Local Similarity 99.0%; Pred. No. 1.9e-121;  
 Matches 502; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY	1	ATGGCTAATCTCGTTTAAATGATCACTTAAATCAGGTTTAAATGATCACCATAATCATCA	60
DB	55	ATGGCTAATCTCGTTTAAATGATCACTTAAATCAGGTTTAAATGATCACCATAATCATCA	114
QY	61	AACGGTATTAATAATGATTAACCTAAATCCCTTAACCTCACCCTCTACCGATCCTTCC	120
DB	115	AACGGTATTAATAATGATTAACCTAAATCCCTTAACCTCACCCTCTACCGATCCTTCC	174
QY	121	ATCATCTCCGACGCTCTCATGACTCGGAACATACACCGTGACCCCGCGCGCGTA	180
DB	175	ATCATCTCCGACGCTCTCATGACTCGGAACATACACCGTGACCCCGCGCGCGTA	234
QY	181	ATCTGCCCTCTCCACCGCTGATATCTCTCGTCTCTCAATAGCCGCAACGGA	240
DB	235	ATCTGCCCTCTCCACCGCTGATATCTCTCGTCTCTCAATAGCCGCAACGGA	294
QY	241	AGTACATTCAGTAGCGGCTCTGCGGACGCTCTTAAAGCGGCAAGCGGTC	300
DB	295	AGTACATTCAGTAGCGGCTCTGCGGACGCTCTTAAAGCGGCAAGCGGTC	354
QY	301	TCCGGGGAGTAATCGTCAACATGAGTGATATCACTGAGTGCTGTTTCAAAAGCAAG	360
DB	355	TCCGGGGAGTAATCGTCAACATGAGTGATATCACTGAGTGCTGTTTCAAAAGCAAG	414
QY	361	AGTACGCTGACGTGGCGGCGGAGCTTATGAGTGATGCTTAAAGAGCGGCGGAG	420
DB	415	AGTACGCTGACGTGGCGGCGGAGCTTATGAGTGATGCTTAAAGAGCGGCGGAG	474
QY	421	AAAGGGGTGTCGCGGTTTCTTGACGGATTATTGCAATATAA-CGGTCGGAGGAACGTT	479
DB	475	AAAGGGGTGTCGCGGTTTCTTGACGGATTATTGCAATATAA-CGGTCGGAGGAACGTT	534
QY	480	GTCGAATGGTGG-AATTGGTGGTCAAG	505
DB	535	NTCNAATGGTGGAAATGGTGGTCAAG	561

RESULT 2  
 CD813279  
 LOCUS  
 DEFINITION  
 sequence.  
 CD813279  
 CD813279.1  
 EST.  
 SOURCE  
 Brassica napus (rape)  
 ORGANISM  
 Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

CD813279 689 bp mRNA linear EST 10-JUL-2003  
 BN15.019B17F020122 BN15 Brassica napus cDNA clone BN15019B17, mRNA  
 accession  
 CD813279  
 CD813279.1  
 GI:32495219

#### REFERENCE

1 (bases 1 to 689)  
 Genoplatte.  
 Genoplatte, a major partnership french program in plant genomics  
 Unpublished (2003)  
 Contact: Genoplatte  
 Genoplatte  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french  
 plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>)  
 and <http://genoplatte-info.infobiogen.fr>.

#### FEATURES

source  
 1..689  
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 /cultivar="Jet neuf"  
 /db\_xref="taxon:3708"  
 /clone="BN15019B17"  
 /tissue\_type="seed"  
 /clone\_lib="BN15"

#### ORIGIN

Query Match 24.5%; Score 368.8; DB 14; Length 689;  
 Best Local Similarity 80.2%; Pred. No. 1.3e-90;  
 Matches 465; Conservative 0; Mismatches 97; Indels 18; Gaps 2;

QY	1	ATGGCTAATCTCGTTTAAATGATCAGTTTAAATCAACGGTTTAAATGA-----	46
DB	102	ATGGCTAATCTCGTTTAAATGATCAGTTTAAATCAACGGTTTAAATGA-----	161
QY	47	-TCACCAAAATCATCAAAACGGTATTAAA---ATTGATTACCTAAATCCCTTAACCTCACC	102
DB	162	TTTGCTAAATCGTCAGAAAGCAGTAAAGTTATTACTTACTTAAAGTCCCTTAAACCTCACC	221
QY	103	CTCTCTACCGATCCTTCCATCATCTCCGAGCTCTCATGACTTCGGAACATAACCAACC	162
DB	222	CTCTCTACCGATCCTTCCATCATCTCCGAGCTCTCATGACTTCGGAACATAACCAACC	281
QY	163	GTGACCCCGCGCGGCTAAATCTGCCCCCTCTCCACCGCTGATATCTCTCTCTCTCCAA	222
DB	282	GTGACCCCGCGCGGCTAAATCTGCCCCCTCTCCACCGCTGATATCTCTCTCTCTCCAA	341
QY	223	TACGCGCAACGGAAGAGTACATTCCTCAAGTAGCGGCTCTGCGCAAGGCACTCTCTTA	282
DB	342	TACGCGCAACGGAAGAGTACATTCCTCAAGTAGCGGCTCTGCGCAAGGCACTCTCTTA	401
QY	283	AACGGCCAAAGCTCGGTCTCGGCGGAGTAAATCGTCAACATGACGTGATCATCTGAGCTG	342
DB	402	AACGGCCAAAGCTCGGTCTCGGCGGAGTAAATCGTCAACATGACGTGATCATCTGAGCTG	461
QY	343	GTGGTTTCAAAGACAAGATGACGTGAGTGGCGCGGAGGCTTATGGTGGATGTG	402
DB	462	ACTGTTTCAAAGACAAGATGACGTGAGTGGCGCGGAGGCTTATGGTGGATGTG	521
QY	403	CTTAAGAGACGCGGAGAAAGGGGTGTGCGCGGTTTCTTTGGACGGATTATTTGCATATA	462
DB	522	CTTAAGAGACGCGGAGAAAGGGGTGTGCGCGGTTTCTTTGGACGGATTATTTGCATATA	581
QY	463	ACCGTCGAGGAAGCTTGTGGAATGGTGGTGAATGGTGGTGAATGGTGGTGAATGGTGGT	522
DB	582	ACCGTCGAGGAAGCTTGTGGAATGGTGGTGAATGGTGGTGAATGGTGGTGAATGGTGGT	641
QY	523	CTTGTGTAGTACGCTCTTGAATTTGACGCTTATTACTGGGA	562
DB	642	CAAAATTAGTAACGCTCTTGAATTTGACGCTTATTACTGGTA	681

#### RESULT 3

BZ006516  
 LOCUS  
 DEFINITION

BZ006516 688 bp DNA linear GSS 07-OCT-2002  
 ceg06a08.g1 B.oleracea002 Brassica oleracea genomic, genomic survey  
 sequence.



BZ006516  
 BZ006516.1 GI:23554774  
 GSS.  
 Brassica oleracea  
 Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 688)  
 Delehaunty, K., Fewell, G., Fulton, L., McCombie, W. R., Miner, T.,  
 Nash, W., Rabinowicz, P. D. and Wilson, R. K.  
 Whole genome shotgun reads from Brassica oleracea  
 Unpublished (2002)  
 Contact: Richard K. Wilson  
 Genome Sequencing Center  
 Washington University School of Medicine  
 Email: submissions@wustl.edu  
 Plate: oeg06 row: a column: 08  
 Seq primer: -28RppOT reverse  
 Class: shotgun  
 High quality sequence start: 16  
 High quality sequence stop: 551.  
 Location/Qualifiers  
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 /db\_xref="taxon:3712"  
 /clone\_lib="B.oleracea002"  
 /note="vector: pOTw13; Whole genome shotgun library from  
 flowering buds. DNA was purified from a crude nuclear  
 prep using Brassica oleracea TOL000DH3 buds provided by  
 Thomas Osborn at the University of Wisconsin. Genomic  
 DNA was provided by Pablo Rabinowicz (CSHL) and the  
 shotgun library prepared at Washington University Genome  
 Sequencing Center."  
 Query Match 23.3%; Score 350.6; DB 28; Length 688;  
 Best Local Similarity 82.7%; Pred. No. 1.4e-85;  
 Matches 401; Conservative 0; Mismatches 84; Indels 0; Gaps 0;  
 78 TTTACCTAAATCCCTTAACTCACCCTCTCTACCGATCCTTCCATCATCTCCGAGCCTC 137  
 29 TCTACCAATCGTTAACTCACCCTCTACCGATCCTTCCGATCCTCCGCGCCTC 88  
 138 TCATGACTCGGAACATACACCGGTACCGCGGCGGCGGTATCTGCCCTCTCCAC 197  
 89 TCACGATTTTGAACATCACTACCGGTATACCGGTGGCGGTGATCTGCCCTCTCC 148  
 198 CGCTGATATCTCGTCTCTCCATACCGCGCAACCGAAAGATACATTCGAAGTAGC 257  
 149 CGCTGATATCTCGTCTCTCCATACCGCGCAACCGAAAGATACATTCGAAGTAGC 208  
 258 GGCTCGTGGCCAGGCCACTCTTAAACGGCGGCGGCTCTCCGCGGAGTAATCGT 317  
 209 AGCTCGGCGCAAGGCCACTCTTAAAGGGTCAAGCAGCAGTCTCTCAACGGAGTAATCGT 268  
 318 CAACATGACGTATCTACCTGAGTGGTGTTCAAAGACAGAGTACGCTGACGTTGC 377  
 269 CAACATGACGTATCTGCTGGGTAGTATTTCAATGACATGATGATGCTGACGTTGC 328  
 378 GGCCTGGAGCTTATGGGTGATGTCTTAAAGAGACGGCGGAGAAAGGGGTGTCGCCGT 437  
 329 CGGTGGAGCTTATGGGTGATGTCTTAAAGAGATACGGCGGAGAAAGGGGTGTCGCCGT 388  
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 389 TTCTTGGAGGATATTTGATATACCTGCGGAGACGTTGTCGAATGTTGAATTTGG 448  
 498 TGGTCAAGTGTTCGAAACGGTCTCTTGTAGTAAACGTCCTTGAATTTGGAGCTTATAC 557  
 449 CGGTGAAGTGTTCGAAACGGTCTCTTGTAGTAAACGTCCTTGAATTTGGAGCTTATAC 508

558 TGGGA 562  
 509 TGGTA 513  
 BH575041  
 BOG8T82TR BOG8 Brassica oleracea genomic clone BOG8T82, genomic  
 survey sequence.  
 BH575041  
 BH575041  
 BH575041.1 GI:17827114  
 GSS.  
 Brassica oleracea  
 Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 838)  
 Town, C.D., Van Aken, S., Uterback, T., Koo, H. and Fraser, C.M.  
 Whole genome shotgun sequencing of Brassica oleracea  
 Unpublished (2001)  
 Other GSSs: BOG8T82TF  
 Contact: Chris Town  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TR  
 Class: sheared ends.  
 Location/Qualifiers  
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 /clone\_lib="BOG8"  
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 Query Match 21.5%; Score 324.4; DB 28; Length 838;  
 Best Local Similarity 74.6%; Pred. No. 2.8e-78;  
 Matches 473; Conservative 0; Mismatches 81; Indels 80; Gaps 2;  
 944 AGTTATTGACATTAACGAAACATTAAGTTACTTCCCGGTTTCATCAATGCAGC 1003  
 640 AGGTGATTGACAGTTAACTAAACCCCTAAGTTACCTGCCCGGTTTATCAATGCAGC 581  
 1004 ACCTGGCTTACTTCGATTTCTTGAACCGTGTACATGTCGAAGAAATAAATCAATCTT 1063  
 580 ACCTGCTCTACTTTGATTTCTTGAACCGTGTACAGTTCAAGTAAGATAAATCAATCTC 521  
 1064 TGGGATTATGGGAATCTCTCATCTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTT 1123  
 520 TGGCTTTATGGGAATCTCTCATCTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTTTCCTT 461  
 1124 TCGATTTTCATACCGGTGTTGTCAAAGACATTTCTTAAAGCAAAATCAGTTTCGGGAC 1183  
 460 TAGATTTCCATAACGGTGTGTTGAAGACATTTCTTCAAGCAGAACTCGATCTTCGGG 401  
 1184 TCGCTCTTCTCTATCAACAAACCGGAATAA-----1214  
 400 TTGCTCTCTCTATCCACCAACCGGAATAAAGTAAGTTATTTCATCTACTAATCTTCAAGAA 341  
 1215 -----ATGGGACAACTCGTAT 1229  
 340 CAAGTAACTAGATCTTGACATAATGTTTTTCTTGTATTATTATTAGATGGGACATGTTAT 281  
 1230 GTCCGCGATGATACACGAGATCGATGAAGATGTTATATATATATATTCATCGGACTACTCAATC 1289

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Db      280  GTCCGCGATGATACCA-----GATGAAGATGTTTCTATGTCGTGGGACTACTACAGGC 227
QY      1290  CGCTACCCCAAGGATCTTCAGAAAGTGGAGAGCGTTAAACGAGAGATATAATTAGGTTTGG 1349
Db      226  AGCTAGCTCACAAAATGTCGAAGAGTGGAGAGTGTAACACGAGCGATCATTAGGTTTGG 167
QY      1350  CAAAGGATTCAGGTATTAAGATTAAACCAATATCTAATGCAATATATACTAGTAAAGAAAGATTG 1409
Db      166  CAAGGATCTCGGATTAAGATTAAAGCAATATCTAATGCAATATATACTAGTAAAGAAAGATTG 107
QY      1410  GATTGAGCATTTGGATCAAAATGGGATGATTTTCGAAGAGGAAAGATCTATTGATCC 1469
Db      106  GGTTCGAACATTTGGATCTAAATGGGGTGCITTTTCGAAGAGGAAAGATCTGTTGATCC 47
QY      1470  CAAAGAACTGTTTATCTCCAGGCGCAAGACATCTTT 1503
Db      46  TAAGAACTATTTATCTCCAGGCGCAAGATATTTT 13

RESULT 5
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LOCUS   AU227876 436 bp mRNA linear EST 23-APR-2002
DEFINITION AU227876 RAFL15 Arabidopsis thaliana cDNA clone RAFL15-29-H04 3',
mRNA sequence.
ACCESSION AU227876
VERSION   AU227876.1 GI:19742523
KEYWORDS  EST.
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 436)
AUTHORS   Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Akiyama,K., Enju,A., Oono,Y., Sakurai,T., Carninci,P., Kawai,J.,
Itoh,M., Ishii,Y., Arahawa,T., Shibata,K., Shinagawa,A.,
Muramatsu,M., Hayashizaki,Y. and Shirozaki,K.
REFERENCE Large scale analysis of Arabidopsis full-length cDNA
JOURNAL   Unpublished (2002)
COMMENT    Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index\_e.html) for further
details.

FEATURES
source
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Location/Qualifiers
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ORIGIN
Query Match 19.3%; Score 290.2; DB 9; Length 436;
Best Local Similarity 95.1%; Pred. No. 6.1e-69;
Matches 311; Conservative 0; Mismatches 13; Indels 3; Gaps 1;

QY      1180  GGACTCGCTCTTCTATCCAAACACCGGATAAATGGGACAATCGTATGCGCGGATG 1239
Db      431  GGACTCGCTCTTCTATCCAAACACCGGATAAATGGGACAATCTATGTC---GGCATG 375

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QY      1240  ATACCAGAGATCGATGAAGATGTTATATATATATATCGGACTACTACAATCGCTACCCCA 1299
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QY      1300  AAGATCTTCCAGAGTGGAGAGCGTTAACGAGAGATATAATTAGGTTTGGAAAGATTCA 1359
Db      314  AAGGATCTTCCAGAGTGGAGAGCGTTACGAGAGATATAATTAGGTTTGGAAAGATTCA 255
QY      1360  GGTATTAAAGATTAAAGCAATATCTAATGCAATATCTAGTAAAGAAAGATTGGATTGAGCAT 1419
Db      254  GGTATTAAAGATTAAAGCAATATCTAATGCAATATCTAGTAAAGAAAGATTGGATTGAGCAT 195
QY      1420  TTTGGATCAAAATGGGATGATTTTCGAAGAGGAAAGATCTATTGATCCCAAGAAACTG 1479
Db      194  TTTGGATCAAAATGGGATGATTTTCGAAGAGGAAAGATCTATTGATCCCAAGAAACTG 135
QY      1480  TTATCTCCAGGCGCAAGACATCTTTTGA 1506
Db      134  TTATCTCCAGGCGCAAGACATCTTTTGA 108

RESULT 6
BZ078445/c
LOCUS   BZ078445 792 bp DNA linear GSS 10-OCT-2002
DEFINITION BZ078445 B.oleracea002 Brassica oleracea genomic, genomic survey
sequence.
ACCESSION BZ078445
VERSION   BZ078445.1 GI:23702365
KEYWORDS  GSS.
SOURCE    Brassica oleracea
ORGANISM  Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 792)
AUTHORS   Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
REFERENCE Whole genome shotgun reads from Brassica oleracea
JOURNAL   Unpublished (2002)
COMMENT    Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: 1lf25 row: a column: 09
Seq primer: -28RPOT reverse
Class: shotgun
High quality sequence start: 12
High quality sequence stop: 551.

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flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea TO1000DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (GSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

ORIGIN
Query Match 19.2%; Score 288.6; DB 28; Length 792;
Best Local Similarity 77.6%; Pred. No. 2.3e-68;
Matches 364; Conservative 0; Mismatches 99; Indels 6; Gaps 1;

QY      1 ATGGCTAATCTTGGTTTAATGATCACTTTAATCAGGTTTAA-----TGATCACCAAA 54
Db      495  ATGGCTAATCTTGGTTTAATGATCACTTTAATCAGGTTTAAATGATCTCTGATTTATTTACTTCAAGC 436
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435 TGATCAATCGTCAGAGATTATTCACCCAAATCGTTAAACCTCACCCCTCTAACCGAT 376
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375 CTTTCGCCCATCTCCGCGCCTCTCAGCATTTTGGAAACATCATCACTACCGTGATACCCGGT 316
175 GCGTAATCTGCCCTCTCTCCACCGCTGATATCTCTCTCTCTCCCAATACGCGCGCAAC 234
315 GCGTGATCTGCCCTCTCTCTCCGCTGAGATATCCGCTCTCTCAGCTACGCTCTAAC 256
235 GGAAAAAGTACATTCGAAGTAGCGCTCTGTCGGCCAGGCCACTCTCTAAACGCGCCAGCC 294
255 GGAAAAAGAAAGTTTCAAGTGGCAGCTCGCGGCCAGGCCACTCTCTTGAAGGGTCAAGCA 196
295 TCGTCTCCGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGTGGTGGTTTCAAAA 354
195 GCATCTCTCAACGAGTATTCGTCACATGACGTGTCTCTCGTGGCTAGTGTAGAT 136
355 GACAAGAGTACGCTGACGTGGCGCGCGGACGTTATGGTGGATGTGCTTTAAGAAGAGC 414
135 GACATGAAGTATGCTGACGTGGCGCGTGGACGTTATGGTGGTGTATGCTGAAAAATACG 76
415 GCGGAGAAAGGGTGTCCGCGGTTTCTTGGACGATTTTGCATATAA 463
75 GCGGAGAAAGCGTTTCCGCGGTTTCTTGGACGATTTTGCATGTTA 27

RESULT 7
BZ030054/c
LOCUS BZ030054
DEFINITION oeg01c05.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
sequence.
ACCESSION BZ030054
VERSION BZ030054.1 GI:23599512
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
REFERENCE 1 (bases 1 to 679)
AUTHORS Delehaunty,K., Fellw.,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
TITLE Whole genome shotgun reads from Brassica oleracea
JOURNAL Unpublished (2002)
COMMENT Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: oeg01 row: c column: 05
Seq primer: -28RPOT reverse
Class: shotgun
High quality sequence start: 8
High quality sequence stop: 551.
FEATURES
Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTw13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea TO1000DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

ORIGIN
Query Match 13.8%; Score 207.4; DB 28; Length 679;
Best Local Similarity 84.1%; Pred. No. 6.4e-46;
Matches 248; Conservative 0; Mismatches 41; Indels 6; Gaps 1;

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1212 TAAATGGGACAAATCGTATGTGCGGATGATACAGAGATCGATGAAGATGTTATATATAT 1271
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1272 TATCGGACTACTACAAATCCGCTACCCCAAGGATCTTCCAGAAAGTGGAGCGTTAAGCA 1331
543 CGTGGGACTACTACAGGCGAGCTAGCTCAGAAATGTGCAAGAGTGGAGAGTGAACGA 484
1332 GAAGATATTAAGTGTTCAGAGGATTCAGGTATTAAGATTAAGCAATATCTAATGCATTA 1391
483 GCGCATCATTAAGTGTTCAGAGGACTCGGTATTAAGATTAAGCAATCTAATGCATTT 424
1392 TACTAGTAAAGAGATTCGATTTGAGCATTTTGGATCAAAATGGGATGATTTTTCGAAG 1451
423 CACCAAGAAAGAGATTCGGTTGAACATTTGGATCTAAATGGGCTGCTTTTCGAAGAG 364
1452 GAAGATCTATTGATCCAGAGAACTCTATCTCCAGGCAAGACATCTTTTGA 1506
363 GAAGATCTGTTTGTATCTTAAGAACTATTATCTCCAGGCAAGATATTTTGA 309

RESULT 8
CB922686
LOCUS CB922686
DEFINITION 626 bp mRNA linear EST 25-APR-2003
VVD086G02_356005 An expressed sequence tag database for abiotic
stressed berries of Vitis vinifera var. Chardonnay Vitis vinifera
cDNA clone VVD086G02 5, mRNA sequence.
ACCESSION CB922686
VERSION CB922686.1 GI:30137348
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
REFERENCE 1 (bases 1 to 626)
AUTHORS Cushman,J.C.
TITLE An expressed sequence tag database for abiotic stressed berries of
Vitis vinifera var. Chardonnay
JOURNAL Unpublished (2002)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer (backward)
BACKWARD: T7 21mer
Plate: 086 row: G column: 02
Seq primer: T3 20mer
High quality sequence stop: 626.
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EcoRI; Site_2: XhoI"

ORIGIN
Query Match 13.5%; Score 203.6; DB 14; Length 626;
Best Local Similarity 62.8%; Pred. No. 7e-45;
Matches 355; Conservative 0; Mismatches 195; Indels 15; Gaps 2;
364 TACGCTGACGTGGCGCGGACGTTATGGTGGATGTCTTAAAGAGAGCGCGGAGAAA 423

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 Qy 424 GGGGTGTCGGCGTTCTTGGACGGATATTGTCATATAACCGTCGAGGAAAGTTGTCG 483  
 Db 130 GGAATTGACCAAGTGTGCTGACTGACTATTGTCACCTAAATGCTGCTGACTCTCT 189  
 Qy 484 AATGTTGGAATTTGGTGTCAAGTCTTTCGAAACGGTCTCTTGTAGTAACGTCCTTGAA 543  
 Db 190 AATGCCGAATAGCGCCAGACATTCGCCATGCTCTCAGATCAGCAGCTGATGAA 249  
 Qy 544 TTGACGCTATTACTGGGAAAGGTGAATGTTGACATGCTGCGACAGCTAAACCCAGAA 603  
 Db 250 ATGATGTTCTTACTGTTAAAGGGAAGTCTGTAAGTTGTTCCAAAGACACAAAGTCTGAG 309  
 Qy 604 TTGTTCTATGAGTCTTAGGAGTTTGGTCAATTTGGAATTAATAAGAGAGCCAGAAAT 663  
 Db 310 CTGTTTTTGGGTTCTTAGGAGTTCTCGGAGCTTTGGGATTATTAAGAAGAGATC 369  
 Qy 664 GTTTTGGACCATGACCTAAACCGGCCAAATGTTTGGATGCTCTACAGTACTTCA 723  
 Db 370 GCTCTAGAACCAGCAGCAAGAGTAAATGGATACAGATGCTTTACGATGACTTCTCC 429  
 Qy 724 ACTTTTCAAGAGACCAAGAGCTTGTATATCAATGGCAACGATATTTGGAGTGCAT 783  
 Db 430 ACAITTTCTAGAGACCAAGAACATTTGATTTCAAT-----CAATGACTGACTAT 480  
 Qy 784 TTAGAAGTCAAAATATTTCTATCAACCGTCTGTTGACACC-----TCTTTTTCCCA 837  
 Db 481 TTGAGGTTCACTCTCCATGCAAAATAGTCTCTCTAATACTGGAGATCTCTTTCTCA 540  
 Qy 838 CTTGAGATCAATCTAAAGTCTGCTGATCTAGTCAAGCAACGCTATCATCTATGTTCTT 897  
 Db 541 CCCTCTGAATCCCGAGAAATATCTTCACTAATATCAAGAAATGGCATCATCTACTGCTT 600  
 Qy 898 GAAGTAGGCAAGTATTATGATGATC 922  
 Db 601 NGAGTGGTCAAGTATACGATGAAC 625

RESULT 9  
 BZ006156/c  
 LOCUS  
 DEFINITION oeg06a08.bi B.oleracea002 Brassica oleracea genomic, genomic survey sequence.  
 ACCESSION BZ006156  
 VERSION BZ006156.1 GI:23554414  
 SOURCE GSS.  
 ORGANISM Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 683)  
 Deléhaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Nash,W., Rabinowicz,P.D. and Wilson,R.K.  
 Whole genome shotgun reads from Brassica oleracea  
 Unpublished (2002)  
 CONTACT: Richard K. Wilson  
 Genome Sequencing Center  
 Washington University School of Medicine  
 Email: submissions@watson.wustl.edu  
 Plate: oeg06 row: a column: 08  
 Seq primer: -21UPPOT forward  
 Class: shotgun  
 High quality sequence start: 32  
 High quality sequence stop: 551.  
 Location/Qualifiers  
 1. .683  
 /organism="Brassica oleracea"  
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 /db\_xref="taxon:3712"  
 /clone\_lib="B.oleracea002"

ORIGIN  
 Query Match 13.3%; Score 200.8; DB 28; Length 683;  
 Best Local Similarity 84.3%; Pred. No. 4.3e-44;  
 Matches 226; Conservative 0; Mismatches 42; Indels 0; Gaps 0;  
 Qy 680 CTAACGGGCGCAAAATGGTTTCGGATGCTCTACAGTATTCACAACTTTTACAAGGACC 739  
 Db 604 CTATGTAGCGCAATGGTTTCGAATGCTGTACAGTCTTACAGCTTTTACAAGGACC 545  
 Qy 740 AAGAAGTTTGATATCAATGGCAACGATATTGGAGTCGACTATTAGAAAGTCAAAATAT 799  
 Db 544 AAGAAGTTTGATATCAATGGCGGATGATGCTGGAGTTGATTATTAGAGTCAACTAT 485  
 Qy 800 TTCTATCAAAACGGTGTGTTGACACCTCTTTTTTCCACCTTTCAGATCAATCTAAAGTCG 859  
 Db 484 TCATGTCAAAACGGCTCGTAGACACCTCTTTTTTCCACAGCTCTAATCAATCTAAATCG 425  
 Qy 860 CTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTTGAAGTAGCCAGTATTATGATG 919  
 Db 424 CTGATTTAGTGAAGACCGCAGGTATCATATATGTTCTTGAAGTAGCCAGTATTATGATG 365  
 Qy 920 ATCCCAATCTCCCATCATCATCAGCAAGGT 947  
 Db 364 ATCCTACACTTCCCATCATTCGCCAGGT 337

RESULT 10  
 BZ500353  
 LOCUS  
 DEFINITION BONRD06TF BO 1.6.2 KB tot Brassica oleracea genomic clone BONRD06, genomic survey sequence.  
 ACCESSION BZ500353  
 VERSION BZ500353.1 GI:27016257  
 KEYWORDS GSS.  
 SOURCE Brassica oleracea  
 ORGANISM Brassica oleracea  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 1 (bases 1 to 776)  
 Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.  
 Whole genome shotgun sequencing of Brassica oleracea  
 Unpublished (2001)  
 Other GSSs: BONRD06TR  
 CONTACT: Chris Town  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TF  
 Class: sheared ends.  
 Location/Qualifiers  
 1. .776  
 /organism="Brassica oleracea"  
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 /db\_xref="taxon:3712"  
 /clone="BONRD06"  
 /clone\_lib="BO 1.6.2 KB tot"  
 /notes="Vector: pBOS1; Site 1: BstXI; 1.6-2 kb sheared total DNA inserted into pBOS1 using BstXI linkers"

ORIGIN

Query Match 13.0%; Score 195.2; DB 28; Length 776;  
 Best Local Similarity 85.2%; Pred. No. 1.6e-42;  
 Matches 218; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 307 GGAGTAATCGTCAACATGAGCGTATCACTGAGCGTGGTTCACAAAGACAAAGATAC 366  
 Db 2 GGAGTGCTTATCAACATGAGCGTGCCTCGCTGACATAACTGTTTCAGAAAGCAAGAGTAT 61

QY 367 GCTGACCTGGCGCGGAGCGTATGAGTGGTGGTCTTAAAGAGACGGCGGAGAAAGGG 426  
 Db 62 GTTACGCTGGCGCGGAGCGTATGAGTGGTGGTCTTAAAGAGACGGCGGAGAAAGGC 121

QY 427 GTGTCGCGGTTCTTGGAGCGATATTTCATATTAACCGTCGGAGAAAGTTCGCAAT 486  
 Db 122 GTTTCGCGGTTCTTGGAGCGATATTTCATATTAACCGTCGGAGAAAGTTCGCAAT 181

QY 487 GGTGGAATGCTGCTCAAGTCTTTCGAAACGCTCTCTGTTAGTACGTCCTTGAATTG 546  
 Db 182 GCTGGAATGCTGCTCAAGTCTTTCGAAACGCTCTCTCAATATTAGTACGTCCTTGAATTG 241

QY 547 GACGTTTACTGGGA 562  
 Db 242 GACGTTTATAATTGGTA 257

RESULT 11  
 AW623777  
 LOCUS EST321722 tomato flower buds 3-8 mm, Cornell University  
 DEFINITION Lycopersicon esculentum cDNA clone cTOB1317 5', mRNA sequence.  
 ACCESSION AW623777  
 VERSION AW623777.1 GI:7336804  
 KEYWORDS EST.  
 SOURCE Lycopersicon esculentum (tomato)  
 ORGANISM Lycopersicon esculentum

REFERENCE  
 AUTHORS van der Hoeven,R.S., Bezzeredes,J.L., Matern,A.L., Holt,I.E.,  
 Liang,F., Hansen,T., Craven,M.B., Bowman,C.D., Roming,C.M.,  
 Niemman,W., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and  
 Tanksley,S.D.  
 TITLE Generation of ESTs from tomato flower tissue, 3-8 mm buds  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: CUGI  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Email: <http://www.genome.clemson.edu/orders/index.html>  
 5 prime sequence.

FEATURES  
 source  
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 /organism="Lycopersicon esculentum"  
 /mol\_type="mRNA"  
 /cultivar="TA496"  
 /db\_xref="taxon:4081"  
 /clone="cTOB1317"  
 /tissue\_type="flower"  
 /dev\_stage="3-8mm buds"  
 /clone\_lib="tomato flower buds 3-8 mm, Cornell University"  
 /note="Vector: pBlueScript SK(-); Site\_1: EcoRI; Site\_2:  
 XhoI; supplier: Tanksley; Flower buds and flowers were  
 taken from greenhouse plants (4-8 wks old, TA496). They  
 were immediately frozen in liquid nitrogen and then  
 size-separated while remaining frozen."

ORIGIN  
 Query Match 12.5%; Score 188.8; DB 10; Length 553;  
 Best Local Similarity 60.4%; Pred. No. 8.3e-41;  
 Matches 332; Conservative 0; Mismatches 212; Indels 6; Gaps 1;

QY 479 TGTCGATGTTGGAATTGGTGGTCAAGTGTTCGAAACGGTCTCTCTTGTAGTAACGTCC 538

Db 3 TCTCTAATGCTGTATTTAGTGGTCAAACTAACCGATATGGTCCCAATAATAGTAACGTAC 62

QY 539 TTGAATTCGGACGTTTACTGGGAAAGGTGAAATGTTGACATGCTCGCGACAGTAAACC 598

Db 63 ATGAGATGGAATTAATACAGTAAAGGGGAATTAATGACTTGTCTCCAAAGATATGAAT 122

QY 599 CAGAAATGTTCTATGAGGTGTAGAGGTTTGGGTCAATTTTGGATTTATAACGAGAGCA 658

Db 123 CAGAAATGTTTGTGGAGTTTGGAGGTTTGGGACAGTTTGGAAATAATAACAAGAGCA 182

QY 659 GAATTTGTTTGGACCATGACCTAAACGGGCAAAATGTTTTCGGATGCTCTACAGTGAAT 718

Db 183 GAATTTGTTTGGATTAAGACCAACAGAGTGAATGGTGAAGATTTATATGATGATTT 242

QY 719 TCACAACCTTTTACAAAGGACCAAGACGTTTGAATATCAATGGCAACGATTTGGAGTCG 778

Db 243 TCTCAAAATTCACAAAGATCAAGAACATCTTAATTTCAATTCATTAATGAATGGATTT 302

QY 779 ACTATTTAGAAGGTCAAATATTCTATCAAAACGGTGTGTTGACA-----CCTCTTTT 832

Db 303 ATGTTGAAGGCTCTTAATGATGGAGCAAGCTCTCTAAATAATTTGGAGATCTTCATTT 362

QY 833 TCCCACTTCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGATCATCATATG 892

Db 363 ATTCACCTTCCCAATCAAAACCAAAATTTGCTTCAATTTATCCAAAATAAAATCATGTAT 422

QY 893 TTCTTGAAGTACCAAGTATTATGATGCCAACTCTCCCATCATCAGCAAGGTTATTG 952

Db 423 GCTTGAATATGTAAGTACTATGATGACCAAAATGCTAATACTATTGTAAGGATTTGA 482

QY 953 ACACATTTAACGAAACATTAAAGTTACTTTCGCCGGTTCATATCAATCAATGACGACGTCCT 1012

Db 483 AGAAGTTGTTAAAGGATTGAAGTATGATGAGTGGATTTATGTTCAAGAAAGATGTGAGTT 542

QY 1013 ACTTCGATTT 1022

Db 543 TTGTGGAATTT 552

CF607152 510 bp mRNA linear EST 30-SEP-2003  
 GEMMA01\_000608 Grape Bud P5P0R1 Library Vitis vinifera cDNA 5',  
 mRNA sequence.  
 CF607152  
 ACCESSION CF607152.1 GI:37187799  
 VERSION CF607152  
 KEYWORDS EST.  
 SOURCE Vitis vinifera  
 ORGANISM Vitis vinifera  
 Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; Vitaceae; Vitis.  
 REFERENCE 1 (bases 1 to 510)  
 AUTHORS Moser,C., Segala,C., Fontana,P., Salakhudinov,I., Gatto,P.,  
 Pindo,M., Zyprian,E., Toepfer,R., Grando,M.S. and Velasco,R.  
 TITLE via E. Mach 1, San Michele all'Adige (TN), I-38010, Italia  
 JOURNAL Tel: 0039-0461-615314  
 COMMENT Fax: 0039-0461-650956  
 Email: claudio.moser@smsa.it  
 The sequencing work has been funded by the 'Fondazione Cassa di  
 Risparmio di Trento e Rovereto'  
 High quality sequence stop: 510.  
 FEATURES  
 source  
 1..510  
 /organism="Vitis vinifera"  
 /mol\_type="mRNA"  
 /cultivar="Pinot noir"

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/sex="Hermaphrodite"  
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/clone\_lib="Grape Bud pSPORT1 Library"  
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ORIGIN

Query Match 12.5%; Score 188.6; DB 14; Length 510;  
Best Local Similarity 64.8%; Pred. No. 9e-41;  
Matches 300; Conservative 0; Mismatches 154; Indels 9; Gaps 1;

QY 364 TACGCTGACGTGGCGCGCGGACGTTAGGTTGGATGCTTAAGAACGCGCGAGAA 423  
DB 48 TATGCTGATGCTGGGGGTGAGCAGCTATGATGATGCTGCAAGCTACGCTCAACAT 107  
QY 424 GGGGTGTCGCCGGTTCTTTGGACGATATTTGTCATATAACCGTCGCGAGAACGTTGCG 483  
DB 108 GCACTGACACAGTGTGCGGACTGACTATTTGTACCTAACAAATGGTGGTACACTCTCT 167  
QY 484 ATGTTGGAATTTGGTGTCAAGTTTCAACGCTCTCTTTGTTAGTAAGTCTCTTCAA 543  
DB 168 AATGCCGAATTAGCGGCCAGACATTCGCCCATGTCCTCAGATCAGAACGCTTATGAA 227  
QY 544 TTGGACGTTTACTGGGAAGGTGAATGTTGACATGCTCGCGACAGCTAAACCCAGAA 603  
DB 228 ATGGATGTTCTTACTGTGTAAGGGAACTGTGACTGTTTCCAAAGACACAACTCCGAG 287  
QY 604 TTGTTCTATGGAGTGTAGAGGTTTGGTCAATTGGAAATTATACGAGACCCAGATT 663  
DB 288 CTGTTTTTTGGGTTTTAGAGGTCCTCGGCGAGTTTGGGATTTATACAGAGCAAGGATC 347  
QY 664 GTTTTGGACCATCACCTAAACGGGCAATGTTTCGGATGCTCTACAGTGATTTTACA 723  
DB 348 GCTCTAGAACCGGCACCAAAAGAGTAAATGGATACAGATGCTTTACGATGACTTCTCC 407  
QY 724 ACTTTTACAAAGACCAAGACGTTTGTATATCAATGGCAAGATATTTGGAGTCACTAT 783  
DB 408 ACATTTTCTAGAGACCAAGAACATTTGATTTCAAT-----CAATGGACTGGACTAT 458  
QY 784 TTAGAGGTCAATATTTCTATCAACGGTGTGTTGACACCT 826  
DB 459 TTGGAAGGTTCACTCTGTATGCAAAATAGTTCTCTTAATACT 501

RESULT 13  
BU025625  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

BU025625 601 bp mRNA linear EST 23-AUG-2002  
Clone QHG10G19, mRNA sequence.  
BU025625 GI:22461145  
EST.  
Helianthus annuus (common sunflower)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; campanulids; Asterales; Asteraceae; Asteroideae;  
Heliantheae; Helianthus.  
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,  
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J.,  
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,  
Lai, Z., Church, S., Jackson, L. and Bradford, K.  
Lettuce and Sunflower ESTs from the Compositae Genome Project  
http://compenomics.ucdavis.edu/  
Unpublished (2002)  
Contact: Alexander Kozik [R.W.Michelmore]  
Department of Vegetable Crops, R.W.Michelmore Lab  
University of California at Davis (UCD)  
Amundson Hall, UCD, Davis, CA 95616, USA  
Tel: 1-(530)-742-1742

Fax: 1-(530)-752-9659  
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]  
singleton, see http://cgpdb.ucdavis.edu/ for details.  
Plate: QHG10 row: G column: 19.  
Location/Qualifiers  
1. .601  
/organism="Helianthus annuus"  
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/cultivar="RHA280"  
/db\_xref="taxon:4232"  
/clone="QHG10G19"  
/lab\_host="E.coli"  
/notes="Vector: pBRCDNASFIAB; The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/  
TAG\_TISSUE=chemical induction  
TAG\_LIB=QH EFGHJ sunflower RHA280  
TAG\_SEQ=IGTAGCCGGG"

ORIGIN

Query Match 12.4%; Score 186.8; DB 13; Length 601;  
Best Local Similarity 63.5%; Pred. No. 3.1e-40;  
Matches 306; Conservative 0; Mismatches 167; Indels 9; Gaps 1;

QY 364 TACGCTGACGTGGCGCGCGGACGTTATGCGGCGGATTTTCATATATACCGTCGCGAGAACGTTGTCG 423  
DB 116 TATGACAGTTTGGAGGTGAGCAGTTATGATAGATGTTTGCACAGCTACGTTATTGTCAT 175  
QY 424 GGGGTGTCGCCGGTTCTTTGGACGATTTATTCATATATACCGTCGCGAGAACGTTGTCG 483  
DB 176 GGACTTGCACCGGTTTCATGACGAGTACTTGTACCTCAGCGTTGGTGGACACACTCTCT 235  
QY 484 AATGTTGGAATTTGGTGTCAAGTTTTCGAAACGGTCTCTTTGTTAGTACGTCCTTGAA 543  
DB 236 AATGCTGGGATTTAGTGGACAAACATCTTTTCATGGGCGCTCAAGTTAGCAATGTTCTTGA 295  
QY 544 TTGGACGTTTACTGGGAAGGTGAATGTTGACATGCTCGCGACAGCTAAACCCAGAA 603  
DB 296 ATGGATGTCATTACTGGGAAGGTGATTTGATTAACCTTGTCTAAGGACATGACTCTGAT 355  
QY 604 TTGTTCTATGGAGTGTAGGAGTTTGGGTCAATTTGGAAATTATACGAGAGCCAGATT 663  
DB 356 CTCTTTTATGCTGTTCTTTGGAGGACCTTGGCCAGTTTGGGATCATAACTAGGCGAAGGATT 415  
QY 664 GTTTTGGACCATGACCTAAACGGGCAAAATGGTTTCGGATGCTCTACAGTGATTTTCA 723  
DB 416 GTTCTAGACAAAGGACCCCAATAGGTCGAATGTTTAAATAATTTACGACGATTTTGCC 475  
QY 724 ACTTTTACAAAGACCAAGAACGTTTGTATATCAATATGGCAACGATATTTGGAGTCACTAT 783  
DB 476 AAGTTTCAAGAGTCAAGAACGCTCTGATATC-----CGTTGATGGGTTTGATTAT 526  
QY 784 TTAGAGGTCAATATTTCTATCAACGGTGTGCTGTCACACCTCTTTTTCACACCTTCA 843  
DB 527 GTAGAGGCTCTTTGATCTTGAATAATAGTCTCGACAGACGCTTTTCTCACCTTCTAAT 586  
QY 844 GA 845  
DB 587 GA 588

RESULT 14  
BQ588342  
LOCUS  
DEFINITION

BQ588342 451 bp mRNA linear EST 06-DEC-2002  
E012308-024-008-P04-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
024-008-P04 5-PRIME, mRNA sequence.

ACCESSION BQ588342  
 VERSION BQ588342.1 GI:26117925  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Beta.  
 REFERENCE 1 (bases 1 to 451)  
 AUTHORS Herwig,R.; Schulz,B.; Weishaar,B.; Hennig,S.; Steinfath,M.; Drungowski,M.; Stah,D.; Wruick,W.; Menze,A.; O'Brien,J.; Lehrach,H. and Radelof,U.  
 TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25 000 potential sugar beet genes  
 JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698  
 COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@piiz-koeln.mpg.de  
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 /clone\_lib="MPIZ-ADIS-024-leaf"  
 /note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatgut AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
 SP6-SalI-CCACGGGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet Project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"  
 ORIGIN  
 Query Match 12.3%; Score 185.2; DB 13; Length 451;  
 Best Local Similarity 66.6%; Pred. No. 7.4e-40;  
 Matches 265; Conservative 0; Mismatches 133; Indels 0; Gaps 0;  
 QY 362 AGTACCTGACGTGGCGCGGACGTTATGGTGGATGCTTAAGAAGACGCGGAGA 421  
 DB 48 AGTATGTAGATGTATGGGGAGGGAATTATGGGTAGATGTTAAAGTGTACGTTAGAT 107  
 QY 422 AAGGGGTGCGCGGTTCTTGACGAGTATTATTCATATAACCGTCGGAGGAGCGTTGT 481  
 DB 108 ATGGATCGACCTTAATCATGACCTGATATTTGTATCTAACGGTGGGTGATGTTGT 167  
 QY 482 CGAATCGTGAATGTGTGTCAAGTGTTCGAAACGGTCCCTTGTGTAGTACGTCCTTG 541  
 DB 168 CTAATGCTGGAATTAGTGACAAGCTTTTAAATCATGGTCCCTCAAAATTGTAACGTTTGT 227  
 QY 542 AATTGACGCTTATCTCGGAGAGTGAATGTGTGACATGCTCGGACAGCTAAACCCAG 601  
 DB 228 AGCTTGATGTGTTCAGGAATGGAGAGCTGTGTGACTTGTTCAGAGAAGAAATTCGG 287  
 QY 602 AATTGTTCTATGAGTGTAGGAGGTTTGGGTCAATTTGGAATTAATAACGAGAGCCAGAA 661  
 DB 288 AGTTGTTTCATGCTGTTTGGGAGGTTTAGGCCAAATTTGGTATTATTACTCGTGTAGGA 347

QY 662 TTGTTTGGACCATGCACCTAAACGGGCCAAATGGTTTCGATGCTCTACAGTGATTCA 721  
 DB 348 TTGCCCTTGAACCTTCTCTCAACGGGTGAGGTGGATAGAGTGTGTACTCCAATTCA 407  
 QY 722 CAACTTTTCAAGAGCACCAAGACGTTTGCATATCAATG 759  
 DB 408 CGCGGTTTCAAAAGATCAAGAGTACTTAAATATCGTTG 445  
 RESULT 15  
 CD843876 707 bp mRNA linear EST 10-JUL-2003  
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 DEFINITION sequence.  
 ACCESSION CD843876  
 VERSION CD843876.1 GI:32525816  
 KEYWORDS EST.  
 SOURCE Brassica napus (rape)  
 ORGANISM Brassica napus  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 REFERENCE 1 (bases 1 to 707)  
 AUTHORS Genoplante.  
 TITLE Genoplante, a major partnership french program in plant genomics  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Genoplante  
 Genoplante  
 93, rue Henri Rochefort 91025 EVRY CEDEX France  
 Tel: 33 1 69 47 54 00  
 Fax: 33 1 69 47 54 10  
 This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (<http://www.genoplante.com>) and <http://genoplante-info.infobiogen.fr>.  
 FEATURES  
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 /tissue\_type="anthers"  
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 Best Local Similarity 55.4%; Pred. No. 1.7e-38;  
 Matches 395; Conservative 0; Mismatches 309; Indels 9; Gaps 2;  
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 DB 1 ACTGATTTCTCTGAATTCACAAGAGATCAAGAAGATTGATATCAGAAACGACGGTTA 60  
 QY 771 --TGGAGTGCATATTTAGAGGTCAATATTTCTATCAACGGTGTGTTGACACCTCT 828  
 DB 61 CATTTCTTGAAGGTTCCGTTATGCTTGACCATGGCCACCTGATTAATCTGGAGATCTACT 120  
 QY 829 TTTTCCACCTTCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACGATATCATC 888  
 DB 121 TACTATCCACGTCGATCACTTGGAGTCTGCTCAATGATCAACGATACCGTGTCTATC 180  
 QY 889 TATGTTCTTGAAGTAGCAAGTATTATGATGATCCCATCTCCCATCATCAGCAAGGTT 948  
 DB 181 TACTGTCTCGAAGTCGCAAGTATTAGCAGCAAACTTCTCAACACTCAGTCAACGAGGAA 240  
 QY 949 ATTGACACATTAAACGAAACATTAAAGTTACTTCCCGGGTTTCTATCAATGACACGCTG 1008  
 DB 241 ATTGAGAGTTTACGAGAGTGTTCGAATGTAAGAGGTTTGTGTACGAGAAGATGTG 300  
 QY 1009 GCCTACTTCGATTTCTTGAACCGGTGTACATGTCGAGAGAAATTAATCAATCACTTTGGGA 1068  
 DB 301 ACGTATATAGATTTCTTGAACCGGGTTTCGAACGCGGAGAGCTAAACCTGTAATCCAAAGGC 360

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QY 1069 TTATGGGAACCTTCCTCACTCTGGCTTAACCTCTACGTTCCCTAAATCTCGGATTCTCGAT 1128
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361 CAATGGGATGTTCCACATCCCATGGCTTAATCTCTTTGTACCAAAATCTCAGATTCAAGA 420
QY 1129 TTTCTAATACGGTGTGTCTAAGACATTTCTTTAAGCAAAATCAGTTCCGGACTCGCT 1188
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421 TTTGATTATGGTGTCTTTAAGGGTATTATCCCTAGAAATACATCACCACCGGTCACCTT 480
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481 CTTGTTTATCCCATGAAGCGCATTTATGTGGAATGATCAAAATGTCTACCGCTATACC---- 536
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655 GTCATACAGTATCTTCTTATCATGCATCACAAGAAGGATGGGTTAGACATTT 707

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Search completed: April 7, 2004, 05:49:25  
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Sequence 20, Appl  
Sequence 18651, A  
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Sequence 55, Appl  
Sequence 177, App  
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Sequence 61, Appl  
Sequence 20, Appl  
Sequence 16, Appl  
Sequence 22, Appl

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ALIGNMENTS

RESULT 1  
US-09-124-541-10  
; Sequence 10, Application US/09124541A  
; Patent No. 6229066  
; GENERAL INFORMATION:  
; APPLICANT: Morris Ph.D., Roy O.  
; TITLE OF INVENTION: A CYTOKININ OXIDASE  
; FILE REFERENCE: UMO1490  
; CURRENT APPLICATION NUMBER: US/09/124,541A  
; CURRENT FILING DATE: 1998-07-29  
; EARLIER APPLICATION NUMBER: 60/054,268  
; EARLIER FILING DATE: 1997-07-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patent in Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 1602  
; TYPE: DNA  
; ORGANISM: Zea mays  
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GenCore version 5.1.6  
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Run on: April 7, 2004, 02:38:39 ; Search time 144 Seconds  
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Minimum DB seq length: 0  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	318.6	21.2	1602	3	US-09-124-541-10
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3	185.2	12.3	1605	3	US-09-124-541-3
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7	40.4	2.7	832	4	US-09-621-976-2813
8	39	2.6	474	4	US-09-621-976-18033
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Query Match 21.2%; Score 318.6; DB 3; Length 1602;  
Best Local Similarity 36.7%; Pred. No. 7.5e-96;  
Matches 543; Conservative 230; Mismatches 636; Indels 72; Gaps 8;

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DB 545 CNGGNATHWSGNGCARGCNTTYMNCAYGNGCNCABATHWSNAAAYGNTNGARATGG 604  
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RESULT 2  
US-09-663-326-10  
Sequence 10, Application US/09663326  
Patent No. 6617497  
GENERAL INFORMATION:  
APPLICANT: Morris Ph.D., Roy O.  
TITLE OF INVENTION: A CYTOKININ OXIDASE  
FILE REFERENCE: UM01490  
CURRENT APPLICATION NUMBER: US/09/663,326  
CURRENT FILING DATE: 2000-09-15  
PRIOR APPLICATION NUMBER: 60/054,268  
PRIOR FILING DATE: 1997-07-30  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 10  
LENGTH: 1602  
TYPE: DNA  
ORGANISM: Zea mays  
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818	TTGACACCTCTTTTTCGCCACTTCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAAC	877
905	CNAAVACNGNTTYTYYACNGAYCNGAYGTNGCMGNATHTGTCGTCNYTNGCNGNGARM	964
878	ACGGT-----ATCATCTATGTTCTTGAAGTAGCCAAGTATATGATGATGCCAATCTCC	931
965	GNAAVGCNACNACNGNTAYWSNATHGARGCNACNTYNAAYTAYGAYAYGCNACNGNG	1024
932	CCATCA-----TCAGCAAGGTTATGACACATTAACGAAACCAATTAAGTTACTTCCCG	985
1025	CNGCNGCNGCTNGAYCARGARYTNGCWSNGNYTNGNACNYTNWSNTAYTNGARG	1084
986	GGTTCAATCAATGCAGCGAGTGGCTACTTTCGATTTCTTGAAACCGTGACATGTCGAAG	1045
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1046	AAAAATAACTCAGATCTTTGGATATATGGGAACCTCCTCATCTCGCTTAACCTCTACG	1105
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1106	TTCTATAATCTCGGATCTCGATTTTCATAACGGGTGTGTCAAAGACATCTCTTTAAGC	1165
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1322	GNATGWSNGCNGCNAACC---NWSNGARGAYGTNTTYTAYGCGNTNWSNYTNTTYW	1378
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1406	ATTGGGATTCAGCATTTTGGAT---CAAAATCGGATGATTTTTCGAGAGGAAAGATCTAT	1462
1499	AYTGGTNGMNCAYTYTGGCNGCNCNARTGGAAYMGNTTYGTNGARATGAARAAVART	1558
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RESULT 3
US-09-124-541-3
/ Sequence 3, Application US/09124541A
/ Patent No. 6229056
/ GENERAL INFORMATION:
/ APPLICANT: Morris Ph.D., Roy O.
/ TITLE OF INVENTION: A CYTOKININ OXIDASE
/ FILE REFERENCE: UMO1490
/ CURRENT APPLICATION NUMBER: US/09/124,541A
/ CURRENT FILING DATE: 1998-07-29
/ EARLIER APPLICATION NUMBER: 60/054,268
/ EARLIER FILING DATE: 1997-07-30
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 3
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US-09-124-541-3

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Best Local Similarity 50.3%; Pred. No. 3.6e-51;
Matches 745; Conservative 0; Mismatches 663; Indels 72; Gaps 9;

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Qy 149 GAAACATACCACTGACCGTGCACCGCGCGCGGTAATCTCCCTCTCCACCGCTATATCT 208
Db 185 GCAACATCACCTGCGCGCTCCCGCGCGGCGGTCCTGTACCGCTGCTCCACGGCGACCTGG 244

Qy 209 CTCGTCTCTCTCAATACGCG---CAAAACGGAAGAACATTCATGAGTACGCTCGTG 265
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Qy 266 GCAAGGCGACTCTTAACGCGCAAGCTCGGTCTCCGCGGAGTATCTCATACATGA 325
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Qy 326 CGTGTATCACTGACGTGGTG-----GTTTCAAAAGACAGAGTACG 367
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Db 485 TGGCGCGCGCTCTGGAACGACTACTCTACCTCACGCTCGCGCGCGCTGTCCAACG 544

Qy 488 GTGGAATTTGGTGTCAAGTGTTCGAAACGGTCTCTTGTAGTAACTCTTGAATGG 547
Db 545 CAGGCATACGCGCGGAGGCTTCGCGACGCGCGCAAGATATCTAACTGCTGGAGATGG 604

Qy 548 ACCTTATTTACTGGAAGTGAATTTGACATGCTCGGACAGCTTAACCCAGAAATGT 607
Db 605 ACCTTATCACGCGCATGGGAGATGTGACGTCTCCAAGCAGCTGAACGCGGACCTGT 664

Qy 608 TCTATGAGTGTAGAGTGTGGTCAATTTGGAATTTAAGAGACCGCAATTTGTT 667
Db 665 TCGACGCGCTCTGGCGGCGCTGGGCGAGTTCGGAGTGATCACCGCGCGCGGATCGCGG 724

Qy 668 TGGACCATGACCTTAACGCGCAATGTTTCGGATGCTCTACAGTATTTTCAACAATT 727
Db 725 TGGACGCGCGCGCGCGCGCGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 784

Qy 728 TTACAAAGGACCAAGAACGTTTGATATCAATGGAACAAAGATATGAGTCTGACTATTAG 787
Db 785 TCAGCGCGGACGAGGAGCGCTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGTGGTGG 844

Qy 788 --AAGTCAATATTTCTATCAACGCGTGTGTTGACACTCTTTTTCCTCCACTTCAGA 845
Db 845 GCGCGATGAGTACGTTGGAAGGTCGTGTGTTGAAACAGAGCTTGGGACCGGACCTGG 904

Qy 846 TCAA-----TCTAAAGTCTGCTGATCTAGTCAAGCAACACGATATCA 886
Db 905 CGAACAGGCGTCTTTCACCGACGCGAGCTCGCGCGGATCGTGGCTCGCGCGGAGC 964

Qy 887 TCTATGTTCTTGAAGTAGCAAGTATATGATATCCATCTCCCATCATCA----- 940
Db 965 GGAACGCCACACCGTGTACAGATCGAGGCGACGCTCAACTACGACCAAGCCACGCGCG 1024

Qy 941 -----GCAAGTTATTGACACATTAACGAAACATTAAGTTACTTCCCG 985
Db 1025 CGGCGCGCGGTGGACGAGGCTCGCTCGCTGGCGACGCTGAGCTAGCTGGAGG 1084

```

RESULT 4

```

US-09-663-326-3
; Sequence 3, Application US/09663326
; Patent No. 6617497
; GENERAL INFORMATION:
; APPLICANT: MORRIS PH.D., ROY O.
; TITLE OF INVENTION: A CYTOKININ OXIDASE
; FILE REFERENCE: UMO1490
; CURRENT APPLICATION NUMBER: US/09/663,326
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/054,268
; PRIOR FILING DATE: 1997-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1605)
US-09-663-326-3

```

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Query Match      12.3%; Score 185.2; DB 4; Length 1605;
Best Local Similarity 50.3%; Pred. No. 3.6e-51;
Matches 745; Conservative 0; Mismatches 663; Indels 72; Gaps 9;

Qy 89 CCCTTAACCTCACCTCTCTACCGATCTTCATCATCTCCGAGCTCTCATGACTTCG 148
Db 125 CTTTGGACGGCAAGCTCCGACCGACAGCAACGGCGCGCGCGCTTCGACGACTTCG 184

Qy 149 GAAACATACCACTGACCGTGCACCGCGCGGTAATCTCCCTCTCCACCGCTATATCT 208
Db 185 GCAACATCACCTGCGCGCTCCCGCGCGGCGGTCCTGTACCGCTGCTCCACGGCGACCTGG 244

Qy 209 CTCGTCTCTCTCAATACGCG---CAAAACGGAAGAACATTCATGAGTACGCTCGTG 265

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Db 245 TGGCGCTGCTGAGCGCGCCAACTCCACCCGGGGTGGCCCTACCATCGCTTCGGG 304  
Qy 266 GCCAAGGCCACTCTTTAAACGGCCCAAGCTTCGCTCGGCGGAGTAATCGTCAACATGA 325  
Db 305 GCCCGCGCCACTCCTCATGGCCAGGCCCTTCGCCCGCGCGGCTCGCTCGTCAACATGG 364  
Qy 326 CGTGTATCACTGACGTGGTG-----GTTTCAAAAGACAAGAGTACG 367  
Db 365 CGTCCCTGGGGAGCCCGCGCGCGCGCGGCATCAACGTGTCCGGGACGGCGCTACG 424  
Qy 368 CTGACGTGGCGCGCGGACGCTTATGGGTGGATGTCCTTAAAGACAGCGCGGAGAAAGGGG 427  
Db 425 TGGACGCGCGCGCGAGCAGGTGTGGATCGACGTGTTCGCGCGGTCTCGTGGCGCGCGG 484  
Qy 428 TGTGCGCGGTTCCTTGGACGATTAATTTGATATAACCGTCGAGGAACTCTTCGATG 487  
Db 485 TGGCGCGCGCTCTTGAAACACTACCTTACCTCACCGTCGCGCGCACCTGTCCAAAG 544  
Qy 488 GTGGAATGTGTGCTCAAGTGTTCGAAACGCTCTCTTTAGTAAAGCTCTTGAATGG 547  
Db 545 CAGGCATCAGCGCGCGCGCTTCGCCAGCGCCACAGATATCAACGTCTGGAGATGG 604  
Qy 548 ACGTTATCTGGGAAGGTGAATGTGATCTCGACATCTCGGACACTAAACCCAGATTTG 607  
Db 605 ACGTTATCACCGGCATGGGAGATGTGACGTCTCAAAGCAGCTGAACCGCGACCTGT 664  
Qy 608 TCTATGAGTGTAGGAGTGTGGTCAATTTGAAATTAACGAGAGCCAGAAATTTT 667  
Db 665 TCGACGCGCTCTGGCGGGCTGGGAGTTCGAGTGATCACCGCGCGCGGATCGCG 724  
Qy 668 TGGACCATGCACTTAACCGGCGCAATGTGTTTCGGATGCTCTACAGTGAATTTCAACTT 727  
Db 725 TGGACGCGCGCGCGCGCGCGGTGGTGGTGTCTGTACACCGACTTCGCGCGT 784  
Qy 728 TTACAAGGACCAAGACGTTTGATATCAATGGCAACGATATTGGAGTCGACTATTAG 787  
Db 785 TCAGCGCGCAACAGAGCGCTGACCGCGCGCGCGCGCGCGCGCTGCTGCTG 844  
Qy 788 --AAGTCAATATTTATCAACGCGTGTGTTGACACCTCTTTTCCACCTTCAGA 845  
Db 845 GCGCGATGAGTACGTGGAAGGTCGTTGCGTGAACGACGAGCTGGCAGCCAGCTGG 904  
Qy 846 TCAG-----TCTAAGTCGTGATCTAGTCAAGCAACACGATCA 886  
Db 905 CGAACCGGGTTCTTACGACGCGGACGCTGCGCGGATGCTGCGCTCGCGGGAGC 964  
Qy 887 TCTATGTTCTTGAAGTAGCCAAATATTATGATGATCCCAATCTCCCAATCA 940  
Db 965 GGAACGCCACCACTGTACAGATCGAGGCGACGCTCACTACGACAAACGCCACGGCG 1024  
Qy 941 -----GCAAGTTATTGACATTAACGAAACATTAACTTACTTCCCG 985  
Db 1025 CGCGCGCGCGGTGACGAGGCTCGCGTCCGCTGGGACGCTGAGCTGAGTGGAGG 1084  
Qy 986 GGTTCATATCAATGACGACGCTGCTACTTTCGATTTCTTGAACGCTGTACATGTCGAAG 1045  
Db 1085 GGTTCGCTTCAGCGCGAGCTGGCTACGCGGGCTTCTTGACCGGCTGCACGCGAGG 1144  
Qy 1046 AAAATAACTAGATCTTGGATTAATGGAACTTCCTCATCTTGGCTTAACTCTACG 1105  
Db 1145 AGGTGCGCTCAACAGCTGGGGCTGTGGCGGGTCCGACCGCTGCTCAACATGTTCG 1204  
Qy 1106 TPCCTAAATCTCGGATCTCGATTTTCAACGCTGTTGTCAAGACATTTCTTTAAGC 1165  
Db 1205 TCGCGCGCTCGCGCATCGCGATTCGACCGCGGGGTGTCAAGGCACTCTGC--AGG 1262  
Qy 1166 AAAATACAGTTCGGGACGTGCTTCTTCTATCCAAACAAACCGGAATAAATGGGCAATC 1225  
Db 1263 CACCGACATCGTCGCGCGCTCA--TCGTCTACCCCTCAACAAATCCATGTGGGACGACG 1321  
Qy 1226 GTATGTCGCGGATGATACGAGATCGATGAAGATGTTATATATATATTCGAGCTACTAC 1285

Db 1322 GCATGTGGCGCGGACGCGC---GTCTGAGGACGTGTTCTACGCGGTGCTGCTCTTCT 1378  
Qy 1286 ATCCGCTACCCCAAGGATCTTCAGAGTGGAGAGCGTTTAAAGAGAGATAATTAGGT 1345  
Db 1379 CGTGGTGGCGCCCAACGACCTTGGCGAGGCTGCAGGACAGAAAGGAGGATCTGCGCT 1438  
Qy 1346 TTTGAAGGATTCAGGTATTAAAGATTAAAGCAATATCTAATCATTTATATAGTAAAGAG 1405  
Db 1439 TCTGCGACTCGCGGGATCCAGTACAAGACCTACCTGGCGGGCACACGACCGCAGTG 1498  
Qy 1406 ATTGATTCAGCATTTTGG---ATCAAAATGGGATGATTTTTCGAGAGGAAAGATCTAT 1462  
Db 1499 ACTGGTTCGCGCACTTCGCGCGCCCAAGTGAATTCGCTTCGTGGAGATGAAGAAAGT 1558  
Qy 1463 TTGATCCCAAGAACTGTTATCTCCAGGCGCAAGACATCTT 1502  
Db 1559 ACGACCCCAAGAGGTGCTCTCCCGCGCAGGACATCTT 1598

## RESULT 5

US-09-124-541-2  
; Sequence 2, Application US/09124541A  
; Patent No. 6229066  
; GENERAL INFORMATION:  
; APPLICANT: Morris Ph.D., Roy O.  
; TITLE OF INVENTION: A CYTOKININ OXIDASE  
; FILE REFERENCE: UMO1490  
; CURRENT APPLICATION NUMBER: US/09/124,541A  
; EARLIER FILING DATE: 1998-07-29  
; EARLIER APPLICATION NUMBER: 60/054,268  
; EARLIER FILING DATE: 1997-07-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 6733  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (1)..(6733)  
; OTHER INFORMATION: genomic sequence for a cytokinin oxidase from Zea  
; OTHER INFORMATION: mays  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1497)..(2111)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2524)..(3216)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (3311)..(3607)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (5697)

US-09-124-541-2

Query Match 7.2%; Score 108.2; DB 3; Length 6733;  
Best Local Similarity 54.5%; Pred. No. 6.6e-25;  
Matches 274; Conservative 0; Mismatches 208; Indels 21; Gaps 2;

Qy 89 CCCTTAACCTCACCTCTCTACCGATCCTTCATCATCTCCGACGCTCTCATGCTCG 148  
Db 1621 CCTTGGACGCAAGCTCCGACGAGCAGCAACGCGCGCGGCTCGACGACTTCG 1680  
Qy 149 GAAACATAACACCGTGACCCCGCGGGGTAACTCTGCCCTCTCCACCGCTGATATCT 208  
Db 1681 GCAACATCAGTCGGCGCTCCCGCGCGGTCTGTACCGTCTCCACGGGCACTGG 1740  
Qy 209 CTGCTCTCTCCAAATAGCGG---CAAAGGAAAAGTACATTCGAAGTAGCGGCTCGG 265  
Db 1741 TGGCGTGTGAGCGCGGCAACTCCACCCCGGGTGGCCCTACACCATCGGCTTCGGG 1800  
Qy 266 GCCAAGGCCACTCTTTAAACGGCAACGCTCGGTCTCCGCGGAGTAAATCGTCAACATGA 325

Db 1801 GCCGGGCACTCCCTCATGAGGCGAGGCTTCGCGCCCGGGCGGCGTGTGCTCAACATGG 1860  
 QY 326 CGTGATCACTGAGTGGTG-----GTTTCAAAAGACAAGAAAGTACG 367  
 Db 1861 CGTCCTGGGAGCGCCCGCGCGCGCGCCGACATCAACGTGTCCGCGGACGGCCGCTACG 1920  
 QY 368 CTGACGTGGCGCGCGGAGCGTATAGGTTGGTGTGTTAGAAAGACGCGCGGAGAAAGGGG 427  
 Db 1921 TGGACCGCGCGCGGAGCAGGTGTGATCGACGTGTTCGCGCGCGTGTGCGCGCGCGG 1980  
 QY 428 TGTGCGCGGTTCTTGGACGAGTATTGTCATATAACCGTCGGAGGAACGTTGTGGAATG 487  
 Db 1981 TGGCGCGCGCTCTGGAAAGACTTCTACCTACCGTCGGCGGACGCTGTCCAAAG 2040  
 QY 488 GTGGAATTTGGTGTCAAGTGTTCGAAACGGTCTCTTTGTTAGTAAAGCTCTTGAATGG 547  
 Db 2041 CAGGCATCAGCGCGCGAGCGTTCCGCCACGCGCCACAGATATCAACGTGTGAGATGG 2100  
 QY 548 ACGTTATTACTGGGAAAGGTGAA 570  
 Db 2101 ACGTTATCACCGGTACGTGTGCA 2123

RESULT 6  
 US-09-663-326-2  
 ; Sequence 2, Application US/09663326  
 ; Patent No. 6617497  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Morris Ph.D., Roy O.  
 ; TITLE OF INVENTION: A CYTOKININ OXIDASE  
 ; FILE REFERENCE: UM01490  
 ; CURRENT APPLICATION NUMBER: US/09/663,326  
 ; CURRENT FILING DATE: 2000-09-15  
 ; PRIOR APPLICATION NUMBER: 60/054,268  
 ; PRIOR FILING DATE: 1997-07-30  
 ; NUMBER OF SEQ ID NOS: 20  
 ; SOFTWARE: Patent In Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 6733  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; NAME/KEY: gene  
 ; LOCATION: (1)..(6733)  
 ; OTHER INFORMATION: genomic sequence for a cytokinin oxidase from Zea  
 ; OTHER INFORMATION: mays  
 ; NAME/KEY: CDS  
 ; LOCATION: (1497)..(2111)  
 ; NAME/KEY: CDS  
 ; LOCATION: (2524)..(3216)  
 ; NAME/KEY: CDS  
 ; LOCATION: (3311)..(3607)  
 ; NAME/KEY: unsure  
 ; LOCATION: (5697)  
 US-09-663-326-2

Query Match 7.2%; Score 108.2; DB 4; Length 6733;  
 Best Local Similarity 54.5%; Pred. No. 6.6e-25;  
 Matches 274; Conservative 0; Mismatches 208; Indels 21; Gaps 2;  
 QY 89 CCCTTACCTCACCTCTCTACCGATCCTTCCATCATCTCCGAGCCTCTCATGACTCG 148  
 Db 1621 CTTTGGACGCACTCCGACCGACAGCAGACGCGAGCGGGCGGCTCGACGACTTCG 1680  
 QY 149 GAAACATPACACCGTGACCCCGGGCGGTAACTCTGGCCCTCTCCACCGCTGATATCT 208  
 Db 1681 GCAACATCAGTGGGCGCTCCCGGCGGCTGTACCGCTGTACCGCTGTCCACGCGGACCTGG 1740  
 QY 209 CTGCTCTCTCAATACCGCG---CAACGGAAGAGTACATCCAAAGTAGCGGCTCGTG 265  
 Db 1741 TGGCGTGTGAGCGCGGCCAATCTCACCCCGGGTGGCCCTACACCATCGCGTCCGCG 1800

QY 266 GCCAAGGCCACTCTCTTAAACGCCCAAGCGTCTCGGCGGAGTAATCTCAACATGA 325  
 Db 1801 GCCGGGCACTCCCTCATGAGGCGAGGCTTCGCGCCCGGGCGGCGTGTGCTCAACATGG 1860  
 QY 326 CGTGATCACTGAGTGGTG-----GTTTCAAAAGACAAGAAAGTACG 367  
 Db 1861 CGTCCTGGGAGCGCCCGCGCGCGCGCCGACATCAACGTGTCCGCGGACGGCCGCTACG 1920  
 QY 368 CTGACGTGGCGCGCGGAGCGTATAGGTTGGTGTGTTAGAAAGACGCGCGGAGAAAGGGG 427  
 Db 1921 TGGACCGCGCGCGGAGCAGGTGTGATCGACGTGTTCGCGCGCGTGTGCGCGCGCGG 1980  
 QY 428 TGTGCGCGGTTCTTGGACGAGTATTGTCATATAACCGTCGGAGGAACGTTGTGGAATG 487  
 Db 1981 TGGCGCGCGCTCTGGAAAGACTTCTACCTACCGTCGGCGGACGCTGTCCAAAG 2040  
 QY 488 GTGGAATTTGGTGTCAAGTGTTCGAAACGGTCTCTTTGTTAGTAAAGCTCTTGAATGG 547  
 Db 2041 CAGGCATCAGCGCGCGAGCGTTCCGCCACGCGCCACAGATATCAACGTGTGAGATGG 2100  
 QY 548 ACGTTATTACTGGGAAAGGTGAA 570  
 Db 2101 ACGTTATCACCGGTACGTGTGCA 2123

RESULT 7  
 US-09-621-976-2813  
 ; Sequence 2813, Application US/09621976  
 ; Patent No. 6639063  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Jobert, S.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
 ; FILE REFERENCE: GENSET.054PR2  
 ; CURRENT APPLICATION NUMBER: US/09/621,976  
 ; CURRENT FILING DATE: 2000-07-21  
 ; NUMBER OF SEQ ID NOS: 19335  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 2813  
 ; LENGTH: 832  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 235..399  
 US-09-621-976-2813

Query Match 2.7%; Score 40.4; DB 4; Length 832;  
 Best Local Similarity 14.5%; Pred. No. 0.0071;  
 Matches 53; Conservative 146; Mismatches 167; Indels 0; Gaps 0;  
 QY 1012 TACTTCGATTTCTTGAACCGTGTACATGTGCAAGAAAATAAATCAGATCTTTGGGATTA 1071  
 Db 40 WRRKKKAWWKYKWTWTWYRYAMNGTYKKKKKAMCRTKKKKKKKYMMWYMGWRRSYM 99  
 QY 1072 TGGGAACCTCTCATCTCTGCTTAACTCTAGCTTCTCTAAATCTCGGATTTCTCGATTTT 1131  
 Db 100 AMWTRTWGAYYRSMYWRKYRCKKAYRKTCTYSSKGTWWRKWKAWITWNNKKT 159  
 QY 1132 CATAACCGTGTGTCAAGACATTTCTTTAAGCAAAAATCAGCTTCGGGACTCGCTCTT 1191  
 Db 160 YYWAATRYMMWMTKWRASWYCMWVGKRWSTWRKSRYSASARSAKRCYCSWSGA 219  
 QY 1192 CTCCTATCCAAACACCGCAATAATGGACATCGTATGTGCGGATGATACACAGATC 1251  
 Db 220 MSWYMMWRWNRWATAGWKAWRSCMRKRYAGSKTSYKSMWNCWTRSWKYCYTKA 279  
 QY 1252 GATGAAGATGTTATATATATATATCGGACTACTACAATCCGCTACCCCAAGGATCTTCCA 1311  
 Db 280 RWTGYCYRKGGMWKGGRWYASKYKWKRWNCWARMYRSTGTTRASMMWRWRYTMM 339  
 QY 1312 GAAGTGGAGCGGTAAACGAAAGATATAGGTTTTGCAAGGATTTCAGGTATTAGATT 1371





COUNTRY: USA  
ZIP: 23113-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
CURRENT APPLICATION DATA:  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935,313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)836-9300  
TELEFAX: (703)683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZ9pt-F1s  
US-08-232-463-14

Query Match 2.5%; Score 38; DB 1; Length 7218;  
Best Local Similarity 2.2%; Pred. No. 0.23;  
Matches 8; Conservative 200; Mismatches 150; Indels 0; Gaps 0;

351 AAAGACAGAGTAGCTGACGTGCGCGCGGACGTTATGGTGGATGCTTAAGAA 410  
1413 RR 1354  
411 GACGGCGGAGAAAGGGTGTGCGCGGTTCTTGGACGGATTATTTGCATATAACGTCGG 470  
1353 RR 1294  
471 AGGAAGTTCGAAATGGTGGATTTGGTCAAGTGTTCGAAACGTCCTCTTGTAG 530  
1293 RR 1234  
531 TAAGCTCTTGAATTGACGTTATTACTGGGAAAGGTGAAATGTCACATGTCGCGACA 590  
1233 RR 1174  
591 GCTAAACCCAGAAATGTTCTATGAGTGTAGAGGTTGGTCAATTTGGAATTATAAC 650  
1173 RR 1114  
651 GAGAGCCAGAAATGTTTGGACCATGACATCAACGCGCAATGTTTCGGATGCTC 708  
1113 RR 1056

RESULT 11  
US-09-103-840A-2  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 441529  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: H37RV  
US-09-103-840A-1

Query Match 2.5%; Score 37.6; DB 3; Length 441529;  
Best Local Similarity 45.1%; Pred. No. 33;  
Matches 139; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

366 CGCTGACGTGCGCGCGGACGTTATGGTGGATGCTTAAGAGACGCGGAGAAAGG 425

; TITLE OF INVENTION: TUBERCULOSIS  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; OTHER INFORMATION: CDC 1551  
; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
; OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 2.5%; Score 37.6; DB 3; Length 4403765;  
Best Local Similarity 45.1%; Pred. No. 33;  
Matches 139; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

366 CGCTGACGTGCGCGCGGACGTTATGGTGGATGCTTAAGAGACGCGGAGAAAGG 425  
Db 4154796 CGCGGACGTGCGCGGACGTTATGGTGGATGCTTAAGAGACGCGGAGAAAGG 4154855  
Qy 426 GGTGTGCGCGGTTCTTGGACGGATTATTTGCATATAACCGTGGAGAACGTTGCGAA 485  
Db 4154856 TCTGTACCATTTGGTGGTTCGCGACGCTGAGGACGATCATATGGCGGAGCGGTCAACCG 4154915  
Qy 486 TGGTGGAAATGGTGGTCAAGTGTTCGAAACGTCCTCTTGTAGTAAAGTCTCTTGAATT 545  
Db 4154916 CTTGGGTATCGAGTGGCGGTCGTTCCGCAACGCGCTGCCCCAGAGTCGCTGGAGAT 4154975  
Qy 546 GGACGTTATTACTGGGAAAGGTGAAATGTTGACATGTCGCGACAGCTAAACCCAGAAATT 605  
Db 4154976 GGATATCTCAGCGCGGACGAGAACTTCTCAGGTCGCGCGGACAGCACTCCGACTT 4155035  
Qy 606 GTTCTATGAGAGTGTAGGAGTTTGGTCAATTTGGAATTATAACGAGAGCCAGAAATTGT 665  
Db 4155036 GTACCGTGCATTCCCTAACTCGTATGGGACATGGGCTATTCAACCGCGGTTTGAATCCA 4155095  
Qy 566 TTTGGACC 673  
Db 4155096 GCTGGAGC 4155103

RESULT 12  
US-09-103-840A-1  
; Sequence 1, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 441529  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: H37RV  
US-09-103-840A-1

Query Match 2.5%; Score 37.6; DB 3; Length 441529;  
Best Local Similarity 45.1%; Pred. No. 33;  
Matches 139; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

366 CGCTGACGTGCGCGCGGACGTTATGGTGGATGCTTAAGAGACGCGGAGAAAGG 425

Db 4162545 CGCCGAGTGGCCGGCATGTCACATACGAGGACCTAATCGCCGCGACACTGACCTACCG 4162604  
Qy 426 GGTGTCCCGGTTCTTGGACGGATTAATGATATACCGTGGAGGAAAGTTGTCGAA 485  
Db 4162605 TCTGTCCACATGTTGGTTCGCGAGCTGAGGACGATCACAATGGGGGGGCGGTACCCGG 4162664  
Qy 486 TGGTGGAAATGGTGTCAAGTGTTCGAAACGGTCTCTTTGTTAGTAAACGTCCTTGAAT 545  
Db 4162665 CTTGGGTATCGAGTCGGCGTCTTCGCAACGGCTGCCACGAGTCGGTGTGGAGAT 4162724  
Qy 546 GGACGTTATTAATCGGAAAGTGAATGTTGACATGTCGGGACAGCTAAACCCAGAAAT 605  
Db 4162725 GGATATCTCACCAGCGGCGAGGAACTTCTCACCGTCTCGCCCGGACAGCACTCCGACT 4162784  
Qy 606 GTTCTATGAGTGTAGGAGTGTGGGTCAATTTGGAATTATACGAGAGCCAGAAATGT 665  
Db 4162785 GTACGTCATCTCCTACTGATGGACACTGGGCTATTCACCCGGCTTCGAATCCA 4162844  
Qy 666 TTTGGACC 673  
Db 4162845 GCTGGAGC 4162852

RESULT 13  
US-09-004-838-39/c  
; Sequence 39, Application US/09004838  
; Patent No. 6350933  
; GENERAL INFORMATION:  
; APPLICANT: Michelmore, Richard W.  
; APPLICANT: Shen, Kathy  
; TITLE OF INVENTION: Procedures and Materials for  
; TITLE OF INVENTION: CONFERRING PEST RESISTANCE IN PLANTS  
; NUMBER OF SEQUENCES: 140  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/004,838  
; FILING DATE: 09-JAN-1998  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/781,734  
; FILING DATE: 10-JAN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Einhorn, Gregory P.  
; REGISTRATION NUMBER: 38,440  
; REFERENCE/DOCKET NUMBER: 023070-078810US  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1441 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: 1..1441  
; OTHER INFORMATION: /note= "RLG2W"  
US-09-004-838-39

Query Match 2.4%; Score 35.6; DB 4; Length 1441;  
Best Local Similarity 63.9%; Pred. No. 0.43;  
Matches 53; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
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Db 237 ATCACTAATATGCGCAACATCGTCAAGTANTATGAGGAACCTAGTCTTACCTCCATCTGA 178  
Qy 943 AAGGTTATTTGACACATTAACGAA 965  
Db 177 ATCTTTTGAACCATTCACGAA 155  
RESULT 14  
US-09-134-001C-812/c  
; Sequence 812, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 812  
; LENGTH: 699  
; TYPE: DNA  
; ORGANISM: Staphylococcus epidermidis  
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Best Local Similarity 49.2%; Pred. No. 0.4;  
Matches 92; Conservative 0; Mismatches 95; Indels 0; Gaps 0;  
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Qy 1098 CCTCTAGTTCCCTAAATCTCGGATTCCTGATTTTATAACGGTGTGTCAAGACATCTT 1157  
Db 134 ACTTAAGTTCTTCGATTTTCAGTATCAATTTGATGATTAATTTGCTAAATATTTTGA 75  
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Qy 1218 GGACAAT 1224  
Db 14 AGCCCAT 8  
RESULT 15  
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; Sequence 28, Application US/09004838  
; Patent No. 6350933  
; GENERAL INFORMATION:  
; APPLICANT: Michelmore, Richard W.  
; APPLICANT: Shen, Kathy  
; APPLICANT: Meyers, Blake  
; TITLE OF INVENTION: Procedures and Materials for  
; TITLE OF INVENTION: CONFERRING PEST RESISTANCE IN PLANTS  
; NUMBER OF SEQUENCES: 140  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California

COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/004,838  
FILING DATE: 09-JAN-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/781,734  
FILING DATE: 10-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Einhorn, Gregory P.  
REGISTRATION NUMBER: 38,440  
REFERENCE/DOCKET NUMBER: 023070-078810US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1500 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..1500  
OTHER INFORMATION: /note= "RLG2B"  
US-09-004-838-28

Query Match 2.3%; Score 35; DB 4; Length 1500;  
Best Local Similarity 63.9%; Pred. No. 0.71;  
Matches 53; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
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QY 943 AAGGTTATTGACACATTAAACGAA 965  
DB 203 ATTCTTTTGAACCATTCACGAA 181

Search completed: April 7, 2004, 05:53:02  
Job time : 166 secs

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Sequence 10804, A  
Sequence 19583, A  
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Sequence 3248, Ap  
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Sequence 33, Appl

US-10-014-101-29  
US-10-311-453-34  
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US-10-326-184-12  
US-10-311-453-25  
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US-10-326-184-15  
US-10-425-114-3248  
US-10-311-453-9  
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US-10-311-453-33

## ALIGNMENTS

## RESULT 1

US-10-311-453-26  
; Sequence 26, Application US/10311453  
; Publication No. US20040031073A1  
; GENERAL INFORMATION:  
; APPLICANT: Schilling, Thomas  
; APPLICANT: Werner, Tom s  
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and  
; TITLE OF INVENTION: physiology  
; FILE REFERENCE: 1226-4  
; CURRENT APPLICATION NUMBER: US/10/311,453  
; PRIOR FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: EP 00870132.8  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: US 60/258,415  
; PRIOR FILING DATE: 2000-12-27  
; PRIOR APPLICATION NUMBER: EP 01870053.4  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 1506  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-311-453-26

Query Match 100.0%; Score 1506; DB 12; Length 1506;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1506; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 ATGGCTAAATCTCGTTTAATGATCACTTTAATCAACGGTTTAAATGATCAACCAATCATCA 60  
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Db 61 AACGGTATTAAATGATTACCTAAATCCCTTAACTCACCCTCTCTACCGATCCTTCC 120

GenCore version 5.1.6  
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Run on: April 7, 2004, 04:38:13 ; Search time 607 Seconds  
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Title: US-10-014-101-26

Perfect score: 1506

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Gapop 10.0 , Gapext 1.0

Searched: 2470632 seqs, 1873875610 residues

Total number of hits satisfying chosen parameters: 4941264

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	1506	100.0	1506	14	US-10-014-101-26
3	1504.4	99.9	1506	14	US-10-326-184-8
4	778.2	51.7	1575	9	US-09-938-842A-2089
5	778.2	51.7	1575	11	US-09-938-842A-2089
6	778.2	51.7	1575	12	US-10-311-453-28
7	778.2	51.7	1575	14	US-10-014-101-28
8	778.2	51.7	1575	14	US-10-326-184-10
9	778.2	51.7	1655	14	US-10-326-184-20
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11	577	38.3	2291	14	US-10-014-101-3
12	470	31.2	1572	12	US-10-311-453-27
13	470	31.2	1572	14	US-10-014-101-27
14	470	31.2	1572	14	US-10-326-184-9
15	306.2	20.3	1611	12	US-10-311-453-29

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 121 ATCATCTCCGAGCCTCTCATGCTTCGGAAACATAACCAACCGTGCACCCGGGGGCTA 180  
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 181 ATCTGCCCTCTCTCCACCGCTGATATCTCTCTCTCCATACGCGCAACGGAATA 240  
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 1201 ACAACCGGATTAATGGGACATCGTATGTCGGCGATGATACCGAGATCGATGAAGT 1260

RESULT 2

US-10-014-101-26  
 ; Sequence 26, Application US/10014101  
 ; Publication No. US20030074698A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schmulling, Thomas  
 ; APPLICANT: Werner, Tom s  
 ; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and  
 ; FILE REFERENCE: 1195-2  
 ; CURRENT APPLICATION NUMBER: US/10/014,101  
 ; CURRENT FILING DATE: 2001-12-10  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/06833  
 ; PRIOR FILING DATE: 2001-06-16  
 ; PRIOR APPLICATION NUMBER: EP 00870132.8  
 ; PRIOR FILING DATE: 2000-06-16  
 ; PRIOR APPLICATION NUMBER: US 60/258,415  
 ; PRIOR FILING DATE: 2000-12-27  
 ; PRIOR APPLICATION NUMBER: EP 01870053.4  
 ; PRIOR FILING DATE: 2001-03-16  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 26  
 ; LENGTH: 1506  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; US-10-014-101-26

Query Match 100.0%; Score 1506; DB 14; Length 1506;  
 Best Local Similarity 100.0%; Pred No. 0;  
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RESULT 3  
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; Sequence 8, Application US/10326184  
; Publication No. US20030163847A1  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Company  
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C3  
; TITLE OF INVENTION: OXIDASE 1  
; FILE REFERENCE: MTC6781.1  
; CURRENT APPLICATION NUMBER: US/10/326,184  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: US 60/343,129  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
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; LENGTH: 1506  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-326-184-8

Query Match 99.9%; Score 1504.4; DB 14; Length 1506;  
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Db 121 ATCATCTCCGAGCTCTCATGACTTCGGAACATTAACACCGTGACCCCGCGCGGTA 180  
Qy 181 ATCTGCCCTCTCCACCGCTGATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
Db 181 ATCTGCCCTCTCTCCACCGCTGATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
Qy 241 AGTACATTCAGATGAGCGGCTCGTGGCCAGGCGACTCTTAAACGGCCAGCGCTCGTC 300  
Db 241 AGTACATTCAGATGAGCGGCTCGTGGCCAGGCGACTCTTAAACGGCCAGCGCTCGTC 300  
Qy 301 TCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGTGTGTTTCAAAAGACAAG 360  
Db 301 TCCGGCGGAGTAATCGTCAACATGACGTGTATCACTGACGTGTGTGTTTCAAAAGACAAG 360  
Qy 361 AAGTACGCTGACGTGGCGCGGACGTTATGGGTGATGCTTAAAGAAGACGGCGGAG 420  
Db 361 AAGTACGCTGACGTGGCGCGGACGTTATGGGTGATGCTTAAAGAAGACGGCGGAG 420  
Qy 421 AAAGGGGTGTCGGCGTTCTTTGACAGGATTAATTTGGCATATAACCGTCGGAGAAAGTTG 480  
Db 421 AAAGGGGTGTCGGCGTTCTTTGACAGGATTAATTTGGCATATAACCGTCGGAGAAAGTTG 480  
Qy 481 TCGAATGCTGAATGCTGGTCAAGTGTTCGAAACGGTCTCTTTAGTAAAGTCTCTT 540

481 TCAGATGCGAATTTGGTGGTCAAGTGTTCGAAACGGTCTCTTTAGTAAACGTCCTT 540  
 541 GAAATGGACGTTATTACTGGGAAGGTGAAATGTTGACATCTCGACAGCTAAACCCA 600  
 541 GAAATGGACGTTATTACTGGGAAGGTGAAATGTTGACATCTCGACAGCTAAACCCA 600  
 601 GAAATGTTCTATAGGAGTGTAGGAGTTGGGTCAATTTGGAAATTAACGAGAGCCAGA 660  
 601 GAAATGTTCTATAGGAGTGTAGGAGTTGGGTCAATTTGGAAATTAACGAGAGCCAGA 660  
 661 ATTGTTTTGGACATGACCTAAACGGGCCAAATGGTTTTGGATGCTCTACAGTATTTC 720  
 661 ATTGTTTTGGACATGACCTAAACGGGCCAAATGGTTTTGGATGCTCTACAGTATTTC 720  
 721 ACAATCTTTACAAAGGACCAAGAAAGTTTGATATCAATGGCAACGATATTGGAGTGAC 780  
 721 ACAATCTTTACAAAGGACCAAGAAAGTTTGATATCAATGGCAACGATATTGGAGTGAC 780  
 781 TATTTAGAGGTCAATATTTCTATCAACGGGTGCTGTTGACACCTCTTTTCCCACT 840  
 781 TATTTAGAGGTCAATATTTCTATCAACGGGTGCTGTTGACACCTCTTTTCCCACT 840  
 841 TCAGATCAATCTAAAGTGGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTGAA 900  
 841 TCAGATCAATCTAAAGTGGCTGATCTAGTCAAGCAACACGGTATCATCTATGTTCTGAA 900  
 901 GTAGCCAGTATATGATGATCCCAATCTCCCATCATCAGCAAGGTATTGACACATTA 960  
 901 GTAGCCAGTATATGATGATCCCAATCTCCCATCATCAGCAAGGTATTGACACATTA 960  
 961 ACGAAACATTAAGTTACTTGCCTGGGTTTCAATCAATGCACGAGCTGGCTTCTTCGAT 1020  
 961 ACGAAACATTAAGTTACTTGCCTGGGTTTCAATCAATGCACGAGCTGGCTTCTTCGAT 1020  
 1021 TTCCTGAAACGTTGATCATGCAAGAAATAAATCAATCTCTGAGTATTGGAACTT 1080  
 1021 TTCCTGAAACGTTGATCATGCAAGAAATAAATCAATCTCTGAGTATTGGAACTT 1080  
 1081 CTTATCTCTGGCTTAACCTCTACGTTCTCTAAATCTCGGATTTCTGATTTTCAATACCGT 1140  
 1081 CTTATCTCTGGCTTAACCTCTACGTTCTCTAAATCTCGGATTTCTGATTTTCAATACCGT 1140  
 1141 GTTGTCAAGACATTTCTTTAAGCAAAATCAGCTTTGGGACTCGCTCTTCTCTATCCA 1200  
 1141 GTTGTCAAGACATTTCTTTAAGCAAAATCAGCTTTGGGACTCGCTCTTCTCTATCCA 1200  
 1201 ACAACCGGAATAAATGGGACATCTGATGTCGGGATGATACAGAGATCGATGAAGAT 1260  
 1201 ACAACCGGAATAAATGGGACATCTGATGTCGGGATGATACAGAGATCGATGAAGAT 1260  
 1261 GTTATATATATTATCGGACTACTACAAATCGCTTACCCCAAGATCTTCCAGAGTGGAG 1320  
 1261 GTTATATATATTATCGGACTACTACAAATCGCTTACCCCAAGATCTTCCAGAGTGGAG 1320  
 1321 AGCGTTAACGAGAGATATTAGTTTTCAGGATTCAGGATTAAGATTAAGCAATAT 1380  
 1321 AGCGTTAACGAGAGATATTAGTTTTCAGGATTCAGGATTAAGATTAAGCAATAT 1380  
 1381 CTAATGCAATTATCTAGTAAGAGATTTGGATTGACATTTTGGATCAAAATGGGATGAT 1440  
 1381 CTAATGCAATTATCTAGTAAGAGATTTGGATTGACATTTTGGATCAAAATGGGATGAT 1440  
 1441 TTTTCGAGAGAGAGATCTATTGATCCCAAGAACTGTTATCTCCAGGCAAGACATC 1500  
 1441 TTTTCGAGAGAGAGATCTATTGATCCCAAGAACTGTTATCTCCAGGCAAGACATC 1500  
 1501 TTTTGA 1506  
 1501 TTTTGA 1506

RESULT 4

US-09-938-842A-2089  
 ; Sequence 2089, Application US/09938842A  
 ; Patent No. US20020160378A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Harper, Jeff  
 ; APPLICANT: Kreps, Joel  
 ; APPLICANT: Wang, Xun  
 ; APPLICANT: Zhu, Tong  
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
 ; FILE REFERENCE: SAME, AND METHODS OF USE  
 ; FILE REFERENCE: SRI21300-3  
 ; CURRENT APPLICATION NUMBER: US/09/938,842A  
 ; CURRENT FILING DATE: 2001-08-24  
 ; PRIOR APPLICATION NUMBER: US 60/227,866  
 ; PRIOR FILING DATE: 2000-08-24  
 ; PRIOR APPLICATION NUMBER: US 60/264,647  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/300,111  
 ; PRIOR FILING DATE: 2001-06-22  
 ; NUMBER OF SEQ ID NOS: 5379  
 ; SEQ ID NO 2089  
 ; LENGTH: 1575  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; US-09-938-842A-2089  
 Query Match 51.7%; Score 778.2; DB 9; Length 1575;  
 Best Local Similarity 72.2%; Pred. No. 4.1e-223;  
 Matches 1093; Conservative 0; Mismatches 363; Indels 57; Gaps 4;  
 Qy 42 AATGATCACCAATCATCAACGCTATTAAATGTTATTTACCTAAATCCCTTAACCTCAC 101  
 Db 63 AACCTTAATCAATCATGATGAGGCAATGATGTTTCTTACCCATATCATCAACCTTAC 122  
 Qy 102 CCTCTCTACCGATCTTCCATCATCTCCGAGCTCTCATGACTTCGGAACATAACCCAC 161  
 Db 123 GGTCTTAACGATCCCTTCTCATCTCTCGCTTCTCAGACTTCGGTAACATAACCGA 182  
 Qy 162 CGTGACCCCGGGGGGTAATCTGCCCTCTCTCCAGCGTGATATCTCTGCTCTCTCC- 220  
 Db 183 CGAAATCCCGGGGGGCTCTCTGCCCTTCTCTCCACACGAGGTGGCTGCTCTCTCCG 242  
 Qy 221 -----AATACGGCGCAACGAAAGTACATTTCCA 251  
 Db 243 TTTGCTAAACGAGGATCTCTTACATAAAGCTCAACACGCGCGCTACTTTCAA 302  
 Qy 252 AGTAGCGGCTCGTGGCCAGGCCACTCTTTAAACGGCCAAAGCTCGGTCTCCGGCGGAGT 311  
 Db 303 AGTGGCTGCTCGAGGCCAAGGCCACTCCCTCCGTGGCCAAAGCTCTGSCACCCGGAGGTGT 362  
 Qy 312 AATCGTCAACATGACGTGATC-----ACTGACGTGGTGGTTTCAAA 353  
 Db 363 CGTGTGAACATGACGTGTCTCGCCATGGCGGCTAAACACAGCGCGGTTGTTATCTCGGC 422  
 Qy 354 AGACAAGAGTACGCTGACGTGGCGCGGACGTTATGGGTGATGTGCTTAAGAGAC 413  
 Db 423 AGACGGACTTACGCTGACGTGGCTGGCGGACGATGTGGGTGATGTTCTGAAGCGCGC 482  
 Qy 414 GCGGAGAAAGGGGTGTCGCGGTTTCTTGGACGATTTTTCATATAACCGTCGAGG 473  
 Db 483 GGTGGATAGAGCGCTCTCGCGGTTACATGACGGAATTTTGTATCTCAGCTCGCGG 542  
 Qy 474 AACGTTGTGGAATGGTGGATTTGGTGTCAAGTGTCTTTCGAAACGGTCTCTTGTAGTAA 533  
 Db 543 GACGTTGTGGAACGCTGGAATCGGTGTGACAGCTTTTAGACACAGCGCTCAGATTAGTAA 602  
 Qy 534 CGTCTTGAATTTGACGCTTATTACTGGGAAGGTGAATGTTGACATGCTCGGACAGCT 593  
 Db 603 CGTTCAATGAGCTTACGCTTATTCGGAAGAGGTGAATGATGACTTGCTCTCCAAAGTT 662  
 Qy 594 AAACCCAGAAATGTTCTATGAGTGTGTAGGAGGTTTGGGTCAATTTTGAATTTATAACGAG 653  
 Db 663 AAACCCGAAATGTTCTATGAGTGTGTAGGAGGTTTGGGTCAATTCGTTATTATAACGAG 722





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Db 843 AGTTGACCTTTTGGAGGTCACCTTAATGATGCAAAATGGCTCGTAGACACCTCTTTCTT 902
Qy 834 CCCACCTTCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGGTATCATCTATGT 893
Db 903 CCCACTCTCCGATCAAAACAGAGTCGATCTCTGTGAATGATGACACCGGATCATCTATGT 962
Qy 894 TCTTGAAGTAGCCAGATTAATGATGATCCATCTCCCATCATCAACAGAGTTATTGA 953
Db 963 TCTGCAAGTAGCCAGATTAATGATGATCCATCTCCCATCATCAACAGAGTTATTGA 1022
Qy 954 CACATTAACGAAACATTAAGTTACTTGGCCGGTTTCAATCAATCAATGACAGCTGGCCTA 1013
Db 1023 CACGTTAAGTAGAATCTAGTTTTCGCTCCAGGTTTATGTTTCTGTAAGATGTTTCCGTA 1062
Qy 1014 CTTTCAATTTCTTGAACCGTGTACATGTCGAAGAAATAAATCAAGATCTTTCGGGATTTG 1073
Db 1083 TTTTCAATTTCTTGAACCGTGTACATGTCGAAGAAATAAATCAAGATCTTTCGGGATTTG 1142
Qy 1074 GGAATCTTCTTCACTCTTGGGTTTAACTCTTACGTTTCTTAAATCTCGGATTTCTCGATTTCA 1133
Db 1143 GGAATCTTCTTCACTCTTGGGTTTAACTCTTACGTTTCTTAAATCTCGGATTTCTCGATTTCA 1202
Qy 1134 TAACGGTGTGTCAGAACATTTCTTCTTAAGCAAAATCAGCTTCGGGACTCGCTTCTTCT 1193
Db 1203 TGATGGTGTATTAATGGCCCTTCTTCTTAACCAAACTCACTTCTGGTGTACTTCTTCT 1262
Qy 1194 CTATCCAAACAAACCGGATTAATGGGACAAATCTATGTCGGGATGATACCAAGATCGA 1253
Db 1263 CTATCCCAACAAACCGGATTAATGGGACAAATCTATGTCGGGATGATACCAAGATCGA 1316
Qy 1254 TGAAGATGTTATATATATATATATGCTTACGTTTCTTAAATCTCGGATTTCTCGATTTCA 1310
Db 1317 CGAAGATGTTTATGATCGATTAATGCTTACGTTTCTTAAATCTCGGATTTCTCGATTTCA 1376
Qy 1311 AGAAGTGGAGGCGTTTAAACGAGAAATTAATAGTTTTCGAGGATTTCAAGGATTTAAAGT 1370
Db 1377 AGAATCTTGAATCTCAACGACAGGTTTATTCAGTTTTCGAGGATTTCAAGGATTTAAAGT 1436
Qy 1371 TAACCAATCTCTAATGATTAATATAGTAAAGAAATGATTTGAGCATTTTGGATCAAA 1430
Db 1437 TAAGGATATTTGATGATTAATCAAGAAATGATTTGAGCATTTTGGATCAAA 1496
Qy 1431 ATGGATGATTTTTCGAGGAAAGATTAATTTGATTTCCCAAGAACTGTTATCTCCAGG 1490
Db 1497 ATGGATGATTTTTCGAGGAAAGATTAATTTGATTTCCCAAGAACTGTTATCTCCAGG 1556
Qy 1491 GCAAGACATCTTT 1503
Db 1557 ACAGACATATTT 1569

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RESULT 6

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US-10-311-453-28
; Sequence 28, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmelling, Thomas
; APPLICANT: Werner, Tom S
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: Physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: BP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: BP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28

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; LENGTH: 1575
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-10-311-453-28

Query Match      51.7%; Score 778.2; DB 12; Length 1575;
Best Local Similarity 72.2%; Pred. No. 4,1e-223;
Matches 1093; Conservative 0; Mismatches 363; Indels 57; Gaps 4;

Qy 42 AATGATCACAAATCATCAACGGTATTAAATTTAGTTTACCTAAATCCCTTAACCTCAC 101
Db 63 AACCTTAATCAAAATCAGATGAGGCAATGATGTTTTTCTTACCCATATCACTCAACCTTAC 122
Qy 102 CCTCTCTACCGATCCTTCCATCATCTCCGACGCTCTCATGACTTCGGGAAACATAAACCCAC 161
Db 123 GGTCTCTAAACCGATCCTTCTCCATCTCTGCGCTTCTCAGACTTCGGTACATACCGA 182
Qy 162 CGTACCCCCCGGGGGGTTAATCTGCCCTCTCTCCACCGCTGATATCTCTCTCTCTCTCC- 220
Db 183 CGAAAAATCCCGCGCGCTCTCTGCCCTCTCTCCACACCGAGGTGGCTCTCTCTCTCCG 242
Qy 221 -----AATACCGCGCAAAACGMAAAAGTACATTTCCA 251
Db 243 TTTTGGCTAACGGGAGGATTTCTTTCAATTAAGGCTCAACAGCCCGCGCTCTATTTCAA 302
Qy 252 AGTAGGGCTCTGTGGCCAAAGGCCACTCTTTAAACGGCCAAAGCTCTGGTCTCCGGCGAGT 311
Db 303 AGTGGCTGTCTGAGGCCAAAGGCCACTCTCTCGTGGCCAAAGCTCTGCAACCGCGAGGTGT 362
Qy 312 AATCGTCAACATGACGTGTATC-----ACTGACGTGGTGGTTTCAAA 353
Db 363 GTCGTGACATGACGTGTCTGCCATCGCGGCTTAAACGAGGGCGTTGTATCTCGGC 422
Qy 354 AGCAAGAAAGTACGTGACGTGGCGGCGGAGCGTTATGGGTGATGTCGTTAAGAGAC 413
Db 423 AGACGGGACTTACGTGACGTGGCTGCGCGGACGATGTGGGTGGATGTCTTGAAGGCGGC 482
Qy 414 GCGGAGAAAGGGGTGTGCGCGGTTTCTTGGACGAGTATTTGCATATAAACCGTCGAGG 473
Db 483 GGTGGATAGAGCGTCTCGCGGTTTACATGACGAGTATTTGTATCTCAGCGTCGCGG 542
Qy 474 AACGTTGTGAAATGGTGAATTTGGTGGTCAAGTGTTCGAAACCGTCTCTCTTTAGTAA 533
Db 543 GACGTTGTGCAACGCTGGAATCGGTGGTCAAGTGTTCGACACCGCTCTCAGATTAGTAA 602
Qy 534 CGTCTTGAATTTGGAGTTTATTTACTTGGGAAAGGTGAAATGTGTGACATGCTCGCACAGCT 593
Db 603 CGTTCATGAGCTTACGTTTATTCGGAAGAGGTGAATGATGACTTGTCTCTCCAAAGTT 662
Qy 594 AAACCCAGAAATTTGTTCTATGAGGTGTAGGAGGTTTGGGTCAATTTGGAATTTAAACGAG 653
Db 663 AAACCCAGAAATTTGTTCTATGAGGTTTTAGGAGGTTTGGGTCAATTTGCGGTATTTAAACGAG 722
Qy 654 AGCCAGAAATTTGTTGGACCATGACCTTAAACCGGCGCAAAATGGTTTCGGATGCTCTACAG 713
Db 723 GGCACGATTTGCGTTGGATCATGCAACCCACCAAGGGTGAATGGTCTCGCATACTCTACAG 782
Qy 714 TGAATTTCAACCTTTTACAAAGGACCAAGAGCGTTTGTATCAATGGAACAGATATGG 773
Db 783 TGACTTCTCGGCTTTTAAAGAGACCAAGAGCGTTTAAATATCAATGACCAATGATCTCGG 842
Qy 774 AGTCGACTATTTAGAGGTCAAAATTTTCTATCAAAACGGTGTCTGTGACACCTCTTTTTT 833
Db 843 AGTTGACTTTTGGAAAGTCAACTTATGATGTCAAAATGGCTTCGTAGACACCTCTTCTT 902
Qy 834 CCCACCTTCAGATCAATCTAAGTCTGCTGATCTAGTCAAGCAACACCGGTATCATCTATGT 893
Db 903 CCCACTCTCCGATCAAAACAGAGTCGATCTCTTGTGAATGATGACACCGGATCATCTATGT 962
Qy 894 TCTTGAAGTAGCCAGATTAATGATGATCCCAATCTCCCAATCATCAAGAGGTTATTGA 953
Db 963 TCTCGAAGTAGCCAGATTAATGATGACAGAAACCAACCTTCCCATTTATGACAGGTTATTGA 1022

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Db	1143	GAAGTTCCTCATCGCTTAACATCTTTGTCCGGGGTCTCGAATCCAAGATTTTCA	1202
Qy	1134	TAACGGTGTTCGAAGACATTTCTTTAAGCAGAAATACGCTTCGGGACTCGCTCTCT	1153
Db	1203	TGATGGTGTTATTAATGGCTTCCTTTAAACCAAACTCAACTCTCTGTGTACTCTCTT	1262
Qy	1194	CTATCCAAACAAACCGGAATAAATGGGACAATCGTATGTCGGCGATGATACAGAGATCGA	1253
Db	1263	CTATCCCAACAAACCGGAATAAATGGGACAATCGGATGTCACGATGACACCC-----GGA	1316
Qy	1254	TGAAGATGTTATATATATATATCGGACTACTCAATCCG-----TACCCCAAGGATCTTCC	1310
Db	1317	CGAAGATGTTTTTATGATCGGATTACTGCAATCAGCTGGTGGATCTCAAAATGGCA	1376
Qy	1311	AGAAATGAGAGCGGTTAAGGAGAAATTAATAGGTTTTGCAAGGATTCAGGATTAAGAT	1370
Db	1377	AGAACTTGAAATCTCAACGACAAAGTTATTCAGTTTTGTGAAACTCGGGAAATTAAGAT	1436
Qy	1371	TAAGCAATCTAATGCAATATACCTAGTAAAGAAATGGAATGAGCATTTTGGATCAAA	1430
Db	1437	TAAGGAATATTTGATGCACTATACAGAAAGAAAGATTTGGGTAAACATTTTGGACCAA	1496
Qy	1431	ATGGGATGATTTTTCGAAGAGAAAGATCTATTTGATCCCAAGAACTGTTATCTCCAGG	1490
Db	1497	ATGGGATGATTTTAAAGAAAGAAATATGTTGATCCCAAGAACTATTTGCTCCAGG	1556
Qy	1491	GCAAGACATCTTT 1503	
Db	1557	ACAAGACATATTT 1569	

RESULT 8

US-10-326-184-10

; Sequence 10, Application US/10326184

; Publication No. US20030163847A1

; GENERAL INFORMATION:

; APPLICANT: Monsanto Company

; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF G

; TITLE OF INVENTION: OXIDASE 1

; FILE REFERENCE: MTC6781.1

; CURRENT APPLICATION NUMBER: US/10/326,184

; CURRENT FILING DATE: 2002-12-20

; PRIOR APPLICATION NUMBER: US 60/343,129

; PRIOR FILING DATE: 2001-12-20

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10

; LENGTH: 1575

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-10-326-184-10

Query Match 51.7%; Score 778.2; DB 14; Length 1575;

Best Local Similarity 72.2%; Pred. No. 4.1e-223; Indels 57; Gaps 4;

Matches 1093; Conservative 0; Mismatches 363;

Qy	42	AATGATCACCACAAATCATCAACCGGTATTAATAATTTGATTTTACCTTAATCCCTTAACCTCAC	101
Db	63	AACCTTAATCAATCAGATGAGGGCATGTGATGTTTTCTTTACCATATCACTCAACCTTAC	122
Qy	102	CTCTCTACCGATCCCTTCATATCTCCGAGCTCTCATGATCTCGGAAACATACCAAC	161
Db	123	GGTCCTAACCGATCCCTTCTCCATCTCTGCGGTCTCTCAGACTTCGGTAAACATACCGA	182
Qy	162	CGTGACCCCGGGGGGTAAATGCGCCCTCTCCACCGCTGATPATCTCTGCTCTCTCC-	220
Db	183	CGAAATCCCGGGCGCTCTCTGCGCTTCTCCACCGAGGAGGTGGCTCGTCTCTCCG	242
Qy	221	-----NATAGCGGCAACCGGAAAGGATACATTTCA	251
Db	243	TTTGCTAACGGAGATTTCTTTACAAATAAAGGCTCAACCGCCCGCGTCTACTTTTCAA	302

Qy	252	AGTAGCGGCTGTGGCCAAAGGCCACTCTCTTAAACCGCCAGCCTCGTCTCTCGGCGGAGT	311
Db	303	AGTGGCTGTCTGAGGCCAAAGGCCACTCTCTCGGTGGCCAAAGCCTCTGCAACCGGAGGTGT	362
Qy	312	AATCGTCAACATGACGTGTATC-----ACTGACGTGGTGGTTTCAAA	353
Db	363	CGTCGTGAACATGACGTGTCTGCCATGCGGCGCTAAACCCAGCGGCGTGTGTATCTCGGC	422
Qy	354	AGACAAAGAGTAGTACGTGACGTGGCGCGCGGACGTATATGGGTGGATGTCTTAAAGAAC	413
Db	423	AGACGGGACTTACGTGACGTGGCTGCCGCGACGATGTGGTGGATGTCTGAAGCGCGC	482
Qy	414	GGCGGAGAAAGGGTGTCCCGGTTTCTTGGACGGAATATTTTGCATATATAACCGTGGAGG	473
Db	483	GGTGGATAGAGGGCTCTCCCGGTTTACATGGACGGAATATTTGTATCTCAGCGTGGCGG	542
Qy	474	AACGTTGTGCAATGTTGGAAATTTGGTCAAGTGTTCGAAACGGTCTCTTTGTAGTAA	533
Db	543	GACGTTGTGCAACGCTGGAATCGTGTGTCAGACGTTTACACACCGGCCCTCAGATTAGTAA	602
Qy	534	CGTCTTGAATTTGGACGTTTACTCGGAAAGGTGAAATTTTGCATGCTCGCGCAGCT	593
Db	603	CGTTCATGAGCTTGACGTTTATACCGGAAAGGTGAAATGATGACTTGTCTTCCAAAGTT	662
Qy	594	AAACCCAGAAATTTCTATGAGGTGTAGGAGGTTTGGGTCAATTTGGAATTAATACGAG	653
Db	663	ARACCTGAAATGTTCTATGAGGTTTTAGGAGGTTTTGGGTCAATTCGGTATTATAACGAG	722
Qy	654	AGCCAGAAATTTTGGACCAATGACCTAAACCGGCCAAATGGTTTCGATGCTCTACAG	713
Db	723	GGCCAGGATTTGGTGGATCATGCACCCCAAGGGTGAAATGGTCTCGGATATCTACAG	782
Qy	714	TGATTTCAACAATTTTACAAAGGACCAAGAACTTTTGATATCAATGGCAACGATATTGG	773
Db	783	TGACTTCTCGGCTTTTAAAGAGACCCAGAGCGTTTAAATATCAATGACCAATGATCTCG	842
Qy	774	AGTCGACTATTAGAGGTCAAATATTTCTATCAAAACGGTGTCTGTGACACCTCTTTTT	833
Db	843	AGTGAATTTTGGAAAGGTCAACTTATGATGTCAAATGGCTCTGTAAGACACCTCTTCT	902
Qy	834	CCCACTTTCAGATCAATCTAAAGTCGCTGATCTAGTCAAGCAACACGGTATCATCTATGT	893
Db	903	CCCACTCTCGATCAACCAAGAGTTCGATCTCTGTGATGACCAACCGATCATCTATGT	962
Qy	894	TCCTGAAGTAGCAAGTATTTATGATGATCCCAATCTCCCATCATCATCAGCAAGGTTATGA	953
Db	963	TCTCGAAGTAGCAAGTATTTATGACAGAACCAACCTTCCCATTTATGACCAAGTGATTGA	1022
Qy	954	CACATTAACGAAACATTTAGTTTACTTGGCCGGTTTCAATATCAATGACGACGTCGCTA	1013
Db	1023	CAGTTAAGTAGAACTCTAGGTTTCGCTCAGGGTTTATGTTCTGTACAGATGTTCCGTA	1082
Qy	1014	CTTCGATTTCTGAAACCGTGTACATGTCGAAGAAAATAAACTCAGATCTTTGGGATATG	1073
Db	1083	TTTCGATTTCTTGAACCGTGTCCGAAACGAAGAATAAACTCAGATCTTTTAGGACTATG	1142
Qy	1074	GGAACTTCTCATCTTGGCTTAACTCTACGTTCTTAATCTCGGATTTCTCGATTTTCA	1133
Db	1143	GGAACTTCTCATCTTGGCTTAACTCTACGTTCTTAATCTCGGATTTCTCGATTTTCA	1202
Qy	1134	TAAAGGTTGTCTCAAGACATTTCTTTAAAGCAAAATACAGTTTCGGGACTCTCTTCT	1193
Db	1203	TGATGGTGTATTAAATGSCCTTCTTCTTAAACCAAAACCTCAACTTCTGGTGTACTCTCT	1262
Qy	1194	CTATCCAAACAAACCGGAAATAAATGGGACATCTGATGTCGGCGATGATACAGAGATCGA	1253
Db	1263	CTATCCCAACAAACCGGAAATAAATGGGACCAACCGGATGTCAACGATGACAC-----GGA	1316
Qy	1254	TGAAGATGTTATATATATATTCGGACTACTTACAAATCCG-----TACCCCAAGGATCTTCC	1310
Db	1317	CGAAGATGTTTTTATGATCGGATTTACTGCAATCAGTGGTGGATCTCAAAATTTGCA	1376
Qy	1311	AGAAATGAGAGCGGTTAAGGAGAAATTAATAGGTTTTTGCAGGATTCAGGATTAAGAT	1370

Db 1377 AGAATTGAAATCTCAACGACAGGTTATTCAGTTTGTGAAACTCGGGAATTAGAT 1436  
 Qy 1371 TAAGCAATATCTAATGCAATATCTAGTAAGAGAGATTGGATTGAGCAATTTGGATCAAA 1430  
 Db 1437 TAAGCAATATTTGATGCACTATACAGAAAGAGATTGGGTTAAACATTTTGGACCAA 1496  
 Qy 1431 ATGGGATGATTTTTCGAGGGAAGATCTATTTTGTATCCCAAGAACTGTTATCTCCAG 1490  
 Db 1497 ATGGGATGATTTTTAAGAAAGAAATATGTTTGTATCCCAAGAACTATGTTCTCAGG 1556  
 Qy 1491 GCAAGACATCTTT 1503  
 Db 1557 ACAAGACATATTT 1569

RESULT 9

US-10-326-184-20  
 ; Sequence 20, Application US/10326184  
 ; Publication No. US20030163847A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Monsanto Company  
 ; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF  
 ; TITLE OF INVENTION: OXIDASE 1  
 ; FILE REFERENCE: MTC6781.1  
 ; CURRENT APPLICATION NUMBER: US/10/326,184  
 ; CURRENT FILING DATE: 2002-12-20  
 ; PRIOR APPLICATION NUMBER: US 60/343,129  
 ; PRIOR FILING DATE: 2001-12-20  
 ; NUMBER OF SEQ ID NOS: 24  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 20  
 ; LENGTH: 1655  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 US-10-326-184-20

Query Match 51.7%; Score 778.2; DB 14; Length 1655;

Best Local Similarity 72.2%; Pred. No. 4.2e-263; Mismatches 363; Indels 57; Gaps 4;

Matches 1093; Conservative 0;

Qy 42 AATGATCACCAAAATCATCAACGGTATTAAATTTGATTTACCTAAATCCCTTAACCTCAC 101  
 Db 63 AACCTTAATCAATCAGATGAGGCATGATGTTTCTTACCCATATCATCTAACCTTAC 122  
 Qy 102 CCTCTTACCGATCTTCCATCATCTCGGAGCCTCTCATGACTTCGGAACATATACAC 161  
 Db 123 GGTCTTAACCGATCCCTTCTCCATCTCTGCGCTTCTCACGACTTCGTAACATAACCGA 182  
 Qy 162 CGTGACCCCGCGGCGTAAATCTGCCCTCTCTCCACGCTGATATCTCTGCTCTCTCC- 220  
 Db 193 CGAAATCCCGCGCGCTCTCTGCCCTCTCTCCACGAGTGGTGGTCTCTCTCCG 242  
 Qy 221 -----AATACGCGCGAAACCGGAAAAAGTACATTTCA 251  
 Db 243 TTTGCTAAACGAGGATTTCTTACAATAAAGGCTCAACAGCCCGCGTCTACTTTCAA 302  
 Qy 252 AGTAGCGCTGTGCGCAAGCCACTCTTAAACGCGCCAGCCTCGTCTCCGCGGAGT 311  
 Db 303 AGTGGCTCTCGAGGCCAAGGCCACTCTCCCTCGTGGCCAGCCCTCTGACCCGAGGTGT 362  
 Qy 312 AATCGTCAACATGACGTGTATC-----ACTGACGTGGTGGTTTCAAA 353  
 Db 363 CGTGTGAACATGACGTGTCTCGCATGGCGGCTAAACCGCGCGGTGTATCTCGG 422  
 Qy 384 AGACAAGAAAGTACGTGACGTGGCGGCGGAGCTATAGGTGATGTGCTTAAGAGAC 413  
 Db 423 AGACGGGACTTACGTGACGTGGTGGCGGAGCATGTGGGTGATGTCTGAAAGCGGCG 482  
 Qy 414 GCGGAGAAAGGGGTGTCGCGGTTCTTGGACGGATTTTTCATATATACCGTCGGAGG 473  
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Qy 474 AACGTTGCGATGGTGAATTTGGTGGTCAAGTGTCTTGGAAACGGTCTCTTGTAGTAA 533  
 Db 543 GACGTTGCGAAGCGTGGAAATCGGTGGTGCACAGTTTAGACACGCGCTCAGATTAGTAA 602  
 Qy 534 CGTCTTGAATTTGGACGTTTATTTACTGGGAAAGGTGAATTTGTGACATGCTCGGACAGCT 593  
 Db 603 CGTTCATGAGCTTGACGTTTATTTACCGGAAAGGTGAATTTGATGACTTGCTCTCCAAAGTT 662  
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 Qy 774 AGTCGACTATTTAGAAAGGTCAAAATTTCTATCAAAACGGTGTGCTGTGACACCTCTTTTT 833  
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 Db 1023 CACGTTAAGTAGAATCTAGGTTTCCGCTCCAGGGTTTATGTTGTTACAGATGTTCCGTA 1082  
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 Db 1557 ACAAGACATATTT 1569

RESULT 10  
 US-10-311-453-3  
 ; Sequence 3, Application US/10311453  
 ; Publication No. US20040031073A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schumling, Thomas  
 ; APPLICANT: Werner, Tom s  
 ; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and  
 ; FILE REFERENCE: 1226-4  
 ; CURRENT APPLICATION NUMBER: US/10/311,453  
 ; CURRENT FILING DATE: 2002-12-16  
 ; PRIOR APPLICATION NUMBER: EP 00870132.8  
 ; PRIOR FILING DATE: 2000-06-16  
 ; PRIOR APPLICATION NUMBER: US 60/258,415  
 ; PRIOR FILING DATE: 2000-12-27  
 ; PRIOR APPLICATION NUMBER: EP 01870053.4  
 ; PRIOR FILING DATE: 2001-03-16  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 US-10-311-453-3  
  
 Query Match 38.3%; Score 577; DB 12; Length 2991;  
 Best Local Similarity 75.9%; Pred. No. 2.6e-162;  
 Matches 852; Conservative 0; Mismatches 40; Indels 231; Gaps 2;  
  
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 DB 1869 ACTGTAATATGGTTCTTTATATATATGTTGTTAATTAATGGGATTGTTTCTCTAAA 1928  
  
 QY 675 TGCACCTAAACGGGCCAAATGGTTTCGGATGCTCTACAGTGAATTTCAACAATTTTACAAA 734  
 DB 1929 TGAATTTGTAGGCCAAATGGTTTCGGATGCTCTACAGTGAATTTCAACAATTTTACAAA 1988  
  
 QY 735 GGACCAAGACGTTTGCATATCAATGGCAACGATATGGAGTCGACTATTTAGAGCTCA 794  
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 QY 795 AATATTTCTATCAAAACGGTGTGGTTCACACCTCTTTTCCACACCTTCAGATCAATCTAA 854  
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 QY 1007 TGGCTACTTCGATTTCTTGAACCGGTACATGTCGAAGAAATTAACATCAGATCTTTGG 1066  
 DB 2409 TGGCTACTTCGATTTCTTGAACCGGTACATGTCGAAGAAATTAACATCAGATCTTTGG 2468  
  
 QY 1067 GATTATGGGAACCTTCCTCATCTTTGGCTTAACCTCTACGTTCTTCAATCTCGAATTCG 1126  
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 QY 1187 CTCTTCTCTATCAACAAACCGGAATAA----- 1214  
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 QY 1404 AGATTGATGAGCATTTTGGATCAAAATGGGATGATTTTTCGAAGAGGAAAGATCTATT 1463  
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 RESULT 11  
 US-10-014-101-3  
 ; Sequence 3, Application US/10014101  
 ; Publication No. US20030074698A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schumling, Thomas  
 ; APPLICANT: Werner, Tom s  
 ; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and  
 ; FILE REFERENCE: 1195-2  
 ; CURRENT APPLICATION NUMBER: US/10/014,101  
 ; CURRENT FILING DATE: 2001-12-10  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/06833  
 ; PRIOR FILING DATE: 2001-06-16  
 ; PRIOR APPLICATION NUMBER: EP 00870132.8  
 ; PRIOR FILING DATE: 2000-06-16  
 ; PRIOR APPLICATION NUMBER: US 60/258,415  
 ; PRIOR FILING DATE: 2000-12-27  
 ; PRIOR APPLICATION NUMBER: EP 01870053.4  
 ; PRIOR FILING DATE: 2001-03-16  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 2991  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 US-10-014-101-3  
  
 Query Match 38.3%; Score 577; DB 14; Length 2991;  
 Best Local Similarity 75.9%; Pred. No. 2.6e-162;  
 Matches 852; Conservative 0; Mismatches 40; Indels 231; Gaps 2;  
  
 QY 615 AGTGTAGGAGTTTGGGTCAATTTGGAATTATAACGAGAGCCAGAAATTTGTTGGACCA 674  
 DB 1869 ACTGTAATATGGTTCTTTATATATATGTTGTTAATTAATGGGATTGTTTCTCTAAA 1928  
  
 QY 675 TGCACCTAAACGGGCCAAATGGTTTGGATGCTCTACAGTGAATTTCAACAATTTTACAAA 734  
 DB 1929 TGAATTTGTAGGCCAAATGGTTTGGATGCTCTACAGTGAATTTCAACAATTTTACAAA 1988

Publication No. US20040031073A1  
 GENERAL INFORMATION:  
 APPLICANT: Schilling, Thomas  
 APPLICANT: Werner, Tom S  
 TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and physiology  
 FILE REFERENCE: 1226-4  
 CURRENT APPLICATION NUMBER: US/10/311,453  
 CURRENT FILING DATE: 2002-12-16  
 PRIOR APPLICATION NUMBER: EP 00870132.8  
 PRIOR FILING DATE: 2000-06-16  
 PRIOR APPLICATION NUMBER: US 60/258,415  
 PRIOR FILING DATE: 2000-12-27  
 PRIOR APPLICATION NUMBER: EP 01870053.4  
 PRIOR FILING DATE: 2001-03-16  
 NUMBER OF SEQ ID NOS: 36  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 27  
 LENGTH: 1572  
 TYPE: DNA  
 ORGANISM: Arabidopsis thaliana  
 US-10-311-453-27

Query Match 31.2%; Score 470; DB 12; Length 1572;  
 Best Local Similarity 58.7%; Pred. No. 2,9e-130;  
 Matches 881; Conservative 0; Mismatches 600; Indels 21; Gaps 3;  
 QY 17 TAATGATCACTTTAATCAACGGTTTAAATGATCACCAATATCAACCGTATTAATAATG 76  
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 Db 1989 GGACCAAGACGTTTGATATCAATGGCAACGATATTTGGAGTGCAGTACTTTAGAGGTCA 2048  
 QY 795 AATATTTCTATCAACGGTTCGTTGACACCTCTTTTCCACCTTTCAGATCAATCTAA 854  
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 Db 2949 TGATCCCAAGAACTGTTATCTCCAGGCGCAAGCATCTTTTGA 2991



716 AACTTGAAGTAGCTCCGAAAGGCGCAAGTGGTTAAAGTTTCTATACATAGATTCTCCG 775  
 725 CTTTTCACAAAGCAACAGAGCTTTGATATCAATGGCAACAGATATTGGAGTC---GACT 781  
 776 AATTACACAGAGATCAAGAACGAGTGTATCGAAACGAGCGGTGTAGATTCTTCTAGAG 835  
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 962 CGAAACATTAAAGTTACTGCCCGGTTCAATCAATGACGACGTCGCTACTTCGATT 1021  
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 1502 TT 1503  
 1550 TT 1551

RESULT 13  
 US-10-014-101-27  
 ; Sequence 27, Application US/10014101  
 ; Publication No. US2003007469A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schmulling, Thomas  
 ; APPLICANT: Werner, Tom  
 ; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and  
 ; TITLE OF INVENTION: physiology  
 ; FILE REFERENCE: 1195-2  
 ; CURRENT APPLICATION NUMBER: US/10/014.101  
 ; CURRENT FILING DATE: 2001-12-10  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/06833  
 ; PRIOR FILING DATE: 2001-06-16

Query Match 31.2%; Score 470; DB 14; Length 1572;  
 Best Local Similarity 58.7%; Pred. No. 2.9e-130;  
 Matches 881; Conservative 0; Mismatches 600; Indels 21; Gaps 3;  
 17 TAATGATCACTTTAAATCAAGGTTTAAATGATCAACCAATCATCAAAACGGTATTAATAATTG 76  
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; PRIOR APPLICATION NUMBER: EP 00870132.8  
 ; PRIOR FILING DATE: 2000-06-16  
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 ; PRIOR FILING DATE: 2000-12-27  
 ; PRIOR APPLICATION NUMBER: EP 01870053.4  
 ; PRIOR FILING DATE: 2001-03-16  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 27  
 ; LENGTH: 1572  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; US-10-014-101-27



842 CAGATCAATCTAAGTCGCTGATCTTAGTCAAGCAACACCGGTATCATCTATGTTCTTTGAAG 901  
896 CCGATCACTTTGAGGATCGCCTCAATGTTCAAGGACATCGTGTATCTACTGCTTGAAG 955  
902 TAGCCAGTATTATGATGCCAATCTCCCATCATCATCAGCAAGGTTATTGACACATTAA 961  
956 TCGTCAAGTATTACGAGCAAACTTCTCAATACAGCTCAACGAGGAATGGAGGATTAA 1015  
962 CGAAAAATTAAAGTTACTTCCCGGGTTTCATATCAATGACAGCTGAGGCTACTTCGATT 1021  
1016 GCGATAGTTTAAACCATGTAAGAGGTTTATGACGAGAAAGATGTGACGTATATGATT 1075  
1022 TCTTGAACGCTGACATGTCGAGAAATAAATCAATCAGATCTTTGGGATATGGAACTTC 1081  
1076 TCTTAAACCGAGTTGCAACCGGAGAGTAAACCTGAAATCAAAGGCCAATGGATGTTTC 1135  
1082 CTCATCTCTGGCTTAACTCTACGTTCTCTAAATCTCGGATTTCTCGATTTTTCATAACGGTG 1141  
1136 CACATCCATGGCTTAACTCTCTTCGTACCAAAAACCTCAAAATCTCCAAATTTGATGATGGTG 1195  
1142 TTGTCAAAGACATTTCTTTAAGCAAAAATCAGCTTCGGGACTCGCTCTCTCTATCCCA 1201  
1196 TTTTAAAGGGTATTATCTTAAGAAATAACATCACTAGCGGTCTGTTCTTTGTTTATCCTA 1255  
1202 CAAACCGGAATAAATGGCAAAATCGTATGTCGGCGATGATACCAAGATCGATGAAGATG 1261  
1256 TGAATCGCAACAAGTGGAAATCGATCGATGTCGCGCTATACCCGAG-----GAAGATG 1309  
1262 TTATATATATTATCGGACTACTCAATCCGCTACCCCAAGGATCTTCCAGAGTGGAGA 1321  
1310 TATTTATCGGTAGGGTTTAAAGATCCCGGGTTTGAATTTGGCAATTTGGGAGGCTTTTGATC 1369  
1322 CGGTTAAGCAGAAATTAATAGGTTTTCAGAGGATTCAGGTATTAAAGATTAAAGCAATATC 1381  
1370 AAGAAACATGGAATACTAGATTTTGTGAGGATGCTAATATGGGGTTTATACAAATATC 1429  
1382 TAATGCATTATACATAGTAAAGAAATGGATGGATTTGGATCAAAATGGGATGATT 1441  
1430 TTCCTTATCATTCATCAAGAAGATGGGTTAGACATTTTGGTCCGAGGTGGAAATATT 1489  
1442 TTTCCAGAGGAAGATCTATTGATCCCAAGAAACTGTTATCTCCAGGGCAAGACATCT 1501  
1490 TCGTAGAGAGAAATATAAATATGATCCCAAAATGATATTATACCGGGACAAATATAT 1549  
1502 TT 1503  
1550 TT 1551

RESULT 14  
US-10-326-184-9  
; Sequence 9, Application US/10326184  
; Publication No. US20030163847A1  
; GENERAL INFORMATION:  
; APPLICANT: Monsanto Company  
; TITLE OF INVENTION: REVERSIBLE MALE STERILITY IN TRANSGENIC PLANTS BY EXPRESSION OF C  
; FILE OF INVENTION: OXIDASE 1  
; FILE REFERENCE: MTC6781.1  
; CURRENT APPLICATION NUMBER: US/10/326,184  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: US 60/343,129  
; PRIOR FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 1572  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-326-184-9

Query Match 31.2%; Score 470; DB 14; Length 1572;  
Best Local Similarity 58.7%; Pred. No. 2.9e-130;

Matches 881; Conservative 0; Mismatches 600; Indels 21; Gaps 3;  
QY 17 TAATGATCATTATTAATCAGCGTTTATATGATCATCAAAATCATCAACGGTATTAAATTTG 76  
Db 56 TCATCATTTACTCTCTCAACTCCGATCAAAACCAACATCAACCAACCATATGGAATATCC 115  
QY 77 ATTTACCTAAATCCCTTAACTCACTCCCTCTCTACCGATCTCTCCATCATCTCCGAGCCT 136  
Db 116 TTTACACAAAGAAATTCGCGGAAATCTCACTCTCTCTCTCTCTCTCTCGATCAAGCGG 175  
QY 137 CTCATGATCTCGGAAACATTAACACCGGTGACCCCGGGGGGTAAATCTGCGCCCTCCCTCA 196  
Db 176 CCACAGATTTCCGCGCACGTCACCAAAATCTTCCCTTCGCGGTCTTAAATCCCTCTCTCCG 235  
QY 197 CGGCTGATATCTCTCGTCTCTCTCAATACCGCGCAACCGGAAAGTACATTCCTCAAGTAG 256  
Db 236 TTGAAGACATACAGATCTTCAAAATCTCTTTGATCTCTCACTGCTCTTTTCTCTTAG 295  
QY 257 CGGCTCGTGGCAAGCGGCACTCTTAAACGGCGCAAGCCTCGGTCTCCGCGGAGTAAATCG 316  
Db 296 CGGCTCGTGGTCAACGACACACGACCGCGTGGCCAGCCTCGGCTAAAGACGAGGTTTGG 355  
QY 317 TCAACATGACGTGATCACTGACGTGG-----TGGTTTCAAAAAGACAAGAGT 364  
Db 356 TCAACATGCGTTCATGTTAATACCGGATCGAGGTATCAAGGTCTTAGGACCTGTTTAT 415  
QY 365 ACGCTGACGTGCGCGCGCGGACGTTTATGGGTGATGTCCTTAAGAAACGGCGGAGAAAG 424  
Db 416 ATGTTGACGTGACGCTCGTGGCTATGGAATGAGGTCTTGAATAAACTTTTGGAGTTAG 475  
QY 425 GGGTGTCCGCGGTTCTTGGACGGAATTTTGCATATAACCGTCCGAGAGAAAGCTTGTGCA 484  
Db 476 GGTTAACCGCGGTTCTTGGACGGAATTTTGTATTTAAACAGTCGTTGGAGCTTATCA 535  
QY 485 ATGTGGGAATGCGTGGTCAAGTGTTCGAAACGGTCTCTTGTATTAGTAACGTCCTTGAAT 544  
Db 536 ACGGCGGAATTAGTGGACAAACGTTTCGTTACGCTCCACAGATCACTAATGTTCTTAGAGA 595  
QY 545 TGAAGTTTACTGCGGAAGTGAATGTTGACATGCTCGGACAGCTAAACCCAGAT 604  
Db 596 TGGATGTTTACTGCGAAAGGAGATGCAACTTTTCCAGGACATGAATCTCGATC 655  
QY 605 TGTTCTATCGAGTGTTAGGAGTTTGGGTCAATTTGGAAATTATAACGAGAGCAGAAATTG 664  
Db 656 TTTTCTTCGCGGTGTAGGAGTTTGGGTCAATTCGGCATTTATAACAGAGCCAGAAITA 715  
QY 665 TTTTGGACCATGCACTTAAACGGGCAATGTTTGGATGCTCTACAGTGATTTTCAAA 724  
Db 716 AACTTGAGTAGTCCGAAAAGGCGCAAGTGGTTAAGGTTTCTATACATAGATTTTCTCG 775  
QY 725 CTTTTCAAAAGGACCAAGAACGTTTGATATCAATGGCAACGATATTGGAGTC---GACT 781  
Db 776 AATTCAAGAGATCAAGAACGAGTATCGAAACGGACGGTGTAGATTTCTTAGAAG 835  
QY 782 ATTTAGAAGTCAATATTCTTATCAACGGTGTGTTGACACCTCTTTTTCCTCCACTT 841  
Db 836 GTTCCATTATGTTGGACCATGTCGCCCAACCGGATAACTGGAGATCCACGTATTATCCACCGT 895  
QY 842 CAGATCAATCTAAAGTCGCTGATAGTCAAGCAACACCGGTATCATCTATGTTCTTTGAAG 901  
Db 896 CCGATCACTTGGAGATCGCTCAATGTTCAACGACATCGTGTCTACTACTGCTTGAAG 955  
QY 902 TAGCCAGTATTATGATGCCAATCTCCCATCATCAACGAGGTTATTGACACATTAA 961  
Db 956 TCGTCAAGTATTACGACGAAACTTCTCAATACACAGTCAACGAGGAATGGAGGAGTTAA 1015  
QY 962 CGAAACATTAAGTTACTTCCCGGGTTTCATATCAATGACAGCTGAGGCTACTTCGATT 1021  
Db 1016 GCGATAGTTTAAACCATGTAAGGAGGTTTATGACGAGAAAGATGTGACGTATATGATT 1075  
QY 1022 TCTTGAACCGGTGATGTCGAGAAATAAATCACTCAGATCTTTTGGGATTTAGGAACTTC 1081  
Db 1076 TCTTAAACCGAGTTCGAAACCGGAGAGTAAACCTGAAATCCAAAGGCCAATGGAGTGTTC 1135

1082	CTCATCTCTGGCTTAACCTCTACGTTCTCTAAATCTCGGATCTTCGATTTTTCATAACGGTG	1141
1136	CACATCCATGGCTTAATCTCTTCGTACCAAAAACTCAAATCTCCAAATTTGATGATGGTG	1195
1142	TTGTCAAAGACATCTCTCTTAGCCAAATAACAGCTTCGGGACCTCGCTCTCTCTATCCAA	1201
1196	TTTTTTAAGGGTATTAATCCCTAGAAATTAACATCACTAGCGGTCTGTCTCTGTTATCCCTA	1255
1202	CAAAACCGGAATAAATGGGCAATTCGTATGTCGGCGATGATACCAGAGATCGATGAAGATG	1261
1256	TGAATCGCAACAAAGTGGAAATGATCGGATGTCGCCGTATACCCGAG-----GAAGATG	1309
1262	TTATATATATATTCGGACACTACAATCGCTACCCCAAGGATCTTCCAGAAGTCGAGA	1321
1310	TATTTTATCGGTAGGTTTAAAGATCCGGGGTTTGGACATTCGGAGGCTTTTGATC	1369
1322	GGCTTAACGAGAAGATAATTAGTTTTTGCAGGATTCAGGTATTAGATTAAACCAATATC	1381
1370	AAGAAACAATCGAAATCTGAACTTTGTGAGATGCTAATATGGGGGTTATACAAATATC	1429
1382	TAATGCATTATATCTAGTAAGAAGATGGATTGAGCATTTTGGATCAAAATGGGATGATT	1441
1430	TTCCCTTATCATTCACAGAAGGATGGGTAGACATTTTGGTCCAGGTGGAAATATTT	1489
1442	TTTTCGAGAGGAAGATCTATTTGATCCCAAGAACTGTTATCTCCAGGGCCAAGACATCT	1501
1490	TCGTAGAGAGAAATATATAATATGAATCCCAAAATGATATTATCACCGGGACAAATATAT	1549
1502	TT	1503
1550	TT	1551

RESULT 15

```

US-10-311-453-29
; Sequence 29, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmilling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 1611
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-311-453-29

```

	Query Match	20.3%	Score 306.2;	DB 12;	Length 1611;
	Best Local Similarity	53.6%;	Prod. No. 6.6e-81;		
	Matches 775;	Conservative	0; Mismatches 628;	Indels 42;	Gaps 5;
Qy	95	ACCTCACCCTCTTACCGATCGTTCCCATCATCTCCGAGCGCTCTCATGACTTCGGAAACA	154		
Dd	110	ACGGCCACTTCACCGTCCACCGTTCGGACTTAGCGCTCGTCTCCFCAGACTTCGGTATGC	169		
Qy	155	TAA---CCACCGTGACCCCCGGCGCGTAATCTGCCCGCTCTCCACCGCTGATATCTCTC	211		
Dd	170	TGAAGTCACTGAAGAGGCATTGGCCCGTGCTTCACTCCATCATCGGCCGAAGACGTGGCAC	229		
Qy	212	GTCCTCTCCAATAFGCCCGCAAACGGAAAAGAATGACATTCCAAGTAGCGGCTCGTGCCCAAG	271		

230	DB	GACTCGTCAGAACAGCTTACGTTACGCCACGGCGTTTCGGTCTCAGCCCGAGGCCACG	289
272	QY	GCCACTCTTAAACGGGCCAACCTCG-----GTCTCCGGCGGAGTAATCG	316
290	DB	GCCATTCATAAACCGACAACGCCGGCGGGAGGAACGGTGTGGTGTGTTGAAATGAACC	349
317	QY	TCACATACACGTGTATCACTCAGCTGTGTGTTTCAAAGACACAAGATACGCTGACGTGG	376
350	DB	ACGGCGTAACCGGGACGCCCAAGCACCTGTCGACCGGATGAATGTATGTGGATGTAT	409
377	QY	CGCCGGGACCTTATGGGTGGATGTCTTAAAGAGACGGCGGAGAAAGGGGTGTCGCGG	436
410	DB	GGGTGGAGAGTTATGGTTCGATGTGTTGAAGAAAACGTTGGAGCATGGCTTAGCACAA	469
437	QY	TTTCTTGACCGGATTTATTTGCATATAACCGTCCGGAGGAACGTGTCGCAATGTTGCAATTG	496
470	DB	AATCATGACCGGATTTGTATCTTAAACCGTTGGAGGTACACTCTCCAATGCAGGAATCA	529
497	QY	GTGTGCAAGTGTTCGAAACCGTCCCTCTGTGTAGTAAGCTCCTTGAATTGGACGTTATTA	556
530	DB	GTGTGCAAGCTTTCCACCATGGTCTCAAAATTAGTTAAGCTCTTGAGCTCGACGTTGTAA	589
557	QY	CTGGGAAAGGTGAATGTGTGATGCTCGGCACAGCTAAACCCAGAAATGTTCTATGAG	616
590	DB	CTGGGAAAGGAGGTGATGAGATGCTCAGAAGAAAGAACACAGGCTATTCATGAG	649
617	QY	TGTTAGGAGGTTTGGGTCAAATTTGGAATTATAACGAGAGCCAGAAATGTTTGGACCATG	676
650	DB	TTCTTTGGTGAATTAGGTCAAATTTGGATCATCACTCGAGCAGCAATCTCTCGAACCCAG	709
677	QY	CACCTAAACGGGCCAATTTGGTTCGGATGCTCTACAGTGAATTCACAACTTTTACAAAG	736
710	DB	CTCCCCAAGGGTGAGTGGATACGGGTATTTGATTCGAGCTTCAAAGTGTTTACGGAG	769
737	QY	ACCAGAAGCTTTGATATCAATGGGCAACGATATTGGAGTCGACTATTTAGAGGTCAAA	796
770	DB	ACCAAGAGTACTTAATCTCAATGCATGGTCAATTAAAGTTTGATTACGTGGAAGGTTTG	829
797	QY	TATTTCTATAACGGTGTGTTGACA-----CCTCTTTTCCACCTTCAGATC	847
830	DB	TGATTTGGACGAAGACTCGTCAACAAATGGAGATCTTCTTTCTCTCCACGTAACC	889
848	QY	AATCTAAAGTCGTGATCTAGTCAAGCAACAGGTATCATCTATGTTCTTGAAGTAGCCA	907
890	DB	CCGTCAAGATCTCTCTGTTAGTTCCAACGGCTCTGTTTGTATTGCTTGAGATCACCA	949
908	QY	AGTATTATGATGATCCCAATCTCCCATCATCAGCAAGGTATTGACACATTAAACGAAA	967
950	DB	AGAACTACCACGACTCCGACTCCGAATCGTTGATCAGGAAGTTGAGATCTCATGAAGA	1009
968	QY	CATTAAAGTTACTTGGCCGGTTCATATCAATGACGACGTGGCTACTTCGATTTCTTGA	1027
1010	DB	AATTGAATTTACCGACATCGTCTTTTACAACGGATTTACAATATGTGGACTTTCTCG	1069
1028	QY	ACCGGTACATGTGCAAGAAAATAAATCAGATCTTTGGATTTATGGGACTTCCTCATC	1087
1070	DB	ACCGGGTACACAGGCCGAATTGAAGCTCCGGTCCAAGAAATTTATGGGAGTTCCACACC	1129
1088	QY	CTTGGCTTAACCTCTACGTTCTCTAAATCTCGGATCTCGATTTTTCATACAGGTGTGTCA	1147
1130	DB	CATGGCTCAACCTCTTCGTGCCAAATCAAGATCTCTGACTTCGATTAAGGCGTTTTCA	1189
1148	QY	AAGACATTTCTTTAAGCAAAAATCAGTTCGGGACTCCGCTCTTCTCTATCCACAAACC	1207
1190	DB	AGGGCATTTTGGGAAATAAAACAA-----GTGGCCCTATCTTATCTACCCCATGAACA	1243
1208	QY	GGATAAATGGGACAATCGTATGTCCGGCATGATAC-----AGAGATCGATGAAG	1258
1244	DB	AAGCAAAATGGGACGAGAGGNGCTCAGCGTGACCGCGGATGAGGAAGTTTCTATCTGG	1303
1259	QY	ATGTTATATATATTCGGACTACTACAATCCCGTACCCCAAGAGGATCTTCCAGAGTGG	1318

Db	1304	TGGCTCTATTGAGATCAGCTTTAACGACGGTGAAGAGACACAGAAGCTAGAGTATCTGA	1363
Qy	1319	AGAGCGTTAACGAGAGATAAATTAGGTTTTCGCAAGGATTTCAGGTATTAAGATTAAAGCAAT	1378
Db	1364	AAGATCAGAACCGTCGGATCTTGGAGTTCTGTGACACAGCCAGATCAATGTGAAGCAGT	1423
Qy	1379	ATCTAATGCATTTATCTAGTAAAGAGATTGGATTGAGCATTTTGGATCAAAATGGGATG	1438
Db	1424	ATCTTCCTCACCCACGCAACACAGGAAGAGTGGTGGCTCATTTTGGGGACAAAGTGGGATC	1483
Qy	1439	ATTTTTCGAAGAGAGAAAGATCTATTTGATCCCAAGAACTGTTTATCTCCAGGGCAAGACA	1498
Db	1484	GGTTCAGAACTTAAGGCTGAGTTTGATCCGCGACACATACTCGCTACTGGTCAGAGAA	1543
Qy	1499	TCTTT 1503	
Db	1544	TCTTT 1548	

Search completed: April 7, 2004, 07:46:10  
 Job time : 620 secs





CC geotropism, leading to an increase in yield; and for screening growth  
 CC promoting chemical of herbicides (I) is useful for increasing the size  
 CC of the root meristem; increasing root size; increasing the size of the  
 CC shoot meristem; delaying leaf senescence and altering leaf senescence;  
 CC increasing leaf thickness; reducing or increasing the vessel size;  
 CC inducing parthenocarp; improving standability of the seedlings;  
 CC increasing branching and for improving lodging resistance. Antibody (III)  
 CC to (II) is useful for identifying and obtaining proteins interacting with  
 CC (II) comprising a screening assay, preferably a two-hybrid screening  
 CC assay. AAU81967-AAU81974 represent Arabidopsis thaliana cytokinin oxidase  
 CC amino acid sequences  
 XX  
 XX Sequence 501 AA;

Query Match 100.0%; Score 2596; DB 5; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-234;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANLRMLTITVLMITKSSNGIKIDLPKSLNLTSTDPISIIASAASHDFGNITVTPGV 60  
 DB 1 MANLRMLTITVLMITKSSNGIKIDLPKSLNLTSTDPISIIASAASHDFGNITVTPGV 60  
 QY 61 ICPSTADISRLQYAANGKSTFOVAARGOGHSLNGQASVSGGIVNMTCITDVVVSXDK 120  
 DB 61 ICPSTADISRLQYAANGKSTFOVAARGOGHSLNGQASVSGGIVNMTCITDVVVSXDK 120  
 QY 121 KYADVAAGTLWVDVLTXTAEKGVSPVSWTDYLTHTVGGTSLNGGIGQVFRNGPLVSNVL 180  
 DB 121 KYADVAAGTLWVDVLTXTAEKGVSPVSWTDYLTHTVGGTSLNGGIGQVFRNGPLVSNVL 180  
 QY 181 ELDVITGKEMLTCSRQLNPFLFYGLGQFGIITRARIIVLDHAPKAKWFRMLYSDF 240  
 DB 181 ELDVITGKEMLTCSRQLNPFLFYGLGQFGIITRARIIVLDHAPKAKWFRMLYSDF 240  
 QY 241 TTFKQERLISMANDIGVDYLEGQIFLSNGVWDTSPFPSPDQSKVADLVKQHGIIYVLE 300  
 DB 241 TTFKQERLISMANDIGVDYLEGQIFLSNGVWDTSPFPSPDQSKVADLVKQHGIIYVLE 300  
 QY 301 VAKYDDPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDLNRVHVEENKLSLGLWEL 360  
 DB 301 VAKYDDPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDLNRVHVEENKLSLGLWEL 360  
 QY 361 PHPWNLVYPKSRILDFHNGVVKDILLKQKASGLALLYPTNRKNWNRMSAMIPEIDED 420  
 DB 361 PHPWNLVYPKSRILDFHNGVVKDILLKQKASGLALLYPTNRKNWNRMSAMIPEIDED 420  
 QY 421 VIYIIGLLQSATPKDLPEVESVNEKIIRFCNDSGKIKOYLMHYTSKEDWIEHFGSKWDD 480  
 DB 421 VIYIIGLLQSATPKDLPEVESVNEKIIRFCNDSGKIKOYLMHYTSKEDWIEHFGSKWDD 480  
 QY 481 FSKRDLFPDKLLSPGQDIF 501  
 DB 481 FSKRDLFPDKLLSPGQDIF 501

RESULT 2  
 ABR63565  
 ID ABR63565 standard; protein; 501 AA.  
 XX  
 AC ABR63565;  
 XX  
 DT 18-SEP-2003 (first entry)  
 XX  
 DE Arabidopsis cytokinin oxidase AtCKX2.  
 XX  
 XX Maize; root growth; root geotropism; cytokinin oxidase; seed size;  
 KW embryo size; cotyledon size; transgenic plant; herbicide.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN WO2003050287-A2.  
 XX  
 PD 19-JUN-2003.

XX 10-DEC-2002; 2002WO-EP013990.  
 XX 10-DEC-2001; 2001US-00014101.  
 PR (SCHM/) SCHMULLING T.  
 PA (WERN/) WERNER T.  
 XX Schmullling T, Werner T;  
 XX WPI; 2003-541577/51.  
 XX  
 PT Stimulating root growth, enhancing lateral or adventitious root formation  
 PT or altering root geotropism comprises increasing plant cytokinin oxidase  
 PT levels or other protein or nucleic acid that reduces active cytokinins in  
 PT a plant.  
 XX  
 PS Example 2; Fig 2; 177pp; English.  
 CC  
 CC The present invention relates to a method for stimulating root growth or  
 CC enhancing the formation of lateral or adventitious roots or altering root  
 CC geotropism, which comprises increasing in a plant or plant part the level  
 CC of a plant cytokinin oxidase or other protein that reduces the level of  
 CC active cytokinins in a plant or plant part. Cytokinin oxidase protein and  
 CC coding sequences from Arabidopsis thaliana are also provided. The method  
 CC is useful in modifying plant morphological, biochemical and physiological  
 CC properties, such as in modifying the initiation, stimulation or  
 CC enhancement of root growth, adventitious root formation, lateral root  
 CC formation, root geotropism, shoot growth, apical dominance, branching,  
 CC timing of senescence, timing of flowering, flower formation, seed  
 CC development and/or seed yield. The present sequence is a protein shown in  
 CC the invention  
 XX  
 XX Sequence 501 AA;

Query Match 100.0%; Score 2596; DB 6; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-234;  
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANLRMLTITVLMITKSSNGIKIDLPKSLNLTSTDPISIIASAASHDFGNITVTPGV 60  
 DB 1 MANLRMLTITVLMITKSSNGIKIDLPKSLNLTSTDPISIIASAASHDFGNITVTPGV 60  
 QY 61 ICPSTADISRLQYAANGKSTFOVAARGOGHSLNGQASVSGGIVNMTCITDVVVSXDK 120  
 DB 61 ICPSTADISRLQYAANGKSTFOVAARGOGHSLNGQASVSGGIVNMTCITDVVVSXDK 120  
 QY 121 KYADVAAGTLWVDVLTXTAEKGVSPVSWTDYLTHTVGGTSLNGGIGQVFRNGPLVSNVL 180  
 DB 121 KYADVAAGTLWVDVLTXTAEKGVSPVSWTDYLTHTVGGTSLNGGIGQVFRNGPLVSNVL 180  
 QY 181 ELDVITGKEMLTCSRQLNPFLFYGLGQFGIITRARIIVLDHAPKAKWFRMLYSDF 240  
 DB 181 ELDVITGKEMLTCSRQLNPFLFYGLGQFGIITRARIIVLDHAPKAKWFRMLYSDF 240  
 QY 241 TTFKQERLISMANDIGVDYLEGQIFLSNGVWDTSPFPSPDQSKVADLVKQHGIIYVLE 300  
 DB 241 TTFKQERLISMANDIGVDYLEGQIFLSNGVWDTSPFPSPDQSKVADLVKQHGIIYVLE 300  
 QY 301 VAKYDDPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDLNRVHVEENKLSLGLWEL 360  
 DB 301 VAKYDDPNLPIISKVIDTLTKTSLYLPGFISMHDVAYFDLNRVHVEENKLSLGLWEL 360  
 QY 361 PHPWNLVYPKSRILDFHNGVVKDILLKQKASGLALLYPTNRKNWNRMSAMIPEIDED 420  
 DB 361 PHPWNLVYPKSRILDFHNGVVKDILLKQKASGLALLYPTNRKNWNRMSAMIPEIDED 420  
 QY 421 VIYIIGLLQSATPKDLPEVESVNEKIIRFCNDSGKIKOYLMHYTSKEDWIEHFGSKWDD 480  
 DB 421 VIYIIGLLQSATPKDLPEVESVNEKIIRFCNDSGKIKOYLMHYTSKEDWIEHFGSKWDD 480  
 QY 481 FSKRDLFPDKLLSPGQDIF 501  
 DB 481 FSKRDLFPDKLLSPGQDIF 501

Db 481 FSKRKDLFPDKKLLSPGQDIF 501

RESULT 3

ABR63569  
ID ABR63569 standard; protein; 501 AA.

XX ABR63569;

DT 18-SEP-2003 (first entry)

XX Arabidopsis cytokinin oxidase-like protein 2.

XX Maize; root growth; root geotropism; cytokinin oxidase; seed size;  
XX embryo size; cotyledon size; transgenic plant; herbicide.

XX Arabidopsis thaliana.

XX WO2003050287-A2.

XX 19-JUN-2003.

XX 10-DEC-2002; 2002WO-EP013990.

XX 10-DEC-2001; 2001US-00014101.

XX (SCHM/) SCHMULLING T.  
XX (WERN/) WERNER T.

XX Schumling T, Werner T;

XX WPI; 2003-541577/51.

XX N-PSDB; ACC85276.

PT Stimulating root growth, enhancing lateral or adventitious root formation  
PT or altering root geotropism comprises increasing plant cytokinin oxidase  
PT levels or other protein or nucleic acid that reduces active cytokinins in  
PT a plant.

PS Claim 19; Page 146-148; 177pp; English.

XX The present invention relates to a method for stimulating root growth or  
XX enhancing the formation of lateral or adventitious roots or altering root  
XX geotropism, which comprises increasing in a plant or plant part the level  
XX of a plant cytokinin oxidase or other protein that reduces the level of  
XX active cytokinins in a plant or plant part. Cytokinin oxidase protein and  
XX coding sequences from Arabidopsis thaliana are also provided. The method  
XX is useful in modifying plant morphological, biochemical and physiological  
XX properties, such as in modifying the initiation, stimulation or  
XX enhancement of root growth, adventitious root formation, lateral root  
XX formation, root geotropism, shoot growth, apical dominance, branching,  
XX timing of senescence, timing of flowering, flower formation, seed  
XX development and/or seed yield. The present sequence is a protein shown in  
XX the invention

SQ Sequence 501 AA;

Query Match 100.0%; Score 2596; DB 6; Length 501;  
Best Local Similarity 100.0%; Pred. No. 1.2e-234;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANLRMITLIIVLMTKSSNGIKIDLPKSNLTLSTDPISIASHDFGNITVTPGV 60

Db 1 MANLRMITLIIVLMTKSSNGIKIDLPKSNLTLSTDPISIASHDFGNITVTPGV 60

QY 61 ICFSTADISRLLQVAANGKSTFQVAARQQGSHLNGQASVSGGVIVNMTCTIDVVVSKDK 120

Db 61 ICFSTADISRLLQVAANGKSTFQVAARQQGSHLNGQASVSGGVIVNMTCTIDVVVSKDK 120

QY 121 KYADVAAGTLWDVLDLKTAEKGVPSVSWTDYLIHTVGGTSLNGGIGGVFRNGPLVSNVL 180

Db 121 KYADVAAGTLWDVLDLKTAEKGVPSVSWTDYLIHTVGGTSLNGGIGGVFRNGPLVSNVL 180

QY	181	ELDVITGKEMLTCSRQNLPELFYCVLGGLGQFGIITRARI	240
Db	181	ELDVITGKEMLTCSRQNLPELFYCVLGGLGQFGIITRARI	240
QY	241	TTFTKQERLISMANDIGDYLEGQIFLSNGVDTSPFP	300
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Db	361	PHPWNLVVPKSRILDFHNGVVKDILLKQKSASGLAL	420
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22

DE Arabidopsis thaliana protein fragment SEQ ID NO: 38445.  
 XX Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 XX Arabidopsis thaliana.

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RESULT 7
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DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38446.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; Genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PA	(WERNER/) WERNER T.			
XX	Schmullling T, Werner T;			
PI				
XX	WPI: 2003-541577/51.			
DR	N-FSDS; ACC85278.			
XX				
PT	Stimulating root growth, enhancing lateral or adventitious root formation			
PT	or altering root geotropism comprises increasing plant cytokinin oxidase			
PT	levels or other protein or nucleic acid that reduces active cytokinins in			
PT	a plant.			
XX				
PS	Claim 2; Page 154-156; 177pp; English.			
XX				
CC	The present invention relates to a method for stimulating root growth or			
CC	enhancing the formation of lateral or adventitious roots or altering root			
CC	geotropism, which comprises increasing in a plant or plant part the level			
CC	of a plant cytokinin oxidase or other protein that reduces the level of			
CC	active cytokinins in a plant or plant part. Cytokinin oxidase protein and			
CC	coding sequences from Arabidopsis thaliana are also provided. The method			
CC	is useful in modifying plant morphological, biochemical and physiological			
CC	properties, such as in modifying the initiation, stimulation or			
CC	enhancement of root growth, adventitious root formation, lateral root			
CC	formation, root geotropism, shoot growth, apical dominance, branching,			
CC	timing of senescence, timing of flowering, flower formation, seed			
CC	development and/or seed yield. The present sequence is a protein shown in			
CC	the invention			
XX				
SQ	Sequence 524 AA;			
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	Best Local Similarity 66.7%; Pred. No. 7.2e-162;			
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DB	69 CPSTTEVARLLRFANGGFSYNGKSTSPASTFKVAAGQGHSLRGQASAPGGVYNNMTCI 128			
QY	112 -----TDVVVSKDKKIVADVAAGTLVVDVLKKTAEKGVSPVSTDLHTVGGTSLNGGI 165			
DB	129 AMAAKPAAVVISADGTADYADAGTMVVDLKAADVDRGVSPVTWTDLYLSVGGTSLNAGI 188			
QY	166 GGOVFRNGPLVSNVLELDVITGEMLTCSRQNLNPELFYGLGGLGQFGIITRAIRVLDPH 225			
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QY	226 APKRAKWRMLYSDFTTFTTKDQRLISMANDIGVDVLEGOIFLNSGVWDTSPFPDQSK 285			
DB	249 APTRVKMSRIYSDFAFKRQDLISMTNDLGVDFLEGQLMNSGVFTSPFPDQTR 308			
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QY	346 HVEENKLSRLGLWELPFWLNLYPKSRILDFHNGVVKDILLKKQKASGLALLYPNRNK 405			
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XX Arabidopsis thaliana protein fragment SEQ ID NO: 37590.

XX Protein identification; signal transduction pathway; metabolic pathway;  
XX hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.

XX Arabidopsis thaliana.

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PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149829P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151066P.  
PR 30-AUG-1999; 99US-0151080P.  
PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155133P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 58.2%; Score 1511.5; DB 3; Length 400;

Best Local Similarity 69.8%; Pred. No. 7.1e-133;

Matches 279; Conservative 55; Mismatches 58; Indels 9; Gaps 3;

QY 108 MTCT-----TDVVSKDKKYADVAAGTLWVDYVKTKTAEGVSPVSWTDTLHITVGGTILS 161

DB 1 MTCLAAKPAAVVISADGTADVAAGTWWVDYKAAVDGRGVSPVTWTDTLYLSVGGTILS 60



Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences

PT from plant with nucleic acid or amino acid sequences from non-plant  
PT organisms.

XX  
XX  
PS Claim 5; SEQ ID NO 3059; 261bp + Sequence Listing; English.

XX  
CC The invention relates to identifying target proteins (ABB90790-ABB94016)  
CC for herbicidally active compounds, comprising aligning and comparing  
CC nucleic acid or amino acid sequences from plant with nucleic acid or  
CC amino acid sequences from non-plant organisms using suitable search  
CC parameters, where plant sequences having an E-value greater by a factor  
CC of 3 than the E-value of most similar non-plant sequences are selected.  
CC The polypeptides or nucleic acids encoding them are useful for  
CC identifying modulators. The identified modulators are useful as  
CC herbicides

XX  
SQ Sequence 523 AA;

Query Match 49.8%; Score 1292; DB 5; Length 523;  
Best Local Similarity 48.5%; Pred. No. 4.6e-112;  
Matches 251; Conservative 106; Mismatches 138; Indels 22; Gaps 6;  
QY 3 NLRMLTILIT--VLMITKSNIGIKIDLPKSLNL-----TLSTDPSIIISAASHDFGN 51  
DB 5 NLRSQVRLIAITVITIIITLSTPITNTSPQWNILSHNEFAGKLTSSSSVESAAATDFGH 64  
QY 52 ITTVPGGVICPSSPADISRLLOVAANGKSTFOVAARGQGHSLNGQASVSGGVVNMTCI 111  
DB 65 VIKIPPSAVLIPSSVEDITDIKLSFDSQSLPFAARGHSHRGQASAKDGVVVNMRSM 124  
QY 112 TD----VVVSKDKKYADVAAGTLWDLVLTAKGKSPVSWTDYLIHTVGGTSLNGGIGG 167  
DB 125 VNDRGIKVRKTCVLYVDAAMLWIEVLNKTLELTPVSWTDYLYLTVGGTSLNGGIGS 184  
QY 168 QVFRNGPLVSNVLELDVITKGEMLTCSRQNLNPELVGVLGQFGIITRARIWLDHAP 227  
DB 185 QTFRYGPQITNVLEMNDVITKGELATCATSKDNNSDLFFAVLGGQFGIITRARIKLEVP 244  
QY 228 KKAQWFRMLYSDFTTFTKQERLISMANDIGVDYLEGQIFLSNGVVD---TSFPFPPSDQS 284  
DB 245 KKAQWLRFLYIDFSEFTRDQERVISKTD--GVDFLEGSIMVDHGPPDNWRSTYPPSDHL 302  
QY 285 KVADLVKQHGIIYVLEVAKYIDDPNLPILSKVIDTLTKTSLYLPGLFISMHDVAYDFELNR 344  
DB 303 RIASVYKRRHVICYCLEVWKYIDETSOYTVNEEMEELSDSLNHVRGFMYEKDVITMDFLNR 362  
QY 345 VHVVENKRLSLGLWELPFWNLVYPKSRILDFHNGVVVKDILLKOKSASGLALLYPTNRN 404  
DB 363 VRTGELNLKSKQWDPVPHWNLVFPKTOISKFDGDFVKGIILRNITSGPVLVYPMNRN 422  
QY 405 KWDNRMSAMIPIDEDVYIIIGLQSATPKDLPEVESVNEKIIRCKDSGKIKIKOYLMMHY 464  
DB 423 KWNDRMSAAIPE--EDVFYAVGFLRSAGFDNWEAFDQENMEILKFCEDANMGVIOYLPYH 480  
QY 465 TSKEDMIEHFGSKWDDFSKRXKDLFDPKLLSPQDIF 501  
DB 481 SSGEGWVRHFGPRWNIFVERKYKYPDKMILSPQNIIF 517

Search completed: April 5, 2004, 17:44:10  
Job time : 62 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 5, 2004, 17:42:01 ; Search time 21 Seconds  
(without alignments)  
2294.855 Million cell updates/sec

Title: US-10-014-101-4  
Perfect score: 2596  
Sequence: 1 MANLRMLTITVLMITKSS.....SKKDLDFPKLLSPQDIP 501

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 78.\*

1: Piri.\*

2: Piri.\*

3: Piri.\*

4: Piri.\*

Pred. No. is the number of results predicted by chance to have a score Greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2579	99.3	515	2 E84577	probable cytokinin
2	1822	70.2	524	2 T09337	cytokinin oxidase
3	1152	44.4	534	2 T51329	cytokinin oxidase
4	1141	44.0	534	2 T01500	cytokinin oxidase
5	1079	41.6	512	2 B96785	hypothetical prote
6	1056.5	40.7	575	2 T00807	probable cytokinin
7	993	38.3	504	2 T49185	cytokinin oxidase-
8	567.5	21.9	438	2 B55578	hypothetical prote
9	429	16.5	447	2 AC1947	hypothetical prote
10	196.5	7.6	470	2 H70795	hypothetical prote
11	196	7.6	479	2 B95997	probable oxidoredu
12	195	7.5	511	2 T48777	6-HYDROXY-D-NICOTI
13	190	7.3	466	2 T49756	related to berber
14	183.5	7.1	459	2 A87201	conserved hypothet
15	177.5	6.8	610	2 T06690	galactonolactone d
16	177	6.8	445	2 T35893	FAD-dependent oxid
17	177	6.8	461	2 H69350	galactonolactone d
18	175.5	6.8	600	2 T14463	galactonolactone d
19	175	6.7	460	2 B68322	probable FAD-link
20	173.5	6.7	466	2 B69842	probable oxidoredu
21	172.5	6.6	461	2 B70697	probable oxidoredu
22	168.5	6.5	539	2 T10626	reticuline oxidase
23	168	6.5	440	1 OXRTGU	L-gulonolactone ox
24	167.5	6.5	461	2 A70687	probable oxidoredu
25	164	6.3	470	2 D69984	galactate oxidase
26	161.5	6.2	540	2 T10625	reticuline oxidase
27	161	6.2	447	2 G70034	reticuline oxidase
28	159	6.1	535	2 T07969	probable reticul
29	154.5	6.0	482	2 C70452	D-lactate dehydrog

mcrA protein - Str  
FAD/FMN-containing  
hypothetical prote  
probable oxidoredu  
hypothetical prote  
D-lactate dehydrog  
hypothetical prote  
D-lactate dehydrog  
reticuline oxidase  
probable sorbitol  
probable oxidase  
probable oxidase  
conserved hypothet  
hypothetical prote  
probable iron-sulf  
probable oxidoredu

30 153.5 5.9 448 2 A55519  
31 152 5.9 467 2 B97213  
32 151.5 5.8 455 2 G81868  
33 150.5 5.8 455 2 A70753  
34 150 5.8 456 2 AC3361  
35 150 5.8 468 2 A13326  
36 150 5.8 530 2 T10628  
37 149.5 5.8 461 2 F82819  
38 149 5.7 538 2 A41533  
39 148 5.7 418 2 T34660  
40 148 5.7 1018 2 B90928  
41 148 5.7 1018 2 F85776  
42 148 5.7 1018 2 AG0703  
43 147 5.7 1000 2 S74069  
44 147 5.7 1018 2 G64926  
45 146.5 5.6 479 2 H70847

## ALIGNMENTS

### RESULT 1

E84577  
probable cytokinin oxidase [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 19-Apr-2002  
C:Accession: E84577  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N  
euss, D.; Nierman, W.C.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.;  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: E84577  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-515 <STO>  
A:Cross-references: GB:AE002093; NID:G4191780; PIDN:AA10149.1; GSPDB:GNC0139  
C:Genetics:  
A:Gene: Ac2g19500  
A:Map position: 2  
C:Superfamily: poppy reticuline oxidase

Query Match	Score	2579	DB 2	Length	515
Best Local Similarity	97.3%	Pred. No.	2e-172	Indels	14
Matches	501	Conservative	0	Mismatches	0
Qy	1	MANLRMLTITVLMITKSSNGIKIDLPKSLNLTSTDPSSIISAASHDFGNITVTTPGGV	60		
Db	1	MANLRMLTITVLMITKSSNGIKIDLPKSLNLTSTDPSSIISAASHDFGNITVTTPGGV	60		
Qy	61	ICPSSSTADISRLLOVAANGKSTFQVAARGQSHLNGQASVSGGVVNMTCITDVVVSXDK	120		
Db	61	ICPSSSTADISRLLOVAANGKSTFQVAARGQSHLNGQASVSGGVVNMTCITDVVVSXDK	120		
Qy	121	KYADVAAGTLWVDVLKKTAEKGVSPVSWTDYLIHTVGGTSLNGGIGGOVFRNGPLVSNVL	180		
Db	121	KYADVAAGTLWVDVLKKTAEKGVSPVSWTDYLIHTVGGTSLNGGIGGOVFRNGPLVSNVL	180		
Qy	181	ELDVIITKGEMLTCSQLNPFLFYGLGLGQFGIITRARIIVLDHAPKAKWFRMLYSDF	240		
Db	181	ELDVIITKGEMLTCSQLNPFLFYGLGLGQFGIITRARIIVLDHAPKAKWFRMLYSDF	240		
Qy	241	TTTKDQOEKLISWANDIGVDYLEGQIFLSNGVVDTSFPPPSQSKVADLVKQHGIIYVLE	300		
Db	241	TTTKDQOEKLISWANDIGVDYLEGQIFLSNGVVDTSFPPPSQSKVADLVKQHGIIYVLE	300		
Qy	301	VAKYDDPNLPITISKVIDTLTKTSLYLPQFISMHDVAVFDFLNRVHVEENKLSRLGLWEL	360		
Db	301	VAKYDDPNLPITISKVIDTLTKTSLYLPQFISMHDVAVFDFLNRVHVEENKLSRLGLWEL	360		
Qy	361	PHPLWMLNLYPKGRILDFFHNGVVKDILLKOKSASGLALIYPNNR	406		

Db 361 PPHWLNLYVPSKRIIDFHNGVVKDILLKQKSGASGLALLYPTRNRKYILLFTHIYLQEPKW 420  
QY 407 DNRMSAMPEIDEDVYIIGLQSTPKDLPEVESVNEKIIRFCCKDSGKIKQVLMHYTS 466  
Db 421 DNRMSAMPEIDEDVYIIGLQSTPKDLPEVESVNEKIIRFCCKDSGKIKQVLMHYTS 480  
QY 467 KEDWIEHFGSKWDDFSKRDLPDPKLLSPGQDIF 501  
Db 481 KEDWIEHFGSKWDDFSKRDLPDPKLLSPGQDIF 515  
RESULT 2  
T09937  
cytokinin oxidase homolog T1614.250 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jun-2002  
C:Accession: T09937  
R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.  
submitted to the Protein Sequence Database, June 1999  
A:Reference number: Z16897  
A:Accession: T09937  
A:Molecule type: DNA  
A:Residues: 1-524 <REV>  
A:Cross-references: EMBL:AL079344; GSPDB:GNC0062; ATSP:T1614.250  
A:Experimental source: cultivar Columbia; BAC clone T1614  
C:Genetics:  
A:Gene: ATSP:T1614.250  
A:Map position: 4  
A:Introns: 210/1; 252/3; 338/3; 428/2  
Query Match 70.2%; Score 1822; DB 2; Length 524;  
Best Local Similarity 66.7%; Pred. No. 1.7e-119; Indels 24; Gaps 5;  
Matches 345; Conservative 69; Mismatches 79; Indels 24; Gaps 5;  
QY 7 MITLIIVLM-----ITKSSNGIKIDLPKSNLTSTDPSSIISAASHDFGNITVTPGGVI 61  
Db 9 LITLITLISLTPLIKSDEGIDVPLPISLNTLTDPSSIISAASHDFGNITDENPGAVL 68  
QY 62 CPSSTADISRLLOYAANG-----KSTQVAARGGSHLSNGOASVGGVIVNMTCI 111  
Db 69 CPSSTTEVARLLRFANGGFSYNGKSTSPASTFKVAARGGSHLSNGOASVGGVIVNMTCL 128  
QY 112 -----TDVVVSKDKKYADVAAGTLMDVVLKKTAEKGVSPVSWTDYLTITVGGTILSNGGI 165  
Db 129 AMAAKPAANVISADGYADVAAGTMVDVLKAAVDRGSPVWTDYLTITVGGTILSNGAI 188  
QY 166 GGQVFRNGPLVSNVLELDVITGKEMLTCSRQNLNPELFGVGLGQFGIITRAIRIVLDH 225  
Db 189 GGQTFRRGQISNVHLELDVITGKEMMTCSKLNPELFGVGLGQFGIITRAIRIALDH 248  
QY 226 APKRAXWFMRLYSDFTFTKQDQRLISMANDIGVDYLEGOIFLSNGVWDTSPFPSPDSQSK 285  
Db 249 APTRVKSRILYSDFAFRKQDQRLISMNDIGVDLEGLQMLMSNGFVDTSPFLSDQTR 308  
QY 286 VADLVKQHGIIYVLEVAKYDDNPLFIISKVIDTLTKLSYLPFGFISMHDVAYFDFLNRV 345  
Db 309 VASLVNDHRIIYVLEVAKYDRTTLPIIDQVIDTLGRTLGAPGFNFVQDVPYDFLNRV 368  
QY 346 HVSEKLRSLGLWELPHPLNLYVPSKRIIDFHNGVVKDILLKQKSGASGLALLYPTRNRNK 405  
Db 369 RNEEDKLRSLGLWELPHPLNLYVPSKRIIDFHNGVVKDILLKQKSGASGLALLYPTRNRNK 428  
QY 406 WDNRMASAMPEIDEDVYIIGLQSA-TPKDLPEVESVNEKIIRFCCKDSGKIKQVLMHY 464  
Db 429 WNNRMSWTMT--DEDVYVIGLQSAAGSQNWQLENLNDKVQFCENSGIKIKEYIMHY 486  
QY 465 TSKEDWIEHFGSKWDDFSKRDLPDPKLLSPGQDIF 501  
Db 487 TRKEDWVYKHFGPKWDDFLRRKIMFDPKRLLLSPGQDIF 523

RESULT 3  
T51929

cytokinin oxidase [imported] - maize  
C:Species: Zea mays (maize)  
C:Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 20-Oct-2000  
C:Accession: T51929  
R:Houba-Herlin, N.; Pethe, C.; D'Alayer, J.; Laloue, M.  
Plant J. 17, 615-626, 1999  
A:Title: Cytokinin oxidase from Zea mays : purification, cDNA cloning and expression in  
A:Reference number: Z25869  
A:Accession: T51929  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-534 <HOU>  
A:Cross-references: EMBL:Y18377; PIDN:CAA77151.1  
A:Experimental source: cultivar mobilis  
C:Genetics:  
A:Gene: cko  
Query Match 44.4%; Score 1152; DB 2; Length 534;  
Best Local Similarity 47.4%; Pred. No. 1.1e-72;  
Matches 235; Conservative 84; Mismatches 149; Indels 28; Gaps 11;  
QY 30 SLNLTSTDPSSIISAASHDFGNITVTPGGVTCPSSTADISRLLOVAANGKS--TFQVAA 87  
Db 42 ALDGLKRTDSNATAAASATDFGNITSPALPAVLPSPSTADLVALLS-AANSTFGWPYTIAP 100  
QY 88 RGQGHSLNGOASVGGVIVNMTCIID-----VVVSKDKKYADVAAGTLMDVVLKKTAEK 141  
Db 101 RGRGHSILMGQAFAPGPGVNVNNSLGDAAAPPRINVSADGRYVDAGGEQVWIDVLRASLAR 160  
QY 142 GVSPVSWTDYLTITVGGTILSNGIGQVFRNGPLVSNVLELDVITGKEMLTCSRQNLNPE 201  
Db 161 GVAPRSWTDYLTITVGGTILSNGISGQAPRHPQISNVLEMDVITGHGEMVTCSKQLNAD 220  
QY 202 LFGVGLGQFGIITRAIRIVLDHAPKAWFMRLYSDFTFTKQDQRLISMANDIG--- 258  
Db 221 LFDVAVGLGQFGVITRAIRIVPEPAPARAWRLVITDFAFSAQDQRLTAPRPGGGGAS 280  
QY 259 ---VDYLEGQIF---LSNGVWDTSPFPSPDSQSKVADLVKQHG--IYVLEVAKYDDPN 309  
Db 281 FGPMSYVEGVSFVFNQSLATDLANTGFTDADVARIVALAGERNATTVYSIEATLNYDNAT 340  
QY 310 --LPIISKVTDLTITLSYLPFGFISMHDVAYFDFLNRVHVEENKLSLGLWELPHPLNLY 367  
Db 341 AAAAADVQELASVLGTLTSYVEGFAFQDVAAYAFDLRVHGEVALNKLGLWVRPHPLNLM 400  
QY 368 YVPSKRIIDFHNGVVKDILLKQKSGASGLALLYPTRNRKNDRMSAMPEIDEDVYIIGL 427  
Db 401 FVPSRIADFDRGVFKGI-LQGTDIVGLVYPLNKSMDGMSAATP--SEDFVYAVSL 457  
QY 428 L-QSATPKDLPEVESVNEKIIRFCCKDSGKIKQVLMHYTSKEDWIEHFG-SKWDDFSKRX 485  
Db 458 LFSSVAPNDLARLQEQNRRIILFCDLAGIQYKTYLARHTDRSDVVRHFGAAKWRNFVEMK 517  
QY 486 LDFDPKLLSPGQDIF 501  
Db 518 NKYPDKRLLLSPGQDIF 533  
RESULT 4  
T01500  
cytokinin oxidase 1 - maize  
C:Species: Zea mays (maize)  
C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 29-Oct-1999  
C:Accession: T01500  
R:Morris, R.O.; Laskey, J.G.  
submitted to the EMBL Data Library, January 1998  
A:Description: A glycosylated cytokinin oxidase from maize.  
A:Reference number: Z14336  
A:Accession: T01500  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-534 <MOR>  
A:Cross-references: EMBL:AF044603; NID:G3341977; PIDN:AAC27500.1; PID:G3341978



C;Genetics:  
A;Gene: cck1  
A;Introns: 206/1; 437/2

Query Match 44.0%; Score 1141; DB 2; Length 534;  
Best Local Similarity 47.0%; Pred. No. 6.5e-72;  
Matches 233; Conservative 83; Mismatches 152; Indels 28; Gaps 11;

QY 30 SINLTSLDPSIIISAASHDFGNIITVTPGGVICPSSSTADISRLQYAANGKS--TFQVAA 87  
DB 42 ALDQKLRDTSNATAAATDFGNIISALPAAYVSSSTGDLVALLS--AANSTPGWPIYIAF 100  
QY 88 RQGHSLNGQASVSGVIVNMTCTD-----VVSKDKKYADVAAGTLVWDVLKTAEX 141  
DB 101 RGRGHSIMGQAFAPGGVVVNMASLGDAAAAPRINVSADGRVYDAGGEQWIDVLRASLAR 160  
QY 142 GVSFVSMTDYLHIITVGGTSLNGGTGGQVFRNGPLVSNVLELDVITGKEMLTCSRQNP 201  
DB 161 GVAPRSWMDYLYLTVGGTSLNAGISGQAFRHPGQPLSNVLEMDVITGHEMTVCSKQLNAD 220  
QY 202 LFYGVGLGGIOPGIIITRARIIVLDHAPKRAKFRMLYSDFTTFTKQDERLISMANDIG--- 258  
DB 221 LFDVAVLGGIOPGVIITRARIIVAPAPARARVRYVYTFDAAFSAQDERLTAPRPGGGGAS 280  
QY 259 ---VDYLEGOIF-----LSNGVVDTSFPPSDOSKVADLVKQHG--IIIVLEVAKYDDPN 309  
DB 281 FQPMYSYVSGSVFNQSLATDLANTGFFTDADVARIVLAGERNATTVYSIEATLYNDAT 340  
QY 310 --LPIISKVIDTLTKTSLYLPGLFISMDHVAYDFLNRVHVVENKLSRLSGLMELPHELPLNL 367  
DB 341 AAAAVDQELASVGLTSLVSEGFARQDVAAFLDRVHGEVALNKLGLRVEPHELPLNM 400  
QY 368 YVPKGRILDFHNGVKDIIILKQKASGLALLYPTNRKNWDMNSAMIPEIDEDVIYIIGL 427  
DB 401 FVPSRIADFRGVFKGI--LOGTDIVGPIVPLNKSMMWDDGMSAATP--SEDVYAYVSL 457  
QY 428 L-QSATPKDLPEVESNEXIIIFKDSGIIKQYIMHYTSKEDWIEHFG-SKWDDFSKRX 485  
DB 458 LFSVAPNDLALQEQNRILAFCDLAGIQYKTYLARHTDRSDWVHRGAARFVEMK 517  
QY 486 DLFPDKKLLSPQDIF 501  
DB 518 NKYDPKRLSLSPQDIF 533

RESULT 5  
B96785  
hypothetical protein F1B16.2 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana [mouse-ear cress]  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C;Accession: B96785  
R;Theologos, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A;Reference number: A86141; MUID:21016719; PMID:11130712  
A;Accession: B96785  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-512 <STO>  
A;Cross-references: GB:AE005173; NID:gl0120443; PIDN:AAG13068.1; GSPDB:GN00141  
C;Genetics:  
A;Gene: F1B16.2  
A;Map position: 1

Query Match 41.6%; Score 1079; DB 2; Length 512;  
Best Local Similarity 45.7%; Pred. No. 1.3e-67;

Matches 218; Conservative 80; Mismatches 137; Indels 42; Gaps 8;  
QY 39 PSIISAASHDFGNI--TTVTPGGVICPSSSTADISRLQYAANGKSTFQVAAARQGHSLNGQ 97  
DB 44 PDLASVSSDFGMLKSPPEPLAVLHPSSAEDVARLVRTAYGSATAPFVSARGHGSINGQ 103  
QY 98 ASVS--GGVIVNM-----TCITDVVSKDKKYADVAAGTLVWDVLKTAEGKSVSWTDYL 152  
DB 104 AAGRNGVVMENHGVGTGTPKPLVRPDEMIVDVGELMVDVLKKTLEHGLAPKSWTDYL 163  
QY 153 HITVGGTSLNGGTGGQVFRNGPLVSNVLELDVITGKEMLTCSRQNPFLVGVGLGQ 212  
DB 164 YLTVGGTSLNAGISGQAFHGFQISNVLELDVIT-----GQ 199  
QY 213 FGIITRARIIVLDHAPKRAKFRMLYSDFTTFTKQDERLISMANDIGVYLEGOIFSLNGV 272  
DB 200 FGIITRARIISLEPAPQVRVIRVLYSSPKVFTDEOBYLISMHGQLKDFYVEGVIVDEGL 259  
QY 273 VD---TSFPPSDOSKVADLVKQHGIIIVLEVAKYDDNPLPIISKVIDTLTKTSLYLP 329  
DB 260 VNNRSFSPRPVFKISSVSSNGSVLYCLETKNVDSDSEIVDOEVLMMKLNFIPT 319  
QY 330 FISMDHVAYDFLNRVHVVENKLSRLSGLMELPHELPLNLVYPKSRILDPHNGVVKOILLKQ 389  
DB 320 SVFTDLQYVDFLDRVHKAELKLSKNLMEVPHPLNLFVPKSRISDFDKGVFKGIL--G 377  
QY 390 KSASGLALLYPTNRKNWDMNSAMIPEIDEDVIYIIGLQSA-----TPKDLPEVESVNE 444  
DB 378 NKTSGFILIYPMKDKWDRSSAVTP--DEEVILVALLRSALTDEGEETQKLEYLKDQNR 435  
QY 445 KIIRFKDSGIIKQYIMHYTSKEDWIEHFGSKWDDFSKRDLPKPKLLSPQDIF 501  
DB 436 RILEFCEQAKINVKQYLPHPHATQEEVVAHFGDKWDRFSRLKAEFDPRHILATGQRI 492

RESULT 6  
T00807  
probable cytochrome oxidase [imported] - Arabidopsis thaliana  
N;Alternate names: cytochrome oxidase protein T32G6.3  
C;Species: Arabidopsis thaliana [mouse-ear cress]  
C;Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 02-Aug-2002  
C;Accession: T00807; F84842  
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,  
submitted to the EMBL Data Library, November 1997  
A;Description: Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence.  
A;Reference number: 214163  
A;Accession: T00807  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-575 <ROU>  
A;Cross-references: EMBL:AC002510; NID:g2618683; PID:g2618686  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; I,  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: F84842  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-575 <STO>  
A;Cross-references: GB:AE002093; NID:g2618686; PIDN:AA84333.1; GSPDB:GN00139  
C;Genetics:  
A;Gene: T32G6.3; At2g941510  
A;Map position: 2  
A;Introns: 223/1; 265/3; 352/3; 440/2  
C;Superfamily: poppy reticuline oxidase

Query Match 40.7%; Score 1056.5; DB 2; Length 575;  
Best Local Similarity 39.8%; Pred. No. 5.9e-66;  
Matches 213; Conservative 102; Mismatches 167; Indels 53; Gaps 12;

118 QKLQVSVDSPPVYVDSGGELWNLNHLHETLKYGLAPKSWTDYHLTVGGTSLNAGISGQ 177

169 VPRNGPLVSNVLELDVITGKGMELTCSQLNPFLFYGLGLGQFGIITRARIVLDAHAK 228

178 APRHGPOISNVHQLIEIVTGKEILNCTKRONSDLFNGVLGLGQFGIITRARIAPAP- 236

229 RAKWFMILYSDFTFTKDOERLISMANDIGVDYLEGQIFLS-NGVVDI--SFFPPSDQS 284

237 -----TMDQELIS-AQGHKFDYIEGFVIINRTGLNWRSLF--TAREP 278

285 KVADLVKQHG-IIVYLEVAKYDDPNLPIISKVIDTLTKTSLYLPFGFSMDHVDAYFDL 343

279 LEASQFKDGRGLYCLELAKYLKQDNKVINQEVKETLSLSYVTSTLTFTTEVAYEAFD 338

344 RVHVENKLRSUGLWELPHEPMLNLYVPKSRILDFHGVVKKIILLKQKASGLALLYPNR 403

339 RVHSEVKLRSQGWEPHEPMLNLYVPRKINEFARGVFGNLL--TDTSGNGPVIVYPVK 396

404 NKWDNRMSAMIEIDEDVDYIIGLQSATP-----KD-LPEVESVNEKIRFCQDSGIK 458

397 SKWDNQTSATPE--EEFYLVAITLSASPGSAGDGVEEILRRNRRLERFSEBAGIGLK 454

459 QYLMYHTSKEDWIEHFGSKWDDFSKRXKOLFDPKLLSPGQDIF 501

455 QYLPHYTTREWRSHFGDKWGFVRKRSRYDPLAILAFGHRIF 497

RESULT 8

E55578

hypothetical protein (ipt 3' region) - Rhodococcus fascians plasmid pFid188

C/Species: Rhodococcus fascians

C/Date: 25-Aug-1995 #sequence\_revision 25-Aug-1995 #text\_change 22-Oct-1999

C/Accession: E55578; S42056

R/Crespi, M.; Vareaecke, D.; Temmerman, W.; Van Montagu, M.; Desomer, J.

J. Bacteriol. 176, 2492-2501, 1994

A/Title: The fas operon of Rhodococcus fascians encodes new genes required for efficient

A/Reference number: A55578; MUID:94222824; PMID:8169198

A/Accession: E55578

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-438 <CRE>

A/Cross-references: EMBL:229635; NID:g455000; PIDN:CAA82745.1; PID:g455005

A/Note: the sequences of residues 107-124 and 126-142 are interchanged in the authors' t

C/Genetics:

A/Genome: plasmid

Query March 21.9%; Score 567.5; DB 2; Length 438;

Best Local Similarity 33.0%; Pred. No. 5.8e-32;

Matches 153; Conservative 65; Mismatches 205; Indels 41; Gaps 10;

QY 37 TDSIISAASHDFGNITTTVTPGVI CPSTADISRLLOYAANGKSTFOVAAACQGHSLNG 96

DB 7 TDDVHLTSAAGDFGNCITHAKPPVYVPTVADYQEAALRYTA--ARNLSLAVRSGSHSTYG 64

QY 97 QASVSGGVIVNM--TCITDVVYSKDKYADVAAGTLWVDVLKKTAEKGVSPVSWTDYLH 153

DB 65 QCAQAGGVVLDMKRFNTVHVDVRSQ-----ATIDAGVRWSDVVAATLSRQQTTPVLTDLG 120

QY 154 ITVGGTSLNGGIGQVFRNGPLVSNVLELDVITGKGMELTCSQLNPFLFYGLGLGQF 213

DB 121 TTVGGTSLVGGFGSGSHGFLQTDNDVSLAVVTGSDFRECSAVSSELEFDAYRGLGQF 180

QY 214 GIITRARIVLDAHAKWFRMLYSDFTFTKQOERLISMANDIGVDYLEGQIFLSNGV 273

DB 181 GVIYNATIRITAAHESVRQKLVSNLGVFLGQQLR--AMSNRL-FDHVGRIRVD---- 233

QY 274 DTSFPFPPSDQSKVADLVKQHGIIIVYLEVAKYDDPNLPIISKVIDTLTKTSLYLPFGISM 333

DB 234 -----AD-----GHLAYRLDLAKYFTPPRP-----DDDALSSLYQDSCAEYN 272

QY 334 HDVAYDFPLNRVHVEENKLSGLWELPHEPMLNLYVPKSRILDFHGVVKKIILLKQKAS 393

DB 273 SDVDYGDGFIRNMAQDELDRHTGWFPHPWASLLIPADKIEQFIE-TTSSSLTDDLGN 331

QY 394 GLALLPTNKNWNRMSAMIPEDIEDVYIIGLLQSAPKDLPEVESNEKILRECKDS 453  
 Db 332 GLIMVYPIPTP---ITAPPPIPHCDTTFMLAVLRTASGAEARMASNRLLYEOARDV 388  
 QY 454 GIKIKOYLHYMTSKEDWIEHFGSKWDDFSKRDLPDKKLLSPG 497  
 Db 389 GGVAAYAVNVPSPGDWCTHFGSRWQALABAKRRFPDYRLAPG 432  
 RESULT 9  
 AC1847  
 hypothetical protein all0324 [imported] - Nostoc sp. (strain PCC 7120)  
 C:Species: Nostoc sp. PCC 7120  
 A:Note: Nostoc sp. Strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002  
 C:Accession: AC1847  
 R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
 Nakazaki, N.; Shimoto, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.  
 DNA Res. 8, 205-213, 2001  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
 A:Reference number: AB1807; MUID:21595285; PMID:11759840  
 A:Accession: AC1847  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-447 <KUR>  
 A:Cross-references: GB:BA000019; PIDN:BAB72282.1; PID:g17129669; GSPDB:GN00179  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: all0324  
 Query Match 16.5%; Score 429; DB 2; Length 447;  
 Best Local Similarity 27.0%; Pred. No. 2.8e-22;  
 Matches 131; Conservative 81; Mismatches 192; Indels 82; Gaps 18;  
 QY 38 DPSIISAASHDFGNITVTPGGVCPSTADISRLLOYAANGKSTFOVAARGOCHSLNGQ 97  
 Db 16 DQSVISVITDFGSLIKNTLGIIRPHNLESLALRFAP--QQNLKARGKGYTOGGQ 73  
 QY 98 ASVSGGVVNMTCITDVVVSXDKKYAD---VAAGTLWVDLTKTAEGVSPVSWTDYLHI 154  
 Db 74 SVAQDAFTLDLRLNH--VSKVDTVAQAIATEAGATWQDIVTTTKYGMPLPCVLPFLNLEQ 131  
 QY 155 TVGGTLNNGGIGGQVFRNGPLVSNVLELDVITGKEMLTCSRQLNPFLFYGLVGLGQFG 214  
 Db 132 TVGGLLSTGGIGSTKTYGPPVAVNIDLIHTNGEYIQCSTQTPEDYHVLVGLGCG 191  
 QY 215 IITRARIIVLDHAPKAKFRMLYSDFTTFKDQERLISVANDIGVDYLEGQIFLS-NGVV 273  
 Db 192 VTASATLALRKTYYRTFHLLYDSLKPWMDH---IFLGRNHQIHLLEGFCWTSAGKIR 248  
 QY 274 DTS-----FPPSDQSKVADLVKQHGIIIVLEKAYDDPNLPIISKVIDTITKTLVILPG 329  
 Db 249 HTTSKKKFF-----AHW-LYGLQVGIEYDEV-APSASDV----- 280  
 QY 330 FTSMDHVAEYDFLNRVHEENK-----LRLSLGWELPHEPMLNLYVPKSRIL 375  
 Db 281 ----LHDLNTRWLF---HTEDETSHVFRYQPRFEWMTSGANQAHWIECFISAEALA 334  
 QY 376 DFHNGVVKDILKQKSASGALLYPTNRKNKDNRSAMIPEIDEDVIYIIGLLQSATP-- 433  
 Db 335 EVLPETLDMPLSLGDGHRAIMVAPDNLFN-----LFWMPFAKN--ILCFAILPMAVPE 387  
 QY 434 --KDLPEVESNEKILRFCKDSGIKIKOYLHYMTSKE--DMTEHFGSKWDDFSKRDLPD 489  
 Db 388 DFKTFDVLSEKVNQLLR---AGG---KRYLSGLWGLSKSNFDMRQHYGTSYKWTWTKQYD 441  
 QY 490 PKKLLS 495  
 Db 442 PSHVLS 447  
 RESULT 10

H70795  
 hypothetical protein RV3719 - Mycobacterium tuberculosis (strain H37RV)  
 C:Species: Mycobacterium tuberculosis  
 C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
 C:Accession: H70795  
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;  
 Connor, R.; Davies, R.; Devlin, K.; Feldwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.;  
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
 Nature 393, 537-544, 1998  
 A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
 A:Reference number: A70500; MUID:98295987; PMID:9634230  
 A:Accession: H70795  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-470 <COL>  
 A:Cross-references: GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA18041.1; PID:el264575  
 A:Experimental source: strain H37RV  
 C:Genetics:  
 A:Gene: RV3719  
 Query Match 7.6%; Score 196.5; DB 2; Length 470;  
 Best Local Similarity 30.6%; Pred. No. 5.4e-06;  
 Matches 57; Conservative 31; Mismatches 91; Indels 7; Gaps 3;  
 QY 111 ITDYY-VSKDKYADVAAGTLWVDLTKTAEGVSPVSWTDYLHITVGGTSLNNGIGGQV 169  
 Db 69 LTGVIGIDPEARTADVAGMCTYEDLIAATLHYGLSPLVVPQLRTITLGGAVTGLIESAS 128  
 QY 170 FRNGPLVSNVLELDVITGKEMLTCSRQLNPFLFYGLVGLGQFGIITRARIIVLDHAPKR 229  
 Db 129 FRNGPLHESVLEMDILTGCAGELLTVSPGQHSDLVRAFPNSYGLTGYSTRILRIQLFVRPP 188  
 QY 230 AKWFRMLYSDFTTFKDQERLISVANDIG--VDYLEGQIFLSNGVVDTSPFPSPQSKVA 287  
 Db 189 VALRHIFRFSLLTAMVAAMERIITDGLDGSVDYLDGVVFS-----DSYLCIGNQTSVP 244  
 QY 288 DLVKOH 293  
 Db 245 GPVSDY 250  
 RESULT 11  
 B95997  
 probable oxidoreductase, oxygen dependent, FAD-dependent protein (EC 1.5.3.-) [imported]  
 C:Species: Sinorhizobium meliloti  
 C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 30-Sep-2001  
 C:Accession: B95997  
 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernanc  
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
 A:Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing endo  
 A:Reference number: A95842; MUID:21396508; PMID:11481431  
 A:Accession: B95997  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-479 <KUR>  
 A:Cross-references: GB:AL591985; PIDN:CAC49642.1; PID:g15141129; GSPDB:GN00167  
 A:Experimental source: strain 1021, megaplasmid pSymB  
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
 Pels, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
 L.; Hyman, R.W.; Jones, T.  
 Science 293, 668-672, 2001  
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kise, B.; Komp, C.; Lelaure,  
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.  
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
 A:Reference number: A96039; MUID:21368234; PMID:11474104  
 A:Contents: annotation  
 C:Genetics:  
 A:Gene: SMB21415  
 A:Genome: plasmid  
 C:Keywords: oxidoreductase  
 Query Match 7.6%; Score 196; DB 2; Length 479;

```

Best Local Similarity   27.4%, Pred. No. 6e-06;
Matches 62; Conservative 45; Mismatches 91; Indels 28; Gaps 7;

Qy      1 MANLRMLTITLVLM-----TKSNGIKIDLPKSLNLTSTDPSSIISAASHDFGNITTVP 57
       :|::||::|
Db      6 LTNLQSITWVSAAIIEAFTARLG-----RVLVATDAAYDEARTIWNGMIDR-RP 55

Qy     58 GGVICPSSTADISRLLOYANGSKTFVOAARGOCHSLNGOASVSGGVIVNMTCITDVVV 117
       :|::||::|
Db     56 GLIVOCAGAADVNVAFFAA--ENQLLVAVRGGGHNIAGNAVCDGGWVIDLTPMKSVRVD 113

Qy    118 KDKKIYADVAAAGTLWVDVLKKT-----AEKGVSFVSWTDYLHITVGGLGQFGVF 171
       :|::||::|
Db    114 ATTKTAWEPCATLADIMETQAFLALPTGIN--STTGIAGLTLG-----GGFGWITRK 166

Qy    172 NGPLVSNVLDELVTGTGEMLTCSRQLNPFLFYGLGGLGQFGIIT 217
       :|::||::|
Db    167 FGIIDNLLEADVVVANGELVRASPTEHRDLFWAIRGGGNGFVVVT 212

RESULT 12
T48777
6-HYDROXY-D-NICOTINE OXIDASE related protein [imported] - Neurospora crassa
N;Alternate names: protein I3E11.250
C;Species: Neurospora crassa
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Aug-2002
C;Accession: T48777
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24541
A;Accession: T48777
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-511 <SCH>
A;Cross-references: EMBL:AL353820; GSPDB:GN00112; NCSP:I3E11.250
A;Experimental source: cosmid contig I3E11; strain 74
C;Genetics:
A;Gene: NCSP:I3E11.250
A;Map position: 2
A;Introns: 32/3
C;Superfamily: poppy reticuline oxidase

```

[illegible]

```

QY 423 -----YI-----IGLQSTPPKDLPEV--- 439
      | : | | | | | | | | | | | | | |
Db 371 LWODHYERLIAAANGTAVTPYLAQRAIPNLVKAMEVNGNALGLKQSDGPLEMLIQVAAQ 430
      | : | | | | | | | | | | | | | |
QY 440 -----ESVNEKIIIRFCXDSGIGIKIQYLMHYT-SKEDWIEHFGSKWDDFSKR 484
      | | | | | | | | | | | | | | | |
Db 431 WPSDALDELWERSSEGVIKINDLAKSRGLSHGFVTVANYAGNSQSVFESYGA--DNEAKL 488
      | | | | | | | | | | | | | | | |
QY 485 KDL---FDPKKLL 494
      | : | | | | | | | | | | | | | |
Db 489 QVAMKWDPEGIL 501

RESULT 13
T49756
related to berberine bridge enzyme [imported] - Neurospora crassa
N/Alternate names: protein B24B19.280
C/Species: Neurospora crassa
C/Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C/Accession: U49756
R/R/Schulte, U.; Aign, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A/Reference number: Z25022
A/Accession: T49756
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-466 <SCH>
A/Cross-references: EMBL:AL356192; GSPDB:GM00116; NCSP:B24B19.280
A/Experimental source: BAC clone B24B19; strain OR74A
C/Genetics:
A/Gene: NCSP:B24B19.280
A/Map position: 6
A/Introns: 83/2; 86/1; 151/3; 193/3

Query Match 7.3%; Score 190; DB 2; Length 466;
Best Local Similarity 21.1%; Pred.No.1.5e-05;
Matches 103; Conservative 80; Mismatches 194; Indels 110; Gaps 20;

```

[illegible]





OM protein - protein search, using sw model

Run on: April 5, 2004, 17:38:21 ; Search time 17 Seconds  
(without alignments)  
1534.538 Million cell updates/sec

Title: US-10-014-101-4  
Perfect score: 2596  
Sequence: 1 MANLRMLTILVIMTKSS.....SKRKDLFPKLLSPGQDIF 501

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2596	100.0	501	1	Q9fuj3 arabidopsis
2	1822	70.2	524	1	Q9fuj2 arabidopsis
3	1292	49.8	523	1	CKX4_ARATH
4	1152	44.4	534	1	CKX3_ARATH
5	1143	44.0	532	1	CKX1_WAIZE
6	567.5	21.9	438	1	CKX1_ORISA
7	214.5	8.3	458	1	FAS5_RHOFA
8	169	6.5	439	1	HNO1_ARTOX
9	159	6.1	535	1	GGLO_RAT
10	153.5	5.9	447	1	RETO_PAPSO
11	153	5.9	439	1	MCPA_STRLA
12	149	5.7	439	1	GGLO_MOUSE
13	148	5.7	418	1	XYOA_STRCO
14	147	5.7	1018	1	YDJ1_ECOLI
15	144.5	5.6	496	1	DLB3_YEAST
16	140	5.4	440	1	GGLO_SCYTO
17	139.5	5.4	587	1	DLB1_YEAST
18	135.5	5.2	1027	1	YDJ1_HAEIN
19	133	5.1	723	1	Y242_HAEIN
20	131	5.0	557	1	ALO_CANAL
21	130.5	5.0	579	1	DLB1_KLULA
22	130	5.0	613	1	ADAS_TRYBB
23	129.5	5.0	526	1	ALO_YEAST
24	126.5	4.9	415	1	XYOA_STRSQ
25	124	4.8	611	1	ADAS_DICDI
26	123	4.7	499	1	GLCD_ECOLI
27	122.5	4.7	530	1	AIPT_YEAST
28	118	4.5	484	1	YGCU_ECO57
29	117	4.5	516	1	DHCR_HUMAN
30	116	4.5	725	1	HX22_HAEIN
31	112	4.3	484	1	YGCU_ECOLI
32	111	4.3	658	1	ADAS_CAVPO
33	110	4.2	1012	1	POLS_BDV5

34	108	4.2	344	1	SVW_CHLPCN
35	108	4.2	512	1	VC02_VACCV
36	108	4.2	561	1	DIM_ARATH
37	108	4.2	658	1	ADAS_HUMAN
38	107.5	4.1	793	1	SYFB_CLOPE
39	107	4.1	662	1	POFA_SCHPO
40	106.5	4.1	512	1	VC02_VACCC
41	106	4.1	1290	1	VACA_HELPY
42	106	4.1	1953	1	BIGA_SALTY
43	105	4.0	513	1	CP12_MOUSE
44	105	4.0	1012	1	POLS_BDV5
45	104	4.0	1012	1	POLS_BDV5

ALIGNMENTS

RESULT 1  
CKX2\_ARATH STANDARD; PRT; 501 AA.  
AC Q9FUJ3; Q9ZUP1;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Cytochrome oxidase 2 precursor (EC 1.4.3.-) (CKO 2).  
GN CKX2 OR AT2G19500 OR F3P11.10.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
CX [1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=21068113; PubMed=11154345;  
RX Blythe K.D., Cole J.L., Laskey J.G., Riekhof W.R., Eparza T.J.,  
RA Kramer M.D., Morris R.O.;  
RT "Molecular and biochemical characterization of a cytochrome oxidase  
from maize";  
RL Plant Physiol. 125:378-386(2001).  
[2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=cv. Columbia;  
RC MEDLINE=20083487; PubMed=10617197;  
RX Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,  
BUELL C.R., Ketchum K.A., Lee J.J., Renning C.M., Koo H., Moffat K.S.,  
RA Cronin L.A., Shen M., Vanden S.E., Umayam L., Tallon L.J., Gill J.E.,  
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,  
RA Salzberg S.L., Fraser C.M., Nierman W.C., White O., Eisen J.A.,  
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis  
thaliana";  
RL Nature 402:761-768(1999).  
CC -!- FUNCTION: Catalyzes the oxidation of cytokinins, a family of  
N(6)-substituted adenine derivatives that are plant hormones,  
where the substituent is an isopentenyl group.  
CC -!- CATALYTIC ACTIVITY: N(6)-(3-methylbut-2-en-1-yl)adenine + H(2)O +  
O(2) = adenine + 3-methylbut-2-enal + H(2)O(2).  
CC -!- COFACTOR: FAD (By similarity).  
CC -!- SUBCELLULAR LOCATION: Extracellular.  
CC -!- SIMILARITY: Belongs to the oxygen-dependent FAD-linked  
oxidoreductase family.  
-----  
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or send an email to license@isb-sib.ch).  
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EMBL; AF303978; AAC30905.1; -;  
EMBL; AC005917; AAD10149.2; -;

DR InterPro: IPR006094; Oxid FAD bind.  
DR InterPro: IPR006093; Oxid FAD BS  
DR InterPro: IPR009014; TransKet\_C\_like.  
DR Pfam: PF01565; FAD\_binding\_4; 1.  
DR ProSite: PS00862; Ox2\_COVAL\_FAD; 1.  
KW Oxidoreductase; Flavoprotein; FAD; Multigene family; Signal;  
FT Glycoprotein.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 501  
FT BINDING 92 92 FAD (COVALENT) (BY SIMILARITY).  
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 137 157  
SQ SEQUENCE 501 AA; 55583 MW; 9F8FOAAEAA4D884A CRC64;  
Query Match 100.0%; Score 2596; DB 1; Length 501;  
Best Local Similarity 100.0%; Pred. No. 4.7e-170;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MANLRLMTLTLYLMTITSSNGIKIDLPKSNLNLSTDPISIIASAHDGPNITVTGGV 60  
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QY 61 ICPSTADISRLLOVAANGKSTFFVAARGQHSLNQASVSGGVVNMTCITDVVVSXDK 120  
DB 61 ICPSTADISRLLOVAANGKSTFFVAARGQHSLNQASVSGGVVNMTCITDVVVSXDK 120  
QY 121 KYADVAAGTLVDVLLKTAEGKSPVSWTDYHLITVGGTSLNGIGQVFRNGPLVSNVL 180  
DB 121 KYADVAAGTLVDVLLKTAEGKSPVSWTDYHLITVGGTSLNGIGQVFRNGPLVSNVL 180  
QY 181 ELDVITGKGMILTCRQLNPFLFYGLGLGQFGIITRAIVLDHAPKRWFRMLYSDF 240  
DB 181 ELDVITGKGMILTCRQLNPFLFYGLGLGQFGIITRAIVLDHAPKRWFRMLYSDF 240  
QY 241 TTFYKQERLSMANDIGVDLEQIFLSNGVWDTFFPPSDQSKVADLVKQGIIVYLE 300  
DB 241 TTFYKQERLSMANDIGVDLEQIFLSNGVWDTFFPPSDQSKVADLVKQGIIVYLE 300  
QY 301 VAKYVDDNPLTISKVIDTLTKTSLYLPFGTSMHDVAYFDFLNRVHVEENKLSLGLWEL 360  
DB 301 VAKYVDDNPLTISKVIDTLTKTSLYLPFGTSMHDVAYFDFLNRVHVEENKLSLGLWEL 360  
QY 361 PPHWNLVVPKSRILDFHNGVVKDILLKQKASGLALLYPTNRKWNRSAMIPDEID 420  
DB 361 PPHWNLVVPKSRILDFHNGVVKDILLKQKASGLALLYPTNRKWNRSAMIPDEID 420  
QY 421 VIYITGLQSATPKDLPVESVNEKIRFCNDSGIKIKQYLMHYTSKEDWIEHFGSKWDD 480  
DB 421 VIYITGLQSATPKDLPVESVNEKIRFCNDSGIKIKQYLMHYTSKEDWIEHFGSKWDD 480  
QY 481 FSKRKDLFPKLLSPGQDIF 501  
DB 481 FSKRKDLFPKLLSPGQDIF 501  
RESULT 2  
CKX4\_ARATH STANDARD; PRT; 524 AA.  
AC Q9FU72; Q9SU77;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Cytochrome oxidase 4 precursor (EC 1.4.3.-) (CKO 4).  
GN CKX4 OR AT3G29740 OR T16L4.250.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosids;  
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN SEQUENCE FROM N.A.  
RP "Empirical analysis of transcriptional activity in the Arabidopsis

MEDLINE=21068113; PubMed=11154345;  
RA Bilyeu K.D., Cole J.J., Laskey J.G., Riekhof W.R., Esparza T.J.,  
RA Kramer M.D., Morris R.O.;  
RT "Molecular and biochemical characterization of a cytochrome oxidase  
from maize."  
RL Plant Physiol. 125:378-386 (2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=20083488; PubMed=10617198;  
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,  
RA Pohl T., Duesenrodt A., Stiekema W., Entian K.-D., Terry N.,  
RA Harris B., Ansoorge W., Brandt P., Grivell L., Rieger M.,  
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,  
RA Kreis M., Delisny M., Puidomenech P., Watson M., Schmidtheini T.,  
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,  
RA Vos P., Hebeisel J., Zimmermann W., Wedler H., Ridley P.,  
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,  
RA Van der Schueren J., Gysmonprez B., Chuang Y.-J., Vandenbussche F.,  
RA Braeken M., Weljens I., Voet M., Bastiaens I., Aert R., Defoor E.,  
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun W.,  
RA Holzer E., Brandt A., Peters S., van Staveren M., Dirke W.,  
RA Moijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,  
RA Bernier S., Hempel S., Feldpausch M., Lamberth S., Van de Daele H.,  
RA De Keyser A., Buyschaert C., Gielens J., Villarroel R., De Clercq R.,  
RA Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,  
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,  
RA Pettett A., Rajandream M.-A., Lyne M., Benes V., Rechmann S.,  
RA Borkova D., Blocker H., Scharfe M., Grimm M., Loeber T.-H.,  
RA Dose S., de Haan M., Maarse A., Schaefer M., Mueller-Auer S.,  
RA Gabel C., Fuchs M., Fartmann B., Graeber K., Dauner D., Herzl A.,  
RA Neumann S., Argirou A., Vitale D., Liguori R., Piravandi E.,  
RA Masson O., Quigley F., Clabaud G., Muendlein A., Felber R.,  
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,  
RA Chafador F., Cooke R., Berger C., Monfort A., Casacuberta E.,  
RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,  
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Raon D., Jesse T.,  
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Biele C.,  
RA Frishman D., Haase D., Lencke K., Mewes H.-W., Stocker S.,  
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,  
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,  
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,  
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,  
RA Lazreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,  
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,  
RA Kramer J., Fulton L., Mardis E., Dente M., Pepin K., Hillier L.W.,  
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,  
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,  
RA Antonou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,  
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,  
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,  
RA Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,  
RA Chen E., Marra M.A., Martensen R., McCombie W.R.;  
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis  
thaliana."  
RL Nature 402:769-777 (1999).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=22954850; PubMed=14593172;  
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,  
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,  
RA Karlth-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,  
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,  
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,  
RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,  
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,  
RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,  
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,  
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,  
RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,  
RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;  
RT "Empirical analysis of transcriptional activity in the Arabidopsis



```

RT genome. ";
CC -!- FUNCTION: Catalyzes the oxidation of cytokinins, a family of
CC N(6)-substituted adenine derivatives that are plant hormones,
CC where the substituent is an isopentenyl group.
CC -!- CATALYTIC ACTIVITY: N(6)-(3-methylbut-2-en-1-yl)adenine + H(2)O +
CC O(2) = adenine + 3-methylbut-2-enal + H(2)O(2).
CC -!- COFACTOR: FAD (By similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced. According to EST
CC sequences;
CC Name=1;
CC IsoId=Q9FUJ2-1; Sequence=displayed;
CC -!- SIMILARITY: Belongs to the oxygen-dependent FAD-linked
CC oxidoreductase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF303980; AAC30907.1; -
DR EMBL; AL079344; CAB45334.1; -
DR EMBL; AL161575; CAB79732.1; -
DR EMBL; AY054460; AAK96652.1; -
DR EMBL; BT000179; AAN15498.1; -
DR PIR; T09937; T09937.
DR InterPro; IPR006094; Oxid_FAD_bind.
DR InterPro; IPR006093; Oxid_FAD_BS.
DR Pfam; PF01565; FAD_binding_4; 1.
DR PROSITE; PS00862; OX2_COVAL_FAD; FALSE NEG.
DR KXW Oxidoreductase; FAD; Flavoprotein; Signal; Glycoprotein;
KW Alternative splicing; Multigene family.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 524 CYTOKININ OXIDASE 4.
FT BINDING 109 109 FAD (COVALENT) (BY SIMILARITY).
FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 15 15 L -> F (IN REF. 1).
SQ SEQUENCE 524 AA; 58061 MW; DBD23A7876DDA171 CRC64;

Query Match 70.28; Score 1822; DB 1; Length 524;
Best Local Similarity 66.78; Pred. No. 4e-117;
Matches 345; Conservative 69; Mismatches 79; Indels 24; Gaps 5;

QY 7 MITLITVLM-----ITKSSNGIKIDLPKSLNLTLDPSIISAASHDFGNITVTPGGVI 61
DB 9 LITLITLFIISLTPTLIKSDGIDVLFPSISLNLVLTDPFSISAASHDFGNITDENPGAVL 68
QY 62 CPSSTADISRLQYAANG-----KSTFOVARGOGHSLNGOASVSGGVVNWTCI 111
DB 69 CPSSTTEVARLLRFANGGFSYNGKSTSPASTFFKVAARGOGHSLRGQASAPGVVNWMTCL 128
QY 112 -----TDVVSVKDKKYADVAAGTLWDVLKTAERGVSFVSTDYLIHTVGGTILSNGGI 165
DB 129 AWAAPAAVVISADGTADVAAAGTMMVDVLKAAVDRGVSFVTWTDYLYLSVGGTILSNAGI 188
QY 166 GGOVFRNGPLVSNVLELDVITGEMLTCSRLNPELFGYVGLGGLGQFGIITRAIVLDH 225
DB 189 GGOVFRNGPQLSNVHELDVITGEMMTCSPLNPELFGYVGLGGLGQFGIITRAIALDH 248
QY 226 APKSAKFRMLYSDFITFTTKDQERLISMANDIGVDYLEGQIFLSNGVWVTPFSFSDQSK 285
DB 249 APTRKVSRLIYSDFAKEDQERLISMTNDLGVDFLEGQLMMSNGFVDTSPFPLSDQTR 308
QY 286 VADLVKQGHIIYVLEVAKYDDNLPITISKVIDTLTKLSYLPGLFISMEDVAVFDFLNRV 345

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## RESULT 3

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CXK3_ARATH STANDARD; PRT; 523 AA.
ID CXK3_ARATH AC Q9LTS3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytokinin oxidase 3 precursor (EC 1.4.3.-) (CKO 3).
GN CXK3 OR ATSG56970 OR MMH17.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21068113; PubMed=11154345;
RA Blayen K.D., Cole J.L., Laskey J.G., Riekhof W.R., Esparza T.J.,
RA Kramer M.D., Morris R.O.;
RA "Molecular and biochemical characterization of a cytokinin oxidase
RT from maize."
RL Plant Physiol. 125:378-386(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,
RA Tabata S.;
RA "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RL clones."
RL DNA Res. 7:31-63(2000).
CC -!- FUNCTION: Catalyzes the oxidation of cytokinins, a family of
CC N(6)-substituted adenine derivatives that are plant hormones,
CC where the substituent is an isopentenyl group.
CC -!- CATALYTIC ACTIVITY: N(6)-(3-methylbut-2-en-1-yl)adenine + H(2)O +
CC O(2) = adenine + 3-methylbut-2-enal + H(2)O(2).
CC -!- COFACTOR: FAD (By similarity).
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- SIMILARITY: Belongs to the oxygen-dependent FAD-linked
CC oxidoreductase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF303979; AAC30906.1; -
DR EMBL; AB024035; BAA97027.1; -
DR InterPro; IPR006094; Oxid_FAD_bind.
DR InterPro; IPR006093; Oxid_FAD_BS.
DR Pfam; PF01565; FAD_binding_4; 1.
DR PROSITE; PS00862; OX2_COVAL_FAD; 1.
KW Oxidoreductase; Flavoprotein; FAD; Multigene family; Signal;

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DB 309 VASLVNDHRIIYVLEVAKYDRTTLPIDQVITLURTLGFAPGMFVQDVPYDFLNRV 368
QY 346 HVEENKRLSIGLWELPFWPLNLYVPKSRILDFHNGVVKDILLKQKASGLALLYPTNRNK 405
DB 369 RNEEDKRLSIGLWELPFWPLNLYVPKSRILDFHNGVVKDILLKQKASGLALLYPTNRNK 428
QY 406 WDNRMASAMIPEDIDVYIIGLQSA-TPKQDLPVSVNEKILRECKDSGKIKQYLWHY 464
DB 429 WNNRMSTMP--DEDVYVIGLQAGSQNQWLENDKVIQFCENSIGIKIYELWHY 486
QY 465 TSKEDWIEHFGSKWDDFSKRKDLFPDKLLSPGQDIF 501
DB 487 TRKEDWVGHFGPKWDDFLRKKIMFDPKLLSPGQDIF 523

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KW Glycoprotein. 1 31 POTENTIAL.  
 FT SIGNAL 32 523 CYTOKININ OXIDASE 3.  
 FT BINDING 105 105 FAD (COVALENT) (BY SIMILARITY).  
 FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 523 AA; 59422 MW; 2324EBFC21D7103A CRC64;  
 Query Match 49.8%; Score 1292; DB 1; Length 523;  
 Best Local Similarity 48.5%; Pred. No. 6.8e-81;  
 Matches 251; Conservative 106; Mismatches 138; Indels 22; Gaps 6;  
 QY 3 NLRMLITLIT--VIMITKSSGKIDLPKSLN-----TLSDPSPISAAASHDRGN 51  
 DB 5 NLRQVRLIAITVILITLPTPTNTSPQWILSHNEFAGKLTSSSSVSAATDEGH 64  
 QY 52 ITTVPGGVCPSTADISLQVAAGKSTFQVAARGQSHLNGASVGGVIVNMTCI 111  
 DB 65 VTKIFPSAVLIPSSVEDITLKLSDFSQLSFPLAARGHSHRGQSAKADGVVNMRS 124  
 QY 112 TD----VVSKOKYADVAAGTLWDVLKTAEGVSPVSWTDYLHITVGGTSLNGGIG 167  
 DB 125 VNRDRGKIVARTCLYVDVDAWLWIEVNLKTELGTPTVSWTDYLVLTGGTSLNGGIG 184  
 QY 168 QVFNGLVSNVLELDVITCKGEMLTCSRLNPELFGVGLGQFGIITRARIIVLDHAP 227  
 DB 185 QTFYRGPQITNVLEMDVITCKGEMLTCSKDMNSDLFFAVLGLGQFGIITRARIKLE 244  
 QY 228 KRAKWFRLYSDFETFTKQOERLISMANDIGVDYLSGQIFLSGVVD---TSFFPSPQS 284  
 DB 245 KRAKWFRLYDFSEFTRQGRVSKTD--GVDFLGSIMVDHPPNDNRSTYPPSDHL 302  
 QY 285 KVADLVKQHGIIYVLEKAYDDPNLPIISKVITLTKLSVLPFGISMHDVAYDFLNR 344  
 DB 303 RIASWVRHRIYVLEKAYDDPNLPIISKVITLTKLSVLPFGISMHDVAYDFLNR 362  
 QY 345 VHVENKLRSLGWLPHPLNLYVPKSRILDFHNGVWKDILLKQXASGLALLVPTNRN 404  
 DB 363 VRTGELMKSGQWDPHPLNLYVPKSRILDFHNGVWKDILLKQXASGLALLVPTNRN 422  
 QY 405 KWDNRMSAMTPEIDEDVIYIIGLQSATPKDLPEVSNVEKIIRPKDSGKIKIKYLMHY 464  
 DB 423 KWDNRMSAAIPE--EDVFAVAGLRSAGFDNWEAFQENNEILKFCEDANMGVQVLPV 480  
 QY 465 TSKEDETEHRSKDDFSKDKLFDPKKLSRGQDIF 501  
 DB 481 SSQEGWVHFGPRNIFVERKIKYDPKAILSPGQINIF 517  
 RESULT 4  
 CKX1 MAIZE STANDARD; PRT; 534 AA.  
 AC O9TON8; 081158;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Cytokinin oxidase 1 precursor (EC 1.4.3.-) (CKO 1).  
 GN CKX1.  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.  
 CX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 417-435; 490-517 AND 524-534.  
 RC STRAIN=cv. Nobilis; TISSUE=kernel;  
 RX MEDLINE=99246676; PubMed=10230061;  
 RA Houben-Herlin N., Pethe C., D'Alayer J., Laloue M.;  
 RT "Cytokinin oxidase from Zea mays: purification, cDNA cloning and  
 expression in moss protoplasts";  
 RL Plant J. 17:615-626(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A., SEQUENCE OF 286-308; 369-377; 398-392 AND 417-431,

AND MASS SPECTROMETRY.  
 MEDLINE=99160863; PubMed=10049708;  
 Morris R.O., Bilyeu K.D., Laskey J.G., Cheikh N.N.;  
 "Isolation of a gene encoding a glycosylated cytokinin oxidase from  
 maize.";  
 Biochem. Biophys. Res. Commun. 255:328-333(1999).  
 [3]  
 RN CHARACTERIZATION, AND TISSUE SPECIFICITY.  
 MEDLINE=21068113; PubMed=11154345;  
 Bilyeu K.D., Cole J.L., Laskey J.G., Riekhof W.R., Esparza T.J.,  
 Kramer M.D., Morris R.O.;  
 "Molecular and biochemical characterization of a cytokinin oxidase  
 from maize.";  
 Plant Physiol. 125:378-386(2001).  
 CC -!- FUNCTION: Catalyzes the oxidation of cytokinins, a family of N(6)-  
 substituted adenine derivatives that are plant hormones, where the  
 substituent is an isopentenyl group. Cleaves zeatin,  
 isopentenyladenine, isopentenyladenosine, zeatin riboside and cis-  
 zeatin, but not dihydrozeatin, kinetin and benzylaminopurine.  
 CC -!- CATALYTIC ACTIVITY: N(6)-(3-methylbut-2-enyl)adenine + H(2)O +  
 O(2) = adenine + 3-methylbut-2-enal + H(2)O(2).  
 CC -!- COFACTOR: FAD.  
 CC -!- ENZYME REGULATION: Competitive inhibition by phenylureas.  
 CC -!- SUBUNIT: Monomer (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Extracellular.  
 CC -!- TISSUE SPECIFICITY: Expressed in immature kernels and unpollinated  
 cobs. Weakly expressed in kernels harvested two weeks after  
 anthesis.  
 CC -!- PMX: Glycosylated, with approximately 10 hexose residues per site.  
 CC -!- SIMILARITY: Belongs to the oxygen-dependent FAD-linked  
 oxidoreductase family.  
 -----  
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 or send an email to license@isb-sib.ch).  
 -----  
 CC EMBL; Y18377; CAA77151.1; .  
 CC EMBL; AF044603; AAC27500.1; .  
 DR PIR; T01500; T01500.  
 DR PIR; T51929; T51929.  
 DR MaizeDB; 194080; .  
 DR InterPro; IPR006094; Oxid FAD bind.  
 DR InterPro; IPR006093; Oxid FAD\_BS.  
 DR Pfam; PF01565; FAD binding\_4; 1.  
 DR PROSITE; PS00862; OX2 COVAL FAD; 1.  
 KW Oxidoreductase; Flavoprotein; FAD; Signal; Glycoprotein.  
 FT SIGNAL 1 18 POTENTIAL.  
 FT CHAIN 19 534 CYTOKININ OXIDASE 1.  
 FT DOMAIN 339 345 POLY-ALA.  
 FT BINDING 105 105 FAD (COVALENT) (PROBABLE).  
 FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 63 63 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 323 323 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 434 434 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 79 79 A -> G (IN REF. 2).  
 FT CONFLICT 168 168 T -> N (IN REF. 2).  
 FT CONFLICT 254 254 L -> F (IN REF. 2).  
 SQ SEQUENCE 534 AA; 57195 MW; 3D5671BC4F40918B CRC64;  
 Query Match 44.4%; Score 1152; DB 1; Length 534;  
 Best Local Similarity 47.4%; Pred. No. 2.6e-71;  
 Matches 235; Conservative 84; Mismatches 149; Indels 28; Gaps 11;  
 QY 30 SLNLTSLDPSISAAASHDFGNITVTPGGVCPSTADISRLQYANGKS--TFQVAA 87  
 DB 42 ALDGKLRDTSNATAAATDFGNITVTPGGVCPSTADISRLQYANGKS--TFQVAA 100

QY 88 RGQHSLSNGASVSGGVVMTCTD-----VVSKDKKYADVAAGTLMVDVLTAKTAEK 141  
Db 101 RGRHSLMGQAFAPGGVNVNMSLGDAAAPRINVSADGRYVDAGGEQVWIDVIRASLAR 160  
QY 142 GVSFVSMTDYLHITVGTSLNGGIGGVFRNGPLVSNVLELDVITGKGMELTCSRLNPE 201  
Db 161 GVAPRSWTDVLYLTGVTSLNAGISGQAFRHGPQISNVLEMDVITGHEWVTCSKQLNAD 220  
QY 202 LFYVGLGLOFGIITRARIIVLDHAPKRWKFMRLISDFTTFYKDOERLISMANDIG--- 258  
Db 221 LFDVAVGLGLOFGVITRARIIVLDHAPKRWKFMRLISDFTTFYKDOERLISMANDIG--- 280  
QY 259 ---VDYLEGGIF---LSNGVVDTSFPPSPQSKVADLVKQHG---IIVYLEVAKYDDPN 309  
Db 281 FGPMYSYVEGVSFVNQSLATLANTGFTDADVARIVALAGERNATTVYSIEATLNDYAT 340  
QY 310 --LPIISKVDTLTKTLYSLPGFTSMHDVAYFDFLNRVHVVEENKLSGLGWELPHEWLN 367  
Db 341 AAAAANDQELASVLGTLISYVEGFAFQFADVAFAELDRVHGEVVALNKLGLWRVPHPLNM 400  
QY 368 YVPSRILDFHNGVVKDILLKOKSASGLALLYPTRNKNWNRMSAMPEIDEDEVIIIGL 427  
Db 401 FVPSRILDFHNGVVKDILLKOKSASGLALLYPTRNKNWNRMSAMPEIDEDEVIIIGL 457  
QY 428 L-QSATPKOLPEVSVNEKIIRPKDSGKIKQVLMHYTSKEDWIEHFG-SKWDDFSRRK 485  
Db 458 LFSSVAPNDLARLOEQNRRIILFCDLAQIKYTLARHTDRSDVWRHFGAAXNRFEVEMK 517  
QY 486 DLFPKLLSPGQDIF 501  
Db 518 NKYDPKLLSPGQDIF 533

RESULT 5  
CKX1\_ORYSA STANDARD; PRT; 532 AA.  
ID Q9JDE6;  
AC 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Probable cytokinin oxidase precursor (EC 1.4.3.-) (CKO).  
GN P0512G09.9.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzoae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cn. Nipponbare;  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Catalyzes the oxidation of cytokinins, a family of  
CC N(6)-substituted adenine derivatives that are plant hormones,  
CC where the substituent is an isopentenyl group.  
CC -!- CATALYTIC ACTIVITY: N(6)-(3-methylbut-2-enyl)adenine + H(2)O +  
CC O(2) = adenine + 3-methylbut-2-enal + H(2)O(2).  
CC -!- COFACTOR: PAD (By similarity).  
CC -!- SUBCELLULAR LOCATION: Extracellular (By similarity).  
CC -!- SIMILARITY: Belongs to the oxygen-dependent PAD-linked  
CC oxidoreductase family.  
CC  
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CC  
CC EMBL; AF002836; BAB07927.1; -;  
CC EMBL; AF002816; BAB03420.1; -;

DR Gramene; Q9LDE6; -;  
DR InterPro; IPR006094; Oxid\_FAD\_bind.  
DR InterPro; IPR006093; Oxid\_FAD\_BS.  
DR Pfam; PFO1565; FAD\_binding\_4; 1  
DR PROSITE; PS00862; OX2\_COVA\_FAD; 1.  
KW Oxidoreductase; Flavoprotein; FAD; 1. Signal; Glycoprotein.  
FT SIGNAL 1 17  
FT CHAIN 18 532  
FT BINDING 105 105  
FT CARBOHYD 52 52  
FT CARBOHYD 63 63  
FT CARBOHYD 133 133  
FT CARBOHYD 321 321  
FT CARBOHYD 432 432  
FT SEQUENCE 532 AA; 56034 MW; B849D646E3B447E CRC64;  
SQ  
Query Match 44.0%; Score 1143; DB 1; Length 532;  
Best Local Similarity 47.1%; Pred. No. 1.1e-70;  
Matches 231; Conservative 75; Mismatches 156; Indels 28; Gaps 8;  
QY 35 LSTDPISIAASHDFGNITTTTPGGVIPCSTADISRLLO--YAANGKSTQVAAAGGCH 92  
Db 47 LRTDPNATVPASMDFGNITAAAPAAVLPFGSPGVAEELRAAYAAPGR-PFTVSPRGKH 105  
QY 93 SLNGQASVSGGVVNMTCI-----TDVVSVKDKKYADVAAGTLMVDVLTAKTAEKSVPS 147  
Db 106 STWQALAGGVVHVHMQSGGGAPRINVSADGAIVDAGGEQLVDVLRALARGVAPRS 165  
QY 148 WTDYHLHTVGGTSLNGGIGGVFRNGPLVSNVLELDVITGKGMELTCSRLNPELFYVL 207  
Db 166 WTDYHLHTVGGTSLNAGVSGQYRHGPQISNVLELDVITGKGMELTCSRLNPELFYVL 225  
QY 208 GGLGQGIITRARIIVLDHAPKRWKFMRLISDFTTFYKDOERLISMANDIG---VDYLEG 264  
Db 226 GGLGQGIITRARIIVLDHAPKRWKFMRLISDFTTFYKDOERLISMANDIG---VDYLEG 285  
QY 265 QIFL-----SNGVVDTSFPPSPQSKVADL--VKQHGIIIVLEVAKYDDPNLP- 311  
Db 286 AVYLAGGLAVALKSSG-----GFFSDADAARVVALAARNATVYSIEATLNYAANATPS 341  
QY 312 IISKVDTLTKTLYSLPGFTSMHDVAYFDFLNRVHVVEENKLSGLGWELPHEWLNLYPK 371  
Db 342 SVDAVAALAGDLHFEFGSFRSDVTFEFLDRVYGEELAEKAGLRVHFWLNLFDVG 401  
QY 372 SRILDFHNGVVKDILLKOKSASGLALLYPTRNKNWNRMSAMPEIDEDEVIIIGLQSA 431  
Db 402 SRIADFRGVFGILQATDITADIAGLIIPVNSKWDAAASAVTPEGEVEFVVSLLFSA 461  
QY 432 TPMDLPEVSVNEKIIRPKDSGKIKQVLMHYTSKEDWIEHFGSKWDDFSKELDFDK 491  
Db 462 VANDVAALAEQNRRIILFCDLAQIKYTLARHTDRSDVWRHFGAKWDRFVORKYDKP 521  
QY 492 KLLSPGQDIF 501  
Db 522 KLLSPGQDIF 531

RESULT 6  
FAS5\_RHOFA STANDARD; PRT; 438 AA.  
ID FAS5\_RHOFA  
AC P46377;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Hypothetical 47.9 kDa oxidoreductase in fasciation locus (ORF5).  
GN FAS5.  
OS Rhodococcus fascians.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Nocardiaceae; Rhodococcus.  
OX NCBI\_TaxID=1828;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=D188;  
RA MEDLINE=94222824; PubMed=8169198;  
RX Crespi M., Vereecke D., Temmerman W., van Montagu M., Desomer J.;  
RT "The fas operon of Rhodococcus fascians encodes new genes required  
for efficient fasciation of host plants.";  
RL J. Bacteriol. 176:2492-2501(1994).  
CC -!- FUNCTION: THE FAS-OPERON ENCODES GENES INVOLVED IN CYTOKININ  
CC PRODUCTION AND IN HOST PLANT FASCINATION (LEAFY GALL).  
CC -!- COFACTOR: FAD (Potential).  
CC -!- INDUCTION: During the interaction with host plants.  
CC -!- SIMILARITY: Belongs to the oxygen-dependent FAD-linked  
CC oxidoreductase family.  
CC  
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CC or send an email to license@isb-sib.ch).  
CC  
CC EMBL; Z296335; CAA82745.1; -  
DR PIR; E55578; E55578.  
DR InterPro; IPR006094; Oxid FAD bind.  
DR Pfam; PF01565; FAD binding\_4; 1.  
DR PROSITE; PS00862; OX2\_COVAL\_FAD; 1.  
KW Hypothetical protein; Oxidoreductase; Flavoprotein; FAD; Plasmid.  
FT BINDING 60 FAD [COVALENT] (BY SIMILARITY).  
SQ SEQUENCE 438 AA; 47889 MW; 5F7FADA0911A0171 CRC64;  
Query Match 21.0%; Score 567.5; DB 1; Length 438;  
Best Local Similarity 33.0%; Pred. No. 1.8e-31;  
Matches 139; Conservative 65; Mismatches 205; Indels 41; Gaps 10;  
QY 37 TDSIISAASHDNGNITVTPGVGICPSSTADISRLQYAAKSTQFVAARGQSHSLNG 96  
DB 7 TDDVHLTSGADGNGICHAQPPVVPVPTVADVQEAALRYTA--ARNLSLAVRSGHSTYV 64  
QY 97 QASVSGGVIVNM---TCITDVVVSCKKYADVAAAGTLWDLVKTKAEKGVSPVSWTDYLH 153  
DB 65 QCQADGGVLDLMDKRFNTVHDVRSQ---ATDAGVNSDVVAATLSRQQTFFVLTDLGL 120  
QY 154 ITVGGTSLNGIGGQVFRNGPLVSNVLELDVITGKEMITCSRQNLNPELFYGVGLGLOF 213  
DB 121 TTVGGTSLVSGFGSGSHGFLQTDNVDLSAVVTGSGDFRECSAVNSSELFDAVRGLGLOF 180  
QY 214 GIITRATVLDHAPKAKFRMLYSDFTTFKDQERLISMANDIGVDYLEGQIFLSNGVV 273  
DB 181 GVIVNATIRLTAAHESVRQKQVNSLGVFLGDLR--AVSNRL-FDHVQGRIRD----- 233  
QY 274 DTSFFPPSDQSKVADLVKQHGIIYVLEVAKYDDPNLPIISKVIDTLTKTSLYLPGFISM 333  
DB 234 -----AD-----GHLAYRLDLAKYFTPPRRP-----DDDALLSSLQYDSCAEYN 272  
QY 334 HDVAYFDLNRVHVVENKLSGLWELPHEMLNLYPKSRILDFHNGVVKDILLKQKSAS 393  
DB 273 SDVDYDGFINRMADQELDRHTGEWFYHPHWASLLIPADKIEQFIE-TTSSSLTDDLGN 331  
QY 394 GLALLYPTNRKWNRMASIMPEIDEDVYIIGLASATPKDLPEVESVNEKILRECKDS 453  
DB 332 GLIMVYIPITP---ITAPIPICDCTFFMLAVLTASPGAEARMIASNRLLYEQARDV 388  
QY 454 GIKIKQVLMHYTSKEDWIEHFGSKWDDFSKRLDFDPKLLSPG 497  
DB 389 GGVAYAYNAVMPSPGDCTHFGSRWQAIARAKRFRDFYRILAPG 432

RESULT 7

HDNO\_ARTOX STANDARD; PRT; 458 AA.  
AC P08159;  
DT 01-AUG-1988 (Rel. 08, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 6-hydroxy-D-nicotine oxidase (EC 1.5.3.6) (6-HDNO).  
OS Arthrobacter oxidans.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Micrococciaceae; Micrococaceae; Arthrobacter.  
OX NCBI\_TaxID=1671;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87304263; PubMed=3622516;  
RA Brandsch R., Hinkkanen A.E., Mauch L., Nagursky H., Decker K.;  
RT "6-hydroxy-D-nicotine oxidase of Arthrobacter oxidans. Gene structure  
of the flavoenzyme and its relationship to 6-hydroxy-L-nicotine  
oxidase";  
RL Eur. J. Biochem. 167:315-320(1987).  
RN [2]  
RP REVISIONS.  
RA Brandsch R.;  
RL Submitted (SEP-1990) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP MUTAGENESIS OF HIS-71.  
RX MEDLINE=90033359; PubMed=2680607;  
RA Mauch L., Bichler V., Brandsch R.;  
RT "Site-directed mutagenesis of the FAD-binding histidine of  
6-hydroxy-D-nicotine oxidase. Consequences on flavinylation and  
enzyme activity";  
RL FEBS Lett. 257:86-88(1989).  
RN [4]  
RP MUTAGENESIS OF ARG-67 AND SER-68.  
RX MEDLINE=90330600; PubMed=2115879;  
RA Mauch L., Bichler V., Brandsch R.;  
RT "Lysine can replace arginine 67 in the mediation of covalent  
attachment of FAD to histidine 71 of 6-hydroxy-D-nicotine oxidase.";  
RL J. Biol. Chem. 265:12761-12762(1990).  
CC -!- CATALYTIC ACTIVITY: (R)-6-hydroxynicotine + H(2)O + O(2) = 1-(6-  
hydroxypyrid-3-yl)-4-(methyamino)butan-1-one + H(2)O(2).  
CC -!- COFACTOR: FAD.  
CC -!- PATHWAY: Degradation of nicotine.  
CC -!- SIMILARITY: Belongs to the oxygen-dependent FAD-linked  
CC oxidoreductase family.  
CC  
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CC  
CC EMBL; X05999; CAA29416.1; -  
DR PIR; S00087; DETOHN.  
DR InterPro; IPR006094; Oxid FAD bind.  
DR InterPro; IPR006093; Oxred\_FAD\_BS.  
DR Pfam; PF01565; FAD binding\_4; 1.  
DR PROSITE; PS00862; OX2\_COVAL\_FAD; 1.  
KW Oxidoreductase; Flavoprotein; FAD.  
FT BINDING 71 71 FAD [COVALENT].  
FT MUTAGEN 67 67 R->A: NO FAD INCORPORATION.  
FT MUTAGEN 67 67 R->K: NO EFFECT ON FAD INCORPORATION, BUT  
FT MUTAGEN 68 68 REDUCED ACTIVITY.  
FT MUTAGEN 68 68 S->A: NO EFFECT ON FAD INCORPORATION OR  
FT MUTAGEN 71 71 ON ACTIVITY.  
FT MUTAGEN 71 71 H->C,Y,S: NO FAD INCORPORATION, ABOLISH  
FT SEQUENCE 458 AA; 48786 MW; 6783E444D66DC841 CRC64;  
OR DIMINISH SIGNIFICANTLY THE ACTIVITY.  
Query Match 8.3%; Score 214.5; DB 1; Length 458;  
Best Local Similarity 24.1%; Pred. No. 2.5e-07;  
Matches 70; Conservative 59; Mismatches 128; Indels 33; Gaps 10;  
QY 27 LPKSLNLTSTDPSTISAASHDFGNITVTPGVGVI-CPS-----STADISRLQYAA-N 78  
DB 1 MSKLATFLSQGVEIVYDDSGFADAIANINWGRHLQRPSPRLARCLISAGDVAKSVRYACDN 60

[illegible]

Reticuline oxidase precursor (EC 1.21.1.3) (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase).

BEEI.

Papaver somniferum (Opium poppy).

Oskaroyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales; Papaveraceae; Papaver.

NCBI\_TaxID=3469;

[1]\_\_TaxID=3469;

SEQUENCE FROM N.A.

STRAIN=cv. Marianne;

MEDLINE=97127853; PubMed=8972604;

Faccini P.J., Penzes C., Johnson A.G., Bull D.;

"Molecular characterization of berberine bridge enzyme genes from opium poppy.";

Plant Physiol. 112:1669-1677(1996).

-!- FUNCTION: Essential to the formation of benzophenanthridine alkaloids in the response of plants to pathogenic attack. Catalyzes the stereospecific conversion of the N-methyl moiety of (S)-reticuline into the berberine bridge carbon of (S)-scoulerine.

-!- CATALYTIC ACTIVITY: (S)-reticuline + O(2) = (S)-scoulerine + H(2)O(2).

-!- COFACTOR: FAD and metal ion.

-!- PATHWAY: Benzophenanthridine alkaloids biosynthesis.

-!- SUBCELLULAR LOCATION: VESICULAR

-!- SIMILARITY: Belongs to the oxygen-dependent FAD-linked oxidoreductase family.

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EMBL: AF025430; AACG61839.1; .

PIR: T07969; T07969.

InterPro: IPR006094; Oxid\_FAD\_bind.

Interpro: IPR006093; Oxired\_FAD\_BS.

Pfam: PF01565; FAD\_binding\_4; 1.

DR PROSITE; PS00862; OX2\_COVAL\_FAD; 1.

KW Oxidoreductase; Signal; Glycoprotein; Flavoprotein; FAD;

KW Alkaloid metabolism.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 535 RETICULINE OXIDASE.

FT BINDING 108 108 FAD (COVALENT) (BY SIMILARITY).

FT CARBOHYD 42 42 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 475 475 N-LINKED (GLCNAC. .) (POTENTIAL).

SEQUENCE 535 AA; 59903 MW; F0341EF38AB41239 CRC64;

Query Match 6.1%; Score 159; DB 1; Length 535;

Best Local Similarity 20.1%; Pred No. 0.002;

Matches 122; Conservative 85; Mismatches 200; Indels 200; Gaps 299

Qy 3 NLRLMITLVIMTKSNGIKID--LPKSLN-----LLISTDPS-----IIISAASHD 48  
: : : : : | : : : : :  
Db 5 SLTLRRFFLFI LLVLTCTVRGGVDNDLLSSCLNSHGHNFTLTSTDNSDYFKLLHSMQN 64  
: : : : : | : : : : :

Qy 49 --EGNITVTGGVTCPSSTADISRLLQYAANGKSTFOVARQGCHSLNGOASVSGG--V 104  
: : : : : | : : : : :

Db 65 PLFAPKTYSKSFSFIVDPGSKEELSTVHCCT--RESWTIRLSGGSHVEGLSYTADTFV 122  
: : : : : | : : : : :

Qy 105 IVNMTCITDVVYSKKYADVAAAGTLWDVLVKTTAEKGVPSPVSWTDYLHIV----- 156  
: : : : : | : : : : :

Db 123 IVDMNNLRISI-----DVLSETAWBSGATLGELYAIAAQSTDTLTGTAQCPTVGS 175  
: : : : : | : : : : :

Qy 157 GGTLSNGIGGOVFRNGPLVSNVLELDVITGGEMLTCRQLNPFLFYGVL--GGLGOFGI 215  
: : : : : | : : : : :

Db 176 GGHSIGGGFGMMSRKYGLAADNVDAILLDSNGAILD--REKMGDDVFWRIRGGGGGWGA 234  
: : : : : | : : : : :

Qy 216 ITRAIRVILDHPAKRAKWFRLYS-----DFTFTTKDQERLIISM-----ANDI 257  
: : : : : | : : : : :

```
Query Match      5.9%; Score 153.5; DB 1; Length 447;
Best Local Similarity 27.5%; Pred. No. 0.0036;
Matches 46; Conservative 31; Mismatches 85; Indels 2; Gaps 2;

QY 57 PGVVICPSTADISRLQYAAANGKSTFCVAAAGQGHSLNGQASVSGGVIVNMTCTIDVV 116
D 30 PAYVVEAADEQEAVALAAEQKRPVGVNATGHPGV---SADDAVLVNTRRMEGVSV 85
QY 117 SKDKKYADVAGTLLVDVLLKTAEGKVPVSWTDYLLHTVGGTSLNGIGGQVFRNGPLV 176
D 86 DAARATAWIEAGARWRKVLHTAHGLAPLNGSS-PNVGAVGYLVGGAGLLGRFQYAA 144
QY 177 SNVLELDVITGKGBMLTCSRLNPELPFYVGLGGQGFQIIRARIVL 223
D 145 DHVRLRLVTDAGRLRDVTAGTDDELDLFWAVRGKDNFGLVGVMEVDL 191

RESULT 11
GGLO MOUSE
ID _GGLO MOUSE STANDARD; PRT; 439 AA.
AC P58710;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE L-gulonolactone oxidase (EC 1.1.1.3.8) (LGO) (L-gulono-gamma-lactone
oxidase) (GLO).
OS GULO.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Colling B., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore I., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshimiki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunatratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerich A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Oxidizes L-gulono-1,4-lactone to hydrogen peroxide and
L-xylulo-5-phosphate.
CC -1- CATALYTIC ACTIVITY: L-gulono-1,4-lactone + O(2) = L-xylulo-5-3-
ascorbate (By similarity).
CC -1- COFACTOR: FAD (By similarity).
CC -1- PATHWAY: Ascorbate biosynthesis; last step.
CC -1- SUBCELLULAR LOCATION: Membrane-associated. Mitochondrial membrane (By
similarity).
CC -1- SIMILARITY: Belongs to the oxygen-dependent FAD-linked
oxidoreductase family.
CC -1- SIMILARITY: SOME, TO YEAST D-LACTATE DEHYDROGENASE [CYTOCHROME].
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; BC019856; AAH19856.1; -.
DR InterPro: IPR007173; ALO.
DR InterPro: IPR006094; Oxid_FAD_bind.
DR InterPro: IPR006093; Oxid_FAD_BS.
DR Pfam; PF04030; ALO; 1.
DR PROSITE; PS00862; Ox2_COVAL_FAD; 1.
DR Oxidoreductase; Flavoprotein; FAD; Ascorbate biosynthesis; Microsome;
KW Transmembrane.
FT INIT_MET 0 0 BY SIMILARITY.
FT BINDING 53 53 FAD (COVALENT) (BY SIMILARITY).
FT TRANSMEM 250 272 POTENTIAL.
SQ SEQUENCE 439 AA; 50361 MW; 52B7E961AA3240A4 CRC64;

Query Match      5.9%; Score 153; DB 1; Length 439;
Best Local Similarity 19.5%; Pred. No. 0.0038;
Matches 92; Conservative 83; Mismatches 188; Indels 108; Gaps 19;

QY 63 PSTADISRLQYAAANGKSTFCVAAAGQGHSLNGQASVSGGVIVNMTCTIDVV-VSKDKK 121
D 26 PTVSGEVREVLARQONKVKV---GGHS-PSDIACDGMHMGKNNRVLQVDKCK 82
QY 122 YADVAAGTLLVDVLLKTAEGKVPVSWTDYLLHTVGGTSLNG---GIGQVFRNGPLVS 177
D 83 QVTVEAGILLTDLHPQLDKGLALSNGAVSDVTVGGVIGSGTHNTGI-----KHGILAT 137
QY 178 NVLELDVITGKGBMLTCSRLNPELPFYVGLGGQGFQIIRARIVLDHAPKAQKFRMLY 237
D 138 QVVALTLMKADGTVLECSSESKADVFQAARVHLGCLGVI---LTVTLCQVPPQ-----PHLE 191
QY 238 SDFTTTKDQERLISMANDIGVDYLEGQI-----FLSNGVVDTSPFPSPDQSKVADLV 290
D 192 TSPFSTLKEV-----LNLSHLKKSEYFRFL-----WPFHSE--NVSIY 230
QY 291 KQHGIIVLEAVKYDDPNLPISKVIDTLTKLSYLP---GFIS----- 332
D 231 QDHNTKPPSSASNNFWD---YAIGFYLLFLLTSTYPLRVGVINFRFFFLFNCKESS 288
QY 333 --MEDVAYPFLNRVHVEENKLSGLWELP-HPWLNLYVPKSRILDFHNGVVKDILLKQ 389
D 289 NLGHKIFSYPCRFQHVQD-----WAIPEKTEALLEKAMLEAHPKVAHYVPEV 340
QY 390 KSASGLIALLYPTNRNKNWDRMSAMPEIDEDVIYIIGLQSATPKOLPEVESVNEKIIRF 449
D 341 RPTRGDDIL-----LSPCFQDSCVMNIIMYRPGKDVPRL----- 376
QY 450 CKDSGIKKIQLVLMHYTSKEDWIEHFGSKWDQFSKRDLF---DPKKLLSP 496
D 377 --DYWLAYETIMKFGGRPHWAKAHNCTRKDFEOWYPAFHKFCDIKELDP 425

RESULT 12
RETO_ESCCA
ID RETO_ESCCA STANDARD; PRT; 538 AA.
AC P30986;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Reticuline oxidase precursor (EC 1.21.3.3) (Berberine-bridge-forming
enzyme) (BBE) (Tetrahydroprotoberberine synthase).
GN BBE1.
OS Eschscholzia californica (California poppy).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
OC Papaveraceae; Eschscholziaceae; Eschscholzia.
OX NCBI_TaxID=3467;
RX [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=92052284; PubMed=1946465;
```

282 DOSKVADVLGHGIIYVLVAKYDDNLPILSKVIDTLTKILSYLP-GFISMDHVAYED 340

356 FTKVY-DLTK- - - - -PLPSKAFVGLLERLSKEPNGFIA - - - - - 388

341 FLNRRVHVVENKLRSGLMELPHPLNLYVPKSRILDFHNGVVDKLLKOKSASGLALLYP 400

389 -LNGFGQMSKISS-DFTFFPH - - - - -RSGRLMVEYI 419

401 TNRNKWDNRMSAMTPEIDEDVIYIIGLQSATPK- - - - -DLPEVESVNEKIIRFCK 451

420 VAWNSEQKKTEFLDWLEKYEFMKPFVSKNPRLGYVNHIDLDLGGIDWGNKTVV- - - 475

452 DSGIKIKQYLMHYTSKEDWIE-HFGSKWDDFSKRDLPDKLLSPQDI 500

476 NNAIEISR- - - - -SWGESYFLSNVERLIRAKTLIDNNVFNHPQSI 516

RESULT 13

XYOA STROCO STANDARD; PRT; 418 AA.

ID -XYOA STROCO STANDARD; PRT; 418 AA.

Q9ZBU1; AC

28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

DE Probable xyloitol oxidase (EC 1.1.3.41).

GN XYOA OR SC06147 OR SCLA9.11C.

OS Streptomyces coelicolor.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycetaceae; Streptomycetaceae; Streptomyces.

NCBI\_TaxID=1902;

[1]

RP SEQUENCE FROM N.A.

RC STRAIN-A3(2) / M145;

RX MEDLINE=1996410; PubMed=12000953;

RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,

RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,

RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,

RA Sanger K., Saunders E., Sharp S., Squares R., Squares S., Taylor K.,

RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,

RA Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces

RT coelicolor A3(2).";

RL Nature 417:141-147(2002).

CC -|- FUNCTION: Catalyzes the oxidation of xyloitol to xylose, also acts

CC on D-sorbitol (by similarity).

CC -|- CATALYTIC ACTIVITY: Xylitol + O(2) = xylose + H(2)O(2).

CC -|- COFACTOR: FAD (by similarity).

CC -|- SIMILARITY: Belongs to the oxygen-dependent FAD-linked

CC oxidoreductase family.

CC

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CC

CC EMBL; AL9139126; CAA22381.1; -

DR PIR; T34660; T34660.

DR InterPro; IPR006094; Oxid\_FAD\_bind.

DR InterPro; IPR006093; Oxred\_FAD\_BS.

DR Pfam; PF01565; Ox2\_Binding\_4; 1.

DR PROSITE; PS00862; OX2\_COVAL\_FAD; FALSE NEG.

DR KX Oxidoreductase; Flavoprotein; FAD; Complete proteome.

KW BINDING 46 46 FAD (COVALENT) (BY SIMILARITY)

FT BINDING 46 46 FAD (COVALENT) (BY SIMILARITY)

SEQUENCE 418 AA; 44346 MW; 2A80DF7735A87DCD CRC64;

Query Match 5.7%; Score 148; DB 1; Length 418;



Matches 50; Conservative 35; Mismatches 82; Indels 12; Gaps 6;  
 QY 50 GNITVTGGVCPSSSTADISRLLOVYANGKSTFQVAAQGHSLNGQASV-SCGVIVNM 108  
 Db 11 GNI-TYAKELLRSHSLDALRALVADSA-----RVRVLGSGHSFNEIAEPFGGGVLLSL 63  
 QY 109 TCITDVV-VSKDKKYADVAAGTLWVDVLTAKTAEKGVSPVSWTDYLTHTVGGTSLNGGIGG 167  
 Db 64 AGLPSVVDVTAARTVRGGVRVAEIARVUHAGLALPNWASLPHLSVAGSVATGTHGS 123  
 QY 168 QVFRNGPLVSNVLELDVITGKGMELTCSRQINPELFGVIGGLGQFGIITRARIIVLDHA 226  
 Db 124 GV-GNGSLASVVRVELVLTADGTSTVIAR--GDERFGAVTSLGALGVVTSLTLDLEPA 179

RESULT 14  
 YDIU\_ECOLI  
 ID YDIU\_ECOLI STANDARD; PRT; 1018 AA.  
 AC P77748;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Hypothetical protein ydiU.  
 GN YDIU OR B1687.  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OC NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.,  
 RA "The complete genome sequence of Escherichia coli K-12."  
 RT Science 277:1453-1474(1997).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=K12;  
 RC MEDLINE=97251357; PubMed=9097039;  
 RX Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,  
 RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,  
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,  
 RA Sampei G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,  
 RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;  
 RT "A 570-Kb DNA sequence of the Escherichia coli K-12 genome  
 corresponding to the 28.0-40.1 min region on the linkage map."  
 RL DNA Res 3:363-377(1996).  
 CC -!- SIMILARITY: STRONG, TO H. INFLUENZA H11N63.  
 CC -!- SIMILARITY: TO MAMMALIAN ALKYLDIHYDROXYACETONEPHOSPHATE SYNTHASES,  
 CC TO YEAST AIP2 AND DLD1 AND TO E. COLI YGCU.  
 CC  
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 CC  
 CC EMBL; AE000263; AAC74757.1; -.  
 CC DR EMBL; D90811; BAA15451.1; -.  
 CC DR PIR; G64926; G64926.  
 CC DR Ecogen; EG13969; ydiU.  
 CC DR InterPro; IPR001450; 4Fe4s ferredoxin.  
 CC DR InterPro; IPR004113; FAD-oxidase C.  
 CC DR InterPro; IPR006094; Oxid FAD bind.  
 CC DR Pfam; PF02913; FAD-oxidase C; 1.  
 CC DR Pfam; PF01565; FAD binding\_4; 1.  
 CC DR PROSITE; PS00198; 4Fe4s\_FERREDOXIN; 1.

KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 1018 AA; 113247 MW; FA93940B0DC8C703 CRC64;  
 Query Match 5.7%; Score 147; DB 1; Length 1018;  
 Best Local Similarity 18.2%; Pred. No. 0.031;  
 Matches 107; Conservative 90; Mismatches 181; Indels 210; Gaps 26;  
 QY 33 LTLSTDPSTIIISAASHDFGNITVTTPGGVCPSSSTADISRLLOVYANGK-STFQVAAQGG 91  
 Db 39 LTMSTDNSIYQ-----LLPDAVVVFRSTADVALIARLAAQERYSSLIPTPRGGG 87  
 QY 92 HSLNGQASVSGGVIVNMTCTID--VVSKDKKYADVAAGTLWVDVLTAKTAEKGVSPVSW- 148  
 Db 88 TGTNGQA-LNQGIIVDMGRHMRNRIIEINPEGVVRVEAG-----VKQOLNQLYLPFGYF 141  
 QY 149 -----TDYLHTITVGGTSLNGG-----ICGVFRNGPLVSNVLE 181  
 Db 142 FAPELSTSNRATLGMINTDASGQSLVYKTSDHVLGVRAVLGGDILDTQPL---PVE 198  
 QY 182 LDVITCKGEML-----TCSRQ-----LNP-----ELF 203  
 Db 199 LAETLGKSNNTTIGRIYNTVYQCRQROQLIINFPLARFLTGYDLRHVFNDWEMTEFDLT 258  
 QY 204 YGVLGGLGQFGIITRARIIVLDHAPKRAKFRMLYSDFTTFTKQBELISMANDIGVDYLE 263  
 Db 259 RLITGSEGLTAFITEARLDITRLPKVRLVNVKYDSFDSALRNAPFMVE-ARALSVEVD 317  
 QY 264 QGIFLSNGVDTSTFFPPSQSKVADLVQK---HGI-----IYVLEVAKYDDP 308  
 Db 318 -----SKVLNAREDIVHVSSELITDVPQDEMGLMIVFAGDD 357  
 QY 309 NLPIISKVIDTLTKLSYLPGFISMHDVAYDFD-----LNRVHVEENKLSRLGLWE- 359  
 Db 358 E-ALIDERNVALCARDEL---LASHQAGVIGVQVCRELAGVERIYAMKK--AVGLLGN 411  
 QY 360 -----LPHWLNLYVPKSR-ILDFHNGVVKDILLKOKSASGLALLYPTNR 403  
 Db 412 AKGAAPPIPAEDTCVPEPEHLADYIAEFRAALDSH-----GLSY-----450  
 QY 404 NKWDNRMSAMIPEIDEDVIILGLQSATPKDLPVEVSNEKIIRFCCKSGIKIKOYLMH 463  
 Db 451 -----GMFHVDAAGLVHVRPALDMPQEQEILMKQISDDVVALTAKYVGLL-----496  
 QY 464 YTSKEDWIEH-----FGSK-WDDFSKRKDLFDPKKLLSPGQ 498  
 Db 497 -----WGERGKGFRABEYSPAFFGESLFAELRKVKAAAFDPHNLNPGK 538

RESULT 15  
 DLD3\_YEAST  
 ID DLD3\_YEAST STANDARD; PRT; 496 AA.  
 AC P39976;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Probable D-lactate dehydrogenase (cytochrome) (D-LCR).  
 GN DLD3 OR YEL071W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OC NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288C / AB972;  
 RX MEDLINE=97313264; PubMed=9169868;  
 RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,  
 RA Arraio R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E.,  
 RA Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,  
 RA Hunnicke-Smith S., Hymann R.W., Kayser A., Komp C., Lashkari D., Lew H.,  
 RA Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,  
 RA Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,  
 RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;

Search completed: April 5, 2004, 17:44:40  
Job time : 20 secs

17 387.5 14.9 137 10 Q94KI5 Q94ki5 triticum ae  
18 376.5 14.5 137 10 Q94KI4 Q94ki4 hordeum vul  
19 226.5 8.7 515 16 Q8NSU5 Q8nsu5 corynebacte  
20 214 8.2 459 2 Q8GAG1 Q8gag1 arthrobacte  
21 206.5 8.0 479 16 Q987W9 Q987w9 rhizobium l  
22 202 7.8 464 2 Q98HK2 Q98hk2 streptomyce  
23 200 7.7 509 16 Q98II2 Q98il2 rhizobium l  
24 196.5 7.6 466 16 Q8VIU9 Q8viu9 mycobacteri  
25 196.5 7.6 470 16 Q69686 Q69686 mycobacteri  
26 196.5 7.6 470 16 Q7TVU9 Q7tvu9 mycobacteri  
27 196 7.6 479 16 Q92U94 Q92u94 rhizobium m  
28 186 7.6 587 10 Q98LW6 Q98lw6 nicotiana t  
29 195 7.5 511 3 Q98FZ1 Q98fz1 neurospora  
30 194 7.5 587 10 Q9FXL9 Q9fxl9 nicotiana t  
31 193.5 7.5 469 16 Q8RD26 Q8rd26 thermosara  
32 192.5 7.4 500 16 Q8F4R3 Q8f4r3 leptospira  
33 192 7.4 461 16 Q87IH1 Q87ih1 vibrio para  
34 192 7.4 588 10 Q8LP11 Q8lp11 lycopersico  
35 185 7.1 439 16 Q82KJ4 Q82kj4 streptomyce  
36 184 7.1 469 16 Q896M6 Q896m6 clostridium  
37 183.5 7.1 459 16 Q69516 Q69516 mycobacteri  
38 182 7.0 581 10 Q92WJ1 Q92wj1 ipomoea bat  
39 181.5 7.0 460 17 Q8PXD0 Q8pxd0 methanosarc  
40 181.5 7.0 481 16 Q8FON1 Q8fon1 leptospira  
41 181 7.0 503 17 Q8TH91 Q8th91 methanosarc  
42 181 7.0 532 10 Q9FKV2 Q9fkv2 arabidopsis  
43 179 6.9 453 16 Q82CC8 Q82cc8 streptomyce  
44 178 6.9 472 2 Q9X5T1 Q9x5t1 streptomyce  
45 178 6.9 488 16 Q8NTW2 Q8ntw2 corynebacte

ALIGNMENTS

RESULT 1  
Q9FE45 PRELIMINARY; PRT; 536 AA.

AC Q9FE45; 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Cytokinin oxidase.  
GN CKO1.  
OS Dendrobium cv. 'Sonia'.  
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales;  
OC Epidendroideae; higher Epidendroideae; Dendrobieae;  
OC Dendrobium.  
OX NCBI\_TaxID=136995;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Yang S., Yu H., Goh C.;  
RT "Molecular cloning and characterization of a cDNA encoding cytokinin  
oxidase in Dendrobium sonia orchid."  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ294543; CAC17753.1; -  
DR EMBL; AJ294542; CAC17752.1; -  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR006094; Oxid\_FAD\_bind.  
DR Pfam; PF01565; FAD\_binding\_4; 1.  
SQ SEQUENCE 536 AA; 60386 MW; ACDF30A77BC940AE CRC64;

Query Match 47.0%; Score 1221; DB 10; Length 536;  
Best Local Similarity 47.9%; Pred. No. 9.9e-80;  
Matches 252; Conservative 82; Mismatches 162; Indels 30; Gaps 11;  
QY 3 NLRIMITLI--TVLMITKSSNGIKIDLPKSLNLTLDPS-----IISAASHDFGN 51  
DB 2 NLHMPFFINPTSLTLLTILMSILIQSPNSLPNTLLTHPTSTHLRFDLSLSAASDFGD 61  
QY 52 ITTVTPGGVCPSTADISRLQYANGKSTFOVAARFGQGHSLNGQASVGGVIVNTCI 111  
DB 62 IIHSLPSAVLPSSPSDIATLLRLSHFSPHSFTVSARGLGHSTRGQAAGFGIVINPMSL 121

OM protein - protein search, using sw model  
Run on: April 5, 2004, 17:41:36 ; Search time 46 Seconds  
(without alignments)  
3436.405 Million cell updates/sec

Title: US-10-014-101-4  
Perfect score: 2596  
Sequence: 1 MANLRMITLITVLMITKSS.....SKKDLFDPKLLSPGQDIF 501

Scoring table: BLCUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : SPTREMBL 25.\*
- 1: sp\_archaea.\*
  - 2: sp\_bacteria.\*
  - 3: sp\_fungi.\*
  - 4: sp\_human.\*
  - 5: sp\_invertebrate.\*
  - 6: sp\_mammal.\*
  - 7: sp\_mhc.\*
  - 8: sp\_organelle.\*
  - 9: sp\_phage.\*
  - 10: sp\_plant.\*
  - 11: sp\_rodent.\*
  - 12: sp\_virus.\*
  - 13: sp Vertebrate.\*
  - 14: sp\_unclassified.\*
  - 15: sp\_virus.\*
  - 16: sp\_bacteriap.\*
  - 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1221	47.0	536	10	Q9FE45	Q9fe45 dendrobium
2	1178	45.4	540	10	Q9FUJ0	Q9fujo arabidopsis
3	1102	42.4	532	10	Q8LJ52	Q8lj52 oryza sativ
4	1091	42.0	558	10	Q94IV9	Q94iv9 oryza sativ
5	1079	41.6	512	10	Q9FWT3	Q9fwt3 arabidopsis
6	1063.5	41.0	525	10	Q8SOF8	Q8sof8 oryza sativ
7	1060	40.8	526	10	Q8H6F6	Q8h6f6 hordeum vul
8	1056.5	40.7	575	10	Q22213	Q22213 arabidopsis
9	1054.5	40.6	520	10	Q84U27	Q84u27 hordeum vul
10	1054	40.6	526	10	Q8S394	Q8s394 hordeum vul
11	993	38.3	504	10	Q9LY71	Q9ly71 arabidopsis
12	991.5	38.2	527	10	Q8LNV6	Q8lnv6 oryza sativ
13	961	37.0	524	10	Q9FUJ1	Q9fuji arabidopsis
14	928.5	35.8	532	10	Q7XKG2	Q7xkg2 oryza sativ
15	498	19.2	458	2	Q84HB2	Q84hb2 streptomyce
16	429	16.5	447	16	Q8YZY0	Q8zyzo anabaena sp

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QY 112 T-DVVVSKDKKYADVAAGTLWDLVLTAKGVSPVSWTDYVLTHTVGGTSLNGIGQGVF 170
DB 122 DGGITVSDGMPVDAGAEQMWDLVRLRHLTPKSWTDYVLTGLGTLNNGISQAF 181
QY 171 ENGLVSNVLELDVITGKGMELTCSRQNLNPELFYVGLGGLGQFGIITRARIIVLDHAPKRA 230
DB 182 LHGPQISNHELDVITGKGMELTCSRQNLNPELFYVGLGGLGQFGIITRARIIVLDHAPKRA 241
QY 231 KWRFLMYSDFTFTTKDQERLISM-ANDIG--VDYLEGQIFLSNGVVD---TSFPFPPSDQS 284
DB 242 RWRMLVW-TDFELFTKQELLISIKAEAGEGKLVNVEGSLLMKSNRSPFFSEKDLK 301
QY 285 KVADLVK-QHGIYVLEVAKYD--DNLPIISKV-----IDTLTKTSLNPLGPFISHMD 335
DB 302 KIKKLASNEGVIYCLEAFYDYGHENFNSRADKAQMDQIEELLRLKSLFVSFGAFRND 361
QY 336 VAYFDLNRVHVEENKLSRLGLWELPHLWLNLYVPKSRILDPHNGVVDKILLLKQKASGL 395
DB 362 VSYMGFLNRVHDGELKRAMGLWDPHPLWLNLFVSKSNIMDFHIGVFVKMGSKS-MGP 420
QY 396 ALLYPTNRKNDNRMSAMTPEIDEDVIYIIGLQSA-TPKDLPEVESVNEKIIRPKCKDSGI 455
DB 421 ILVYPTKSKDKRMSTSP--DEEVYSIGILLSEMNDELHLSHNAEILKPCDQOGM 478
QY 456 KIKQYLMHYTSKEDWIEHFGSKWDDFSKSKDLDPKLLSPQDIF 501
DB 479 NYKQYLPHTYS-EDMKKHFGKWERFVEMKSRVDPKAILSPQKIF 524

RESULT 2
QYFUJ0 PRELIMINARY; PRT; 540 AA.
AC Q9FUJ0;
AT 01-MAR-2001 (T-EMBLrel. 16, Created)
DT 01-MAR-2001 (T-EMBLrel. 16, Last sequence update)
DE 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Putative cytochrome oxidase.
GN CXX6.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Billye K.D., Laskey J.G., Riekhof W.R., VanVickle S., Morris R.O.;
RT "A family of cytochrome oxidases from Arabidopsis thaliana.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF033982; AAC03090.1;
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006094; Oxid_FAD_bind.
DR Pfam; PF01565; FAD binding 4; 1.
DR PROSITE; PS00862; OX2 COVAL FAD; 1.
SQ SEQUENCE 540 AA; 60389 MW; D74DD0D50CEBA76F CRC64;

Query Match 45.4%; Score 1178; DB 10; Length 540;
Best Local Similarity 48.6%; Pred. No. 1.3e-76;
Matches 232; Conservative 84; Mismatches 143; Indels 18; Gaps 7;

QY 39 PSIISAASHDFGNI-TTVTPGGVICSPSTADISRLQYANGKSTFQVAARGQCHSLNGQ 97
DB 48 PSDLASVSSDFGMLKSPPEPLAVLHPSAEDVARLVRTAGSATAPVSAARGHGHISNGQ 107
QY 98 ASVS-GGVVNM-----TCITDVVVSKDKKYADVAAGTLWDLVLTAKGVSPVSWTDYL 152
DB 108 AAGRGVVMNMHGVGTGPKPLRPDEMVDVWGGELWDLVLTAKGVSPVSWTDYL 167
QY 153 HITVGGTSLNGIGQVFRNGPLVSNVLELDVITGKGMELTCSRQNLNPELFYVGLGGLGQ 212
DB 168 YLTVGGTSLNAGISQALHHPQISNVLELDVITGKGMELTCSRQNLNPELFYVGLGGLGQ 227
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QY 213 FGIITRARIIVLDHAPKRAKWFRLMYSDFTFTTKDQERLISMANDIGVDYLEGQIFLSNGV 272
DB 228 FGIITRARIIVLDHAPKRAKWFRLMYSDFTFTTKDQERLISMANDIGVDYLEGQIFLSNGV 287
QY 273 VD---TSFPFPPSDQSKVADLVKQHGIIYVLEVAKYDDPNLPIISKVIDTLTKTSLYLP 329
DB 288 VNNWRSFSPRPVNVKISSVSGNSGVLYCLEITKNYHSDSEIVDQEVIELMKLNFPT 347
QY 330 FISMHDVAVFELNRVHVEENKLSRLGLWELPHLWLNLYVPKSRILDPHNGVVDKILLLKQ 389
DB 348 SVFTTDLQVDFLDRVHKAEELKLSRLGLWELPHLWLNLYVPKSRILDPHNGVVDKILLLKQ 405
QY 390 KASAGLALLYPTNRKNDNRMSAMTPEIDEDVIYIIGLQSA-----TPKDLPEVESVNE 444
DB 406 NKTSGPILYPMKDKWDRSSAVTP--DEEVYVALLRSALTDEETQKLEYLKDQNR 463
QY 445 KIRPKCKDSGIKQYLMHYTSKEDWIEHFGSKWDDFSKSKDLDPKLLSPQDIF 501
DB 464 RILEFCEQAKINVKYLPHPATQEWVAHFQKDRFRSLKAEFFDPRHLATGQRI 520

RESULT 3
Q8LJ52 PRELIMINARY; PRT; 532 AA.
ID Q8LJ52
AC Q8LJ52;
AT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DE 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Putative cytochrome oxidase.
GN P0413G02.1.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa japonica (G3) genomic DNA, chromosome 1, PAC clone:P0413G02.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003344; BAC07345.1;
DR Gramene; Q8LJ52;
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006094; Oxid_FAD_bind.
DR Pfam; PF01565; FAD binding 4; 1.
DR PROSITE; PS00862; OX2 COVAL FAD; 1.
SQ SEQUENCE 532 AA; 58016 MW; C3B56144953DE2FF CRC64;

Query Match 42.4%; Score 1102; DB 10; Length 532;
Best Local Similarity 45.5%; Pred. No. 3.9e-71;
Matches 222; Conservative 89; Mismatches 151; Indels 26; Gaps 9;

QY 35 LSTDPISIISAASHDFGNI-TTVTPGGVICSPSTADISRLQYANGKSTFQVAARGQCHSL 94
DB 41 LSVPSDVMSEASLDFGLTSAEPLAVFHPRGAGDVAALVKAAYGASGIRVSARGHHSI 100
QY 95 NQASVSGGVVNM-----CITDVVVSKDKKYADVAAGTLWDLVLTAKGV 143
DB 101 SQQAAGGVVVDMSHGWRAEAEERTLPVYSPALGGHYIDVWGGELWDLVLTAKGV 160
QY 144 SPVSWTDYVLTHTVGGTSLNGIGQVFRNGPLVSNVLELDVITGKGMELTCSRQNLNPELF 203
DB 161 APRSWTDYVLTHTVGGTSLNGIGQVFRNGPLVSNVLELDVITGKGMELTCSRQNLNPELF 219
QY 204 YGVGLGGLGQFGIITRARIIVLDHAPKRAKWFRLMYSDFTFTTKDQERLISM-NDIGVYL 262
DB 220 FGALGGLGQFGIITRARIIVLDHAPKRAKWFRLMYSDFTFTTKDQERLISM-NDIGVYL 279
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QY 98 ASVS--GGVIVNM-----TCITDVVSKDKYADVAAGTLWVDVLKKTAEKGVSPVSWTDYL 152  
Db 104 AAGRNGVVENMNGVGTGPKFLVRPDENVYDVWGGELWVDVLKKTLEHGLAPKSWTDYL 163  
QY 153 HITVGGTSLNSGIGGVFRNGPLVSNVLELDVITGKGEMLTCSRQLNPFLFYGVGLGQ 212  
Db 164 YLTVGGTSLNAGISGQAFHGGPOISNVLELDVIT-----GQ 199  
QY 213 FGIITRARIIVLDHAPKRAKFWMLYSDFTTFTKDOERLISMANDIGVDVLEGOIFLSNGV 272  
Db 200 FGIITRARIISLPAPQVRVIRVILYSSPKVFTEDEQYILSMHGQKPFYVGGFVIVDEGL 259  
QY 273 VD---TSFPPPSDQSKVADLVKQHGIIYVLEVAKYDDPNLPIISKVIDTLTKLSVLP 329  
Db 260 VNNWSSFFSPNPVKISSVSSNGSVLYCLEITKNYHSDSEIVDQVEIILMKLNFIPT 319  
QY 330 FLSMDVAYFDLNRVHVVEENKRLSLGLWELPWPMLNLYPKSRILDFHNGVWQDILLKQ 389  
Db 320 SVFTTDLQVDFLDVHKAELKRLSKNLWEVPHWNLVFPKSRISDFDKGVFKIL--G 377  
QY 390 KSGASGLALYPTNRNKNWNRMSAMIPEDIDVYIIGLIQSA-----TPKOLPEVESVNE 444  
Db 378 NKTSGPILYPNKKNWDRSSAVTP--DEEVFYLVALLSALTDGEETQKLEYLKQDN 435  
QY 445 KIIRFKOSGIKIQLMYHTSKEDWIEHFGSKWDDFSKRDLPFKLLSPGQDIF 501  
Db 436 RILEFCEQAKINQVLPHPATQEWVAHFGDKWDRFSLKAEFDFRHLATGQRI 492

RESULT 6  
Q8SOF8 PRELIMINARY; PRT; 525 AA.  
ID Q8SOF8  
AC Q8SOF8; 21, Created  
DT 01-JUN-2002 (TREMREL. 21, Last sequence update)  
DT 01-JUN-2002 (TREMREL. 21, Last sequence update)  
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)  
DE Putative cytokinin oxidase.  
GN B1150F11.19.  
OS Oryza sativa (japonica cultivar-group).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Nipponbare;  
RA Sasaki T., Matsumoto T., Yamamoto K.;  
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, BAC  
clone:B1150F11."  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AP003412; BAB90259.1; -  
DR Gramene; Q8SOF8; -  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR006094; Oxid\_FAD bind.  
DR InterPro; IPR006093; Oxid\_FAD BS.  
DR Pfam; PF01565; FAD binding\_4; 1.  
DR PROSITE; PS00862; OX2 COVAL\_FAD; 1.  
SQ SEQUENCE 525 AA; 58011 MW; D10B03BFD4259DDD CRC64;

Query Match 41.0%; Score 1063.5; DB 10; Length 525;  
Best Local Similarity 43.3%; Pred. No. 2.3e-68;  
Matches 205; Conservative 94; Mismatches 153; Indels 21; Gaps 8;  
QY 44 AASHDFGNITVTGGVICPSSTADISRLQ--YAANGKSTFQVARGGSHSLGQASVS 101  
Db 50 AAARDFNRCSLLPAAVHLFGSVSDVAATVRVFLQGRSPLTVARGHSHSLGQSA 109  
QY 102 GGVIVNMTCITDV-----VVSDDKDYADVAAGTLWVDVLKKTAEKGVSPVSWTDYL 155  
Db 110 GGVIVNMESLAAAAARAVRHGGASPHVADPGGELWNLVHLTKHGLAPRSMTDYL 169  
QY 156 VGGTSLNSGIGGVFRNGPLVSNVLELDVITGKGEMLTCSRQLNPFLFYGVGLGQ 215

Db 170 VGGTSLNSGIGGVFRNGPLVSNVLELDVITGKGEMLTCSRQLNPFLFYGVGLGQ 229  
QY 216 ITRARIIVLDHAPKRAKFWMLYSDFTTFTKDOERLISMANDIGVDVLEGOIFLS--NGVD 274  
Db 230 ITRARIALPAPQVRVIRVILYSDFTTFTKDOERLISMANDIGVDVLEGOIFLS--NGVD 287  
QY 275 T--SFPPPSDQSKVADLVKQHGIIYVLEVAKYDDPNLPIISKVIDTLTKLSVLP 332  
Db 288 NWRTSFKPDPVQASQFQSDGRVLYCLEITMNFNDEADIMEQEVGALLSRLSIFST 347  
QY 333 MHDVAYFDLNRVHVVEENKRLSLGLWELPWPMLNLYPKSRILDFHNGVWQDILLKQ 392  
Db 348 YTDVTVLEFDLNRVHVVEENKRLSLGLWELPWPMLNLYPKSRILDFHNGVWQDILLKQ 405  
QY 393 SGLALYPTNRNKNWNRMSAMIPEDIDVYIIGLIQSA---DLPEVSVNEKIIR 448  
Db 406 NGPILYPTNRNKNWNRMSAMIPEDIDVYIIGLIQSA---DLPEVSVNEKIIR 463  
QY 449 FCKDSGIKIQLMYHTSKEDWIEHFGSKWDDFSKRDLPFKLLSPGQDIF 501  
Db 464 FCKNGVGMKQYLAFTTQKQKHAHFGARWETFERKRTYDPLAILAPQRI 516

RESULT 7  
Q8H6F6 PRELIMINARY; PRT; 526 AA.  
ID Q8H6F6  
AC Q8H6F6; 23, Created  
DT 01-MAR-2003 (TREMREL. 23, Last sequence update)  
DT 01-MAR-2003 (TREMREL. 23, Last sequence update)  
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)  
DE Cytokinin dehydrogenase 2 (EC 1.5.99.12).  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Luxor;  
RA Galuszka P., Frebort I.;  
RT "Cytokinin dehydrogenase genes in barley."  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF540382; AAN16383.1; -  
DR GO; GO:0019139; F:cytokinin dehydrogenase activity; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR006094; Oxid\_FAD bind.  
DR InterPro; IPR006093; Oxid\_FAD BS.  
DR Pfam; PF01565; FAD binding\_4; 1.  
DR PROSITE; PS00862; OX2 COVAL\_FAD; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 526 AA; 58848 MW; 9443FF33C75D2C2F CRC64;

Query Match 40.8%; Score 1060; DB 10; Length 526;  
Best Local Similarity 42.2%; Pred. No. 4.2e-68;  
Matches 215; Conservative 100; Mismatches 174; Indels 20; Gaps 10;  
QY 6 LMITLITVMTIKSSNGIKIDPLKSLNLTSTDPESI---ISAASHDFGNITVTGGVIC 61  
Db 9 LKLFLLGLGAVTRAHVHLKHDVLAISLG-TLPDGHFSFHDLSAAMDGNLSFPFVAVL 67  
QY 62 CPSSTADISRLQ--YAANGKSTFQVARGGSHSLGQASVSQGVIVNMTCITDV--VV 116  
Db 68 HFGSVADIATTVRHVFLMGEHSALTVAARGHSHSLGQASQAGGIVIRKMSLSRVKQVH 127  
QY 117 SKDKKYADVAAGTLWVDVLKKTAEKGVSPVSWTDYLITVGGTSLNSGIGGVFRNGPLV 176  
Db 128 PGASPYVDASGGELWNLVHLTKYGLAPKSWTDYHLTVGGTSLNAGVSGQTFRHGP 187  
QY 177 SNVLELDVITGKGEMLTCSRQLNPFLFYGVGLGQFGLITRARIIVLDHAPKRAKFW 236  
Db 188 SNVLELDVITGKGEMLTCSRQLNPFLFYGVGLGQFGLITRARIIVLDHAPKRAKFW 247

QY 237 YSDETTTQDOERLISMANDIGVDYLEGQIFLS-NGVVDI--SFFPPSDOSKVADLVKQH 293  
Db 248 YLDFMSTEDDEMISAEKTF--DYIEGFVNIIRTGILNWRSFNQDPERASRETDR 305  
QY 294 GIIYVLEAKYDDPNLPIISKVIDTTLTKLSYLPGFISMHDVAYDFLNRVHVEENKLR 353  
Db 306 KVLFCLEMTKNFNEPEADIMEQVEHALLSQLRYTPASLFHTDVTYIEFLDRVHSSEMKLR 365  
QY 354 SLGLWELPHPLNLYVPKSRILDFHNGVVKDILLKQKSASGLALLYPTNKNKDNMSAM 413  
Db 366 AKGLWEVPHPLNLYIPRSTIHTTAEQVFGKIL--EDNNNGPILLYPVKSRDNRTSVV 423  
QY 414 IPEIDEDVIYIIGLQSAT--PKDLPEVESVNEKIIREFCKSGIKIKQYLMHYTSKEDWIE 472  
Db 424 IP--DEEVYLVGLFSSAIGSHSIEHTLNLNQIIEFSNKAISGVQYVLPNTYTEPEWKA 481  
QY 473 HFGSKWDDFSKRKDLFDPKLLSPGQDIF 501  
Db 482 HYGARWDAFOQRKNYTDPLAILAPGQKIF 510

RESULT 8  
O22213 PRELIMINARY; PRT; 575 AA.  
AC O22213;  
DT 01-JAN-1998 (TREMELrel. 05, Created)  
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE Putative cytokinin oxidase.  
GN AT2G41510.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=20083487; PubMed=10617197;  
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,  
RA Buehl C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,  
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,  
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,  
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,  
RA Salzberg S.L., Fraser C.M., Venter J.C.;  
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis  
thaliana."  
RL Nature 402:761-768 (1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RA Lin X.;  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; ACC02510; AAB84333.1; -.  
DR F01; T00807; T00807.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR006094; Oxid\_FAD\_bind.  
DR InterPro; IPR006093; Oxred\_FAD\_BS.  
DR Pfam; PF01565; FAD binding 4; 1.  
DR PROSITE; PS00862; OX2\_COVAL\_FAD; 1.  
SQ SEQUENCE 575 AA; 64924 MW; 3005D391A6F4C192 CRC64;

Query Match 40.7%; Score 1056.5; DB 10; Length 575;  
Best Local Similarity 39.8%; Pred. No. 8,7e-68;  
Matches 213; Conservative 102; Mismatches 167; Indels 53; Gaps 12;

QY 9 TLITVLM-----TKSSNGIKIDLPKSNLTLSTDPSTISAA----- 45  
Db 16 TLFGIEMILVLSICPOTNLCSNHSVSTPKELP---SSNPDIRSLVSLDLEGYISFDD 72

QY 46 ----SHDFGNITVTPGGVICPSPSTADISRILQVAAN--GKSTFOVAARGQCHSLNGQAS 99  
Db 73 VHNVAKDFGNRYQLPPLAILHPRSVDFDISSMKHIVHLGSTNLNVAARGHSHLQGOAL 132  
QY 100 VSGGVIVNMTCI--TDVVVSKDKK-YADVAAGTLWVDLKKTAEGVSPVSTDLHLTV 156  
Db 133 AHQGVVIRKESURSDIRIYKGRQYVDVSGGEIWINILRETLKYGLSPKSWTDHLTV 192  
QY 157 GGTLSNGGIGGVFRNGPLVSNVLELDVITKGEMLTCSRQLNPFLFYVGLGLQGFII 216  
Db 193 GGTLSNAGISGQAFKHGQPINNVYQLEIVTGKGVVTCSEKNSSELFFSVLGLGLQGFII 252  
QY 217 TRARIVLHAPRAKRWKMLISDFITFTYKQBERLISMANDIGVDYLEGQIFLSNGVWD-- 274  
Db 253 TRARISLEAPHWKRWIRVLYSDFSFAFSRDQSYLLSKETP--DYVEGVFIINR--TDLL 308  
QY 275 ---TFFPPSDOSKVADLVKQHGIIYVLEVAKYDDPNLPIISKVIDTLTKLSYLPGR 331  
Db 309 NNWRSSFSPNDSTQASRFKSDGKTLVLEVVKYFNPEEASSMDQBTGKLSELNVPSTL 368  
QY 332 SMHDVAYDFLNRVHVEENKLRSLGLWELPHPLNLYVPKSRILDFHNGVVKDILLKQKS 391  
Db 369 FSSEVPYIEFLDRVHIAERKLRAGLWEPHPWLNLLIPKRSIYQFATEVFNILTSNN- 427  
QY 392 ASGLALLYPTNKNKDNMSAMIPEDIEDVIYIIGLQSATP-----KDLPEVESVNEKI 446  
Db 428 -NGPILLYPVNQSCKKHTSLTP--NEDIFVYVAFLPSPVNSSGKNDLLEVLLKQNRV 484  
QY 447 IRPKDSGIIKQYLMHYTSKEDWIEHFGSKVDPSKRKDLFDPKLLSPGQDIF 501  
Db 485 MNFCAAAANLVKYLPHYETQKEMSHFGKRWETFAQRKQAYDPLAILAPGORIF 539

RESULT 9  
Q84U27 PRELIMINARY; PRT; 520 AA.  
AC Q84U27;  
DT 01-JUN-2003 (TREMELrel. 24, Created)  
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE Cytokinin dehydrogenase 3 (EC 1.5.99.12).  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Luxor;  
RA Galuska P., Frebort I.;  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY209184; AAC50082.1; -.  
DR GO; GO:0019139; F:cytokinin dehydrogenase activity; IEA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR GO; GO:0006118; P:electron transport; IEA.  
DR InterPro; IPR006094; Oxid\_FAD\_bind.  
DR InterPro; IPR006093; Oxred\_FAD\_BS.  
DR Pfam; PF01565; FAD binding 4; 1.  
DR PROSITE; PS00862; OX2\_COVAL\_FAD; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 520 AA; 58163 MW; A6FE752806458AD0 CRC64;

Query Match 40.6%; Score 1054.5; DB 10; Length 520;  
Best Local Similarity 43.4%; Pred. No. 1e-67;  
Matches 213; Conservative 96; Mismatches 161; Indels 21; Gaps 11;

QY 24 KIDLPKSNLTLSTDPSTISAA-----ISASHDFGNITVTPGGVICPSPSTADISRILQ--YAA 77  
Db 27 KYDVLASLG-TLFDGHFSFHDLPAAARDFENLSSPPFVAVLHPGSVADIAITVRHVFLM 85  
QY 78 NGKSTFOVAARGQCHSLNGQASVSGGVIVNMTCTIDV---VSKDKKYADVAAGTLWVDV 134

Db 86 GBHSLTVAARGHSHLYGQSQAGGIIVIRMESLOSVMQVHPGASPVVDASGGELWINV 145  
QY 135 LKTAEGKVPVSWTDYLIHTVGGTSLNGGIGGQVFRNGPLVSNVLELDVITGEMLTIC 194  
Db 146 LNKTLKYGLAPKSWTDYLIHTVGGTSLNAGVSGQTFRHGPGQISNVNELEIVTGRDITC 205  
QY 195 SRQLNPELFYVGLGGLGQFGIITRARIIVLDHAPKAKFRWMLYSDFTFKDKQERLISMA 254  
Db 206 SPQNSDLFHAALGGLGQFGIITRARIILEPAPQVWVRVIRVLYLDFMSLTEDQEWLISAE 265  
QY 255 NDIGVYLEGQIFLS-NGVVDTF--SFFPPSQSKVADLVKQHGIIYVLEVAKYDDNLP 311  
Db 266 KTF--DYIEGFVSNRTGILNWRSSFPQPERASQFETDRKVLFCLEMTKNF-NPEEA 322  
QY 312 IISKVIDTLTKTSLYLPFGFISMHDVAYDFNVRVVEENKLSLGLWELPFWNLNLYPK 371  
Db 323 GIMEQIHALLSQRVTPPSLFTDVTYMEFLDRVHSSSEIKLRAKGLWEVFWNLNLIIPR 382  
QY 372 SRILDFHNGVVKDILLKQKASGLALLYPTNRKNWDRMSAMIPEDSDVYIIGLQSA 431  
Db 383 STVHTFAKQVFGKIL--EDNNGNPILLYPVNKSRRWDRNRTSVLP--DEEVSYLVGFLPSA 438  
QY 432 T-PKOLPEVESNEXIIRFCKDSGKIKOYLMHVTSKEDWIEHFGSKWDDFSKRLDFDP 490  
Db 439 MGFHSIKRTLNLNQIIEFSNKASIGVQOYLPHYSTEPWKAHYGARWDATQQRKNYIDP 498  
QY 491 KKLSPGQDIF 501  
Db 499 LAILAPGORIF 509  
  
RESULT 10  
Q8S394 PRELIMINARY; PRT; 526 AA.  
AC Q8S394;  
DT 01-JUN-2002 (T-EMBLrel. 21, Created)  
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)  
DE Cytokinin dehydrogenase 2 (EC 1.5.99.12).  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;  
OC Triticeae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Galuszka P., Frebort I.;  
RT "Cytokinin dehydrogenase genes in barley."  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AP490591; AM08400.2;  
DR GO: GO:0019139; F.cytokinin dehydrogenase activity; IEA.  
DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
DR GO: GO:0006118; P:electron transport; IEA.  
DR InterPro: IPR006094; Oxid\_FAD\_bind.  
DR InterPro: IPR006093; Oxid\_FAD\_BS.  
DR Pfam: PF01565; FAD\_binding\_4; 1.  
DR PROSITE: PS00862; OX2\_COVAL\_FAD; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 526 AA; 58814 MW; 97207FD3C090E62F CRC64;

Query Match 40.6%; Score 1054; DB 10; Length 526;  
Best Local Similarity 42.0%; Pred. No. 1.1e-67;  
Matches 214; Conservative 100; Mismatches 175; Indels 20; Gaps 10;  
  
QY 6 LMITLITVLMITKSSNGIKIDLPKSLNLTSTDPISL-----ISAASHDFGNITVTTPGGVI 61  
Db 9 LKFLLLGLGAVTAHVHVKHDVLASLG-TLPDGHFSFHDLSAAMDFFGNLSFPFPAVL 67  
  
QY 62 CPSTADISRLQ--YAANGKSTFQVAARGQSHLNGQASVSGGVIVNMTCTDV---VV 116  
Db 68 HPGSVADIATTVRHVFLMGHSHSALTVAARGHSHLYGQSQAGGIIVIRMESLRVQMWH 127  
QY 117 SKDKKYADVAGTLWVDVLKTAEGKVPVSWTDYLIHTVGGTSLNGGIGGQVFRNGPLV 176

Db 128 PGASPVVDASGGELMINVLNKLKYGLAPKSWTDYLIHTVGGTSLNAGVSGQTFRHGPGQI 187  
QY 177 SNVLELDVITGKEMLTCSRQINPELFYVGLGGLGQFGIITRARIIVLDHAPKAKFRWML 236  
Db 188 SNVNELEIVTGRDITCSPQNSDLFHAALGGLGQFGIITRARIILEPAPQVWVRVIRV 247  
QY 237 YSDFTFTTKDQERLISMANDIGVYLEGQIFLS-NGVVDTF--SFFPPSQSKVADLVKQH 293  
Db 248 YLDFMSLTEDQEWLISAEKTF--DYIEGFVSNRTGILNWRSSFPQPERASQFETDR 305  
QY 294 GIIVYLEVAKYDDNLPILISKVIDTLTKTSLYLPFGFISMHDVAYDFNVRVVEENKLSL 353  
Db 306 KVLFCLEMTKNFPEADIMEQEVHALLSQRVTPPSLFTDVTYMEFLDRVHSSSEIKLR 365  
QY 354 SLGLWELPFWNLNLYPVNKSRIILDFHNGVVKDILLKQKASGLALLYPTNRKNWDRMSAM 413  
Db 366 AKGLWEVFWNLNLIIPRSTIHTFAQVFGKIL--EDNNGNPILLYPVNKSRRWDRNRTSV 423  
QY 414 IPEDSDVYIIGLQSAT-PKOLPEVESNEXIIRFCKDSGKIKOYLMHVTSKEDWIE 472  
Db 424 IP--DEEVSYLVGFLPSAIGPHSIEHTLNQIIEFSNKASIGVQOYLPHYSTEPWKA 481  
QY 473 HFGSKWDDFSKRLDFDPKLLSPGQDIF 501  
Db 482 HYGARWDATQQRKNYIDPLAILAPGORIF 510  
  
RESULT 11  
Q9LY71 PRELIMINARY; PRT; 504 AA.  
AC Q9LY71;  
DT 01-OCT-2000 (T-EMBLrel. 15, Created)  
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)  
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
DE Cytokinin oxidase-like protein.  
GN MAA21.70.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsiis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W., Rudd S.,  
RA Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA EU Arabidopsis sequencing project;  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL163818; CAB87797.1; -;  
DR PIR: T49185; T49185  
DR GO: GO:0006118; P:electron transport; IEA.  
DR InterPro: IPR006094; Oxid\_FAD\_bind.  
DR Pfam: PF01565; FAD\_binding\_4; 1.  
SQ SEQUENCE 504 AA; 56519 MW; 203961A475847F8D CRC64;

Query Match 38.3%; Score 993; DB 10; Length 504;  
Best Local Similarity 41.5%; Pred. No. 2.8e-63;  
Matches 217; Conservative 100; Mismatches 152; Indels 54; Gaps 14;  
  
QY 6 LMITLITVLMIT-----KSSNGIKIDLPKSLNLTSTDPISLISAASHDFGNITTV 55  
Db 2 LIVRSFTLLSCIAFKLACCFSS-----ISSLKALFLVGHLEFHVHASKDFGNRYQL 57  
  
QY 56 TPGGVICPSSPADISRLQ--YAANGKSTFQVAARGQSHLNGQASVSGGVIVNMTCTID 113  
Db 58 IPLAVLHPKSVSDIASIRHITWMTGTHSOLTVARGHSHLYGQSQAGQTRHGVIVHMSLHP 117  
QY 114 -----VVVSKDKKYADVAGTLWVDVLKTAEGKVPVSWTDYLIHTVGGTSLNGGIGGQ 168  
Db 118 QKLVYSVDSAPYVDVSGGELWINILHETLKYGLAPKSWTDYLIHTVGGTSLNAGISGQ 177



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QY 169 VFRNGPLSVNLELDVITGKGMELTCSRQLNPFLFYGLVGLGQFGIITRARIIVLDHAPK 228
DB 178 AFRGPOISNVHQLIEITVGRKEILNCRQNSDLFNGVLGQFGIITRARIIVLEPAP- 236
QY 229 RAKFRMLYSDFTTFTKDOERLISMANDIGVDYLEGOIFLS-NGVDT---SFEPSDQS 284
DB 237 -----TMDQEQILS-AQHKFDYIEGFVINRTGLLNSWLSLSP--TAEEP 278
QY 285 KVADLVKQHG-IIVVLEVAKYDDPNLFIISKVITDTLTKLSLPGFISMHDVAYFDLFLN 343
DB 279 LEASQKFDGRTLYCLELAKYLKQNDKVINCEVKETLSLSYVTSTLFTTEVAYEAFLD 338
QY 344 RVHVEENKRLSLGWELPHPLNLYVPKSRILDFHNGVGVKDLKQKASGLALLYPTNR 403
DB 339 RVHSEVKLRSGQWEPHPNLLVPRSKINEFARGVFGNILL--TDTSGNPVIVPVNK 396
QY 404 NKWDRNSAMPEIDEDVIYIIGLQSATP-----KD-LPEVESVNEKIIIRFCDSGKIK 458
DB 397 SKNDNQTSAVTPE--EEVFYILVAILTSASPOSAGKGVVEILRRNRILFESEAGLKL 454
QY 459 QYLMHYTSKDWIEHFGSKWDFSKDLDFPKLLSPGQDIF 501
DB 455 QYLPHTYTREWRSHFGKGEFVRKSRYPDLAILAPGHRIF 497

RESULT 12
Q8LNV6 PRELIMINARY; PRT; 527 AA.
AC Q8LNV6;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DE Putative cytochrome oxidase.
GN OSUNBA0012L23.33.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]_TaxID=39947;
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,
RA Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.,
RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
RA Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSUNBA0012L23 genomic sequence.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
RT chromosome 10.";
RL Science 300:1566-1569 (2003).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC051632; AA091887.1; -
DR EMBL; AB017106; AAP54326.1; -
DR Gramene; Q8LNV6; -
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006094; Oxid FAD bind.
DR Pfam; PF01565; FAD binding 4; 1.
SQ SEQUENCE 527 AA; 58428 MW; 9EB8175695F49265 CRC64;

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Query Match 38.2%; Score 991.5; DB 10; Length 527;  
 Best Local Similarity 42.4%; Pred. No. 3.8e-63;  
 Matches 211; Conservative 94; Mismatches 146; Indels 47; Gaps 14;

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QY 311 LNLTLSTPDSIISAASHDFGNITVTGVCIPSTADISILLOYAAN---GKSTFQVAA 87
DB 35 LNLTLPTT-----TTASSDFGRILFHSPSAVLKQPAPRDISLLSFLSPGKVT--VAA 87
QY 88 RQGHSLNGQASVSGVIVNMTCTIIVVV-----SKDKYADVAAGTLDVLDVLTAKSG 142
DB 88 RGAGSHIHQAQALDGIIVVEMSSLSPEIEFYRRGGDVSYADVGGIIMWIELLEQSLKIG 147
QY 143 VSPVSWTDYHLITVGGTSLNGIGGQVFNGLVSNVLELDVITGKGMELTCSRQLNPFL 202
DB 148 LAPRSWTDYLYTIGTGLSNAGISQITFKHGQISNVQLQLEVVTGGEIVTCSPTKDAEL 207
QY 203 FYGVGLGQFGIITRARIIVLDHAPKRAKWFMLYSDEFTTFTKDOERLISMANDIGVDYL 262
DB 208 FNAVGLGQFGIITRARIIVLDHAPKRAKWFMLYSDEFTTFTKDOERLISMANDIGVDYL 265
QY 263 EGQIFLNSGVDTSS---FPPPSQSKVADLVKQHG-----IIVVLEVAKY-YDDNLPIL 313
DB 266 EGQIFLNEQSLHSSSIATFTN-----VDFNPDFGTNNPKIYICIEFAVHD;QNNKIN-V 319
QY 314 SKVIDTLTKLTVLPGLFISMHDVAYFDLNRVHVVENKRLSLGLWELPHPLNLYVPKSR 373
DB 320 EQVEVISRQMSHIAHLSYSEVSFYDFLNRVMEEMSLRNSGLNEVHPHPLNMFVPSAG 379
QY 374 ILDFHNGVVKDILLKOKSA---SGLALYPTNRNKNWDRNSAMPE--IDEDVIYIIGL 428
DB 380 ISDF-----RDLMDSISPDNFEGLIYIPLLRHKWDINTSVLPDPSGSTDQVMYAVGIL 434
QY 429 QSATPKDLPEVESVNEKIIRF-----CKDSGKIKQYLMHYTSKDWIEHFGSKWDDFSK 483
DB 435 RSANPDGCSHHCQLQELLRHRRLAGAAAGLGAQYLAHHTPAGWRHFRGWRWERFAD 494
QY 484 RKDLDFPKLLSPGQDIF 501
DB 495 RKARDFPRCILGPGQIF 512

RESULT 13
Q9FUJ1 PRELIMINARY; PRT; 524 AA.
AC Q9FUJ1;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DE 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Cytochrome oxidase (FAD-linked oxidoreductase family).
GN CKX5.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bilyeu K.D., Laskey J.G., Riekhof W.R., VanVickle S., Morris R.O.;
RT "A family of cytochrome oxidases from Arabidopsis thaliana.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Town C.D., Haas B.J., Maiti R., Hannick L.I., Chan A.P., Renning C.M.,
RA Smith Jr R.K., Arbogast T., Tallon L.J., Utterback T.R., VanAken S.E.,
RA Feldblyum T.V., Yu C., Wortman J.R., White O., Fraser C.M.;
RT "Arabidopsis thaliana chromosome 5 BAC F13M11 genomic sequence.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF303981; AAC30908.1; -
DR EMBL; AC140977; AAC073882.1; -
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR006094; Oxid FAD bind.
DR Pfam; PF01565; FAD binding 4; 1.
SQ SEQUENCE 524 AA; 57975 MW; 9ADB3BE97A7F063C CRC64;

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Query Match 37.0%; Score 961; DB 10; Length 524;

Best Local Similarity 41.0%; Pred. No. 6e-61; Mismatches 91; Indels 30; Gaps 12;  
Matches 207; Conservative 91; Mismatches 177; Indels 30; Gaps 12;  
QY 18 KSSNGIKIDLPKSNL--TLSTDPSTIISAASHDFGNITVTPGGVICSADISRLQY 75  
Db 25 KSTGVS---ESLNIQEIILCGGAADIAIGDEFGMCVKFLAVRFPVGPEDIAAGVK- 79  
QY 76 AANGKSTFOVARGGCHSLNGQASVSGGVIVNMTCTD-----VVSKDKKDYADYAG 128  
Db 80 AALRSKDLTVARGNGHSINGQAAEGGLVVDMSSTAENHFEVGLSGGDATFVDVSGG 139  
QY 129 TLWVDVLKK-TAEKGVSPVSWTDYHLHTVGGTSLNGGIGGVFRNGPLVSNVLELDVITG 187  
Db 140 ALWEDVLKRCVSEYGLAPRSWTDYGLVGGTSLNAGVSGQAFRGVPGQTSNVTELDVVTG 199  
QY 188 KGEMLTCSRQNLNPELFGVGLGQFGIITRARIIVLDHAPKRWFRMLYSDFTTFYKQ 247  
Db 200 NGDVVTCSEIENSELFFSLGGLGQFGIITRARIIVLDHAPKRWFRMLYSDFTTFYKQ 259  
QY 248 ERLISWANDIGVDYLEGQIFLSNGVVDTSFPP-----PSDOSKQADLVKQHG-IYVLEV 301  
Db 260 EWLVSQKNESDYVEGFVV-NGADPVGWTFVPLHDPHDFPRLPQSGSVLYCLEL 318  
QY 302 AKYY-DDPNLPIISKVIDTLTKTSLYLPFGFISMHDVAFDFLNRVHVVENKLSGLWEL 360  
Db 319 GLHYRDSNSIDKVRERLIGRLRFNEGLRPEVDLPYVDLFLRVKRESEIAKENGWTET 378  
QY 361 PFWNLNLYPKSRILDFHNGVVKDILLKQKASGLALYPTNRKNDNRMSAMIDEIDED 420  
Db 379 PFWNLNLYPKSRILDFHNGVVKDILLKQKASGLALYPTNRKNDNRMSAMIDEIDED 420  
QY 421 VYIIGLQSATP-----KDLPEVESVNEKIIIFKCDGSKIKIYLMHYTSKEDTIEHFGS 476  
Db 436 IFVIVALLRFVPPCAKVSSEKMAQNEIHWCKVNGIDYKLYLPHYKSBQEWIRHFGN 495  
QY 477 KWDFFSKRDLDPKLLSPGQDIF 501  
Db 496 RMSRFVDRKAMFDPMAILSPGQKIF 520  
RESULT 14  
Q7XKQ2 PRELIMINARY; PRT; 532 AA.  
AC Q7XKQ2; Q7XKQ2;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE OSTNB0065J09.7 protein.  
GN OSTNB0065J09.7  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzoae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Han B., Feng Q., Huang Y.C., Li Y., Zhu J.J., Zhao Q.J., Hu X.,  
RA Lu Y.L., Mu J., Yu Z., Chen L., Fan D.L., Meng Q.J., Zhang L.,  
RA Lu Y.Q., Yu S.L., Liu X.H., Lu T.T., Zhang Y.J., Lu Y., Li C., Li T.,  
RA Zhang Y., Hu H., Jia P.X., Qian Y.M., Ying K., Zhou B., Chen Z.H.,  
RA Hao P., Zhang L., Wu M., Zhang R.Q., Guan J.P., Fu G., Wang S.Y.,  
RA Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F., Jia J., Yin H.F.,  
RA Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y., Shao C.Y., Sun Y.,  
RA Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W., Sheng H.H.,  
RA Gu J.L., Chen S.T., Ni L., Zhu P.H., Hong G.F.,  
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL663010; CAB05711.1; -.  
SQ SEQUENCE 532 AA; 57618 MW; 78D3740726B60A2C CRC64;  
Query Match 35.8%; Score 928.5; DB 10; Length 532;  
Best Local Similarity 41.7%; Pred. No. 1.4e-58;  
Matches 224; Conservative 76; Mismatches 182; Indels 55; Gaps 15;

QY 4 LRLMITLITVLMITKSSNGIKIDLPKS-INLTLSTDPSTIISAASHDFGNITVTPGGVIC 62  
Db 3 LKAVLYAAVLAVLTCSSVNFQSPDVLGPVALLPTSSA--RDFGAVVSDAPFAVVR 60  
QY 63 PSTADISELL---QYANGKSTFOVARGGCHSLNGQASVSGGVIVNMTCTD-VV 116  
Db 61 PESPDDIALLLGALSSTAPSPAT--VAAGVAGHSLHGOAQARDGIVVETRALPDRHV 118  
QY 117 SKD-----KKYADVAAGTLDVVLKTAEGVSPVSWTDYHLHTVGGTSLNGGIG 166  
Db 119 SARAHGGDDATVAVADVAGALWVEVLEBCLGLAPPSTWTDYLYLTVGGTSLNGG 178  
QY 167 GQVFRNGPLVSNVLELDVITGKEMLTCSRQNLNPELFGVGLGQFGIITRARIIVL 226  
Db 179 GQTFKHGQPLSNVLELDVITGKEMLTCSRQNLNPELFGVGLGQFGIITRARIIVL 238  
QY 227 PKBAKFRMLYSDFTTFKQBELISMANDIGVDYLEGQIFLSNGVVDTSF-----F 278  
Db 239 PPKVRVAFYDSFETFTGQELLVSMPEQ--VDYVEGFWLNEQSLHSSVAFPAQLNF 296  
QY 279 PPSDQSKVADLVKQHGIIYVLEKAYVDDPNLPIISKVIDTLTKTSLYLPFGFISM 338  
Db 297 SPDFGSK-----GRKKVYICIEFAVHDFQDSSRADHVVVKLVSAKLSYLPHV 351  
QY 339 FDFLNRVHVVENKLSGLWELPFWNLNLYPKSRILDFHNGVVKDILLKQKSA---S 395  
Db 352 FDFLNRVHVVENKLSGLWELPFWNLNLYPKSRILDFHNGVVKDILLKQKSA---S 395  
QY 396 ALLYPTNRKNDNRMSAMIDEIDEDVYIIGLQSATPKDLPE--YESVNEKIIIF- 449  
Db 407 ILVYPLLTLDKWDGNTSAVVPAAPDGVMYIFGVLRSTDPARCGRACVDSIMARH 466  
QY 450 CKDS-----GIKIKVLMHYTSKEDTIEHFGSKWDDFSKRLDFPKLLSPGQDIF 501  
Db 467 CRDGGGGGIGAKQYLARQSPARWRDHFAGNGRFAAKARFDPHLVLPFGQGI 523  
RESULT 15  
Q84HB2 PRELIMINARY; PRT; 458 AA.  
AC Q84HB2;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Oxidase.  
OS Streptomyces carzinostaticus subsp. neocarzinostaticus.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=167636;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Liu W., Nonaka K., Nie L., Bae J., Zazopoulos E., Farnet C.M.,  
RA Shen B.;  
RA "Biosynthesis of the chromoprotein enediynes neocarzinostatin in  
RT Streptomyces carzinostaticus: analysis of the gene cluster and  
RT deduction of the biosynthetic pathway.";  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY117439; AAM78001.1; -.  
DR GO; GO:0006118; P-electron transport; IEA.  
DR InterPro; IPR006094; Oxid\_FAD\_bind.  
DR Pfam; PF01565; FAD\_binding\_4; 1.  
SQ SEQUENCE 458 AA; 48784 MW; 3606B6C8E881D5D4 CRC64;  
Query Match 19.2%; Score 498; DB 2; Length 458;  
Best Local Similarity 32.2%; Pred. No. 1.5e-27;  
Matches 141; Conservative 80; Mismatches 155; Indels 62; Gaps 14;  
QY 15 MITKSSNGIKIDLPKSNLTLSTDPSTIISAASHDFGNITVTPGGVICSADISRLQ 74  
Db 24 ILRSRGPFSRLGLP-LLRGLTSLTRDSDLTAAARDFGNRIHURPVAVLHPADAEDV 82  
QY 75 YA-ANGKSTFOVARGGCHSLNGQASVSGGVIVNMTCTITDVVSKDKKYADYAGTLM 133

Db	83	FGRENG---FAVVRGAACSVGQQTSDGIVVDSLSLS-AVGEPAPSLVRVDGGARWEA	138
Qy	134	VLKKTAEKGVSPVSWTDYHLITVGGTILSNGIGGQVFRNGPLVSNVLELDVITGKGEMLT	193
Db	139	VLEATLPGGRVPLVPPHGLSVGGTILSVGGIGGTSHRYGVSADNVLELEVVTASGDLIT	198
Qy	194	CSROLNPELFYVGLGGLGQFGIITRARIVLDPHAKRAKWERMLYSOFTTTTKDQERLISM	253
Db	199	CSPVRPELFDVAVRGSJGRYGIITGATLALTGARSSARTYRLVTHDCAAFIADQORLV--	256
Qy	254	ANDIGVDYLEQIIFLSNGVDTSPFPDQSKVADLVKQHGIIYVLEVAKYDDPNLPPII	313
Db	257	-HERRFEHVEGHARSG-----TS-----GWLFLVLEAMQSFDTPHEPDD	294
Qy	314	SKVIDTLTKLSYLPFGFISMHDVAYDFLNRVHVEENKLSGLWE-LPHWNLNLYVPKS	372
Db	295	TALLEGLTH-----HHVDTIETVSYRDFLGRVAPLEARQALGSMQHHPHRCNVLLP--	347
Qy	373	RILDFHNGVVKDILLKOKSA-----SGLALLYPTNRKNKNDNRMSAMIPEIDE--DV	421
Db	348	-----GLEBALITRILAGITEEDIGFGGSVLLYPIP-----TARLAA--PHVPKARDA	394
Qy	422	IYIIGLLQSATPKDLPEV	439
Db	395	LTVVFGLOQTAPPDQPEL	412

Search completed: April 5, 2004, 17:45:39  
Job time : 49 secs



OM protein - protein search, using sw model

Run on: April 5, 2004, 17:43:01 ; Search time 22 Seconds  
(without alignments)  
1175.664 Million cell updates/sec

Title: US-10-014-101-4  
Perfect score: 2596  
Sequence: 1 MANRLMITLITVIMTKSS.....SKRKDLFPKLLSPQDIF 501

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Issued Patents AA.\*
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  - 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
  - 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
  - 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
  - 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*
  - 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1141	44.0	534	3	US-09-124-541-1
2	1141	44.0	534	4	US-09-663-326-1
3	214.5	8.3	458	4	US-08-624-447-4
4	193.5	7.5	495	3	US-09-217-490-2
5	183.5	7.1	459	4	US-08-311-731A-47
6	178	6.9	472	4	US-09-266-965-128
7	177.5	6.8	610	4	US-09-630-983A-1
8	175.5	6.8	600	4	US-09-423-468A-13
9	175.5	6.8	600	4	US-09-630-983A-3
10	174	6.7	468	4	US-09-328-352-6023
11	169	6.5	440	4	US-09-630-983A-9
12	168.5	6.5	540	4	US-09-647-390-18
13	166.5	6.4	592	4	US-09-423-468A-15
14	166	6.4	1036	4	US-09-489-039A-10266
15	160	6.2	1019	4	US-09-543-681A-4447
16	159	6.1	535	4	US-09-589-733C-18
17	155.5	6.0	538	4	US-09-647-390-16
18	154	5.9	529	4	US-09-589-733C-17
19	153.5	5.9	448	4	US-08-624-447-5
20	151	5.8	529	4	US-09-589-733C-16
21	149	5.7	538	4	US-09-589-733C-19
22	146.5	5.6	514	4	US-09-266-965-114
23	142.5	5.5	542	4	US-09-589-733C-2
24	142.5	5.5	542	4	US-09-589-733C-20
25	129.5	5.0	526	4	US-09-630-983A-5
26	129.5	5.0	526	4	US-09-630-983A-7
27	126.5	4.9	643	4	US-09-252-991A-23842

28	126	4.9	473	4	US-09-540-236-3656	Sequence 3656, Ap
29	116	4.5	529	4	US-09-252-991A-27777	Sequence 27777, A
30	116	4.5	725	3	US-08-425-843-2	Sequence 2, Appli
31	115	4.4	488	4	US-09-540-236-3681	Sequence 2681, Ap
32	113	4.4	529	4	US-09-433-248A-6	Sequence 6, Appli
33	113	4.4	614	4	US-09-328-352-4369	Sequence 4369, Ap
34	113	4.4	3169	4	US-09-453-702B-257	Sequence 257, App
35	110	4.2	422	4	US-09-634-238-227	Sequence 227, App
36	108	4.2	344	4	US-09-198-452A-857	Sequence 857, App
37	108	4.2	1012	1	US-08-219-262B-9	Sequence 9, Appli
38	108	4.2	1012	3	US-09-031-655-9	Sequence 9, Appli
39	105.5	4.1	527	4	US-09-252-991A-23709	Sequence 23709, A
40	105	4.0	715	3	US-08-425-843-7	Sequence 7, Appli
41	105	4.0	1012	1	US-08-219-262B-5	Sequence 5, Appli
42	105	4.0	1012	3	US-09-031-655-5	Sequence 5, Appli
43	104	4.0	816	4	US-09-328-352-6677	Sequence 6677, Ap
44	104	4.0	1012	1	US-08-219-262B-7	Sequence 7, Appli
45	104	4.0	1012	3	US-09-031-655-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1  
US-09-124-541-1  
; Sequence 1, Application US/09124541A  
; Patent No. 6229056  
; GENERAL INFORMATION:  
; APPLICANT: Morris Ph.D., Roy O.  
; TITLE OF INVENTION: A CYTOKININ OXIDASE  
; FILE REFERENCE: UMO1490  
; CURRENT APPLICATION NUMBER: US/09/124,541A  
; CURRENT FILING DATE: 1998-07-29  
; EARLIER APPLICATION NUMBER: 60/054,268  
; EARLIER FILING DATE: 1997-07-30  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 534  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-09-124-541-1

Query Match 44.0%; Score 1141; DB 3; Length 534;  
Best Local Similarity 47.0%; Pred. No. 2.3e+105;  
Matches 233; Conservative 83; Mismatches 152; Indels 28; Gaps 11;

Qy	30	SLNLTSTDPISIIASAASHDFGNITVT	PGGVICPSSTADISRLQVAANGKS--TFQVAA	87
Db	42	ALDGKRTSNATRAASTDFGNITTSALP	AVLPSTGDLVALLS-AANSTPGWPYIAF	100
Qy	88	RGQGHSLNGQASVSGVIVNMTCTD-----	VVVSQKKYADVAAGTLWVDVLKKTAEK	141
Db	101	RGRGHSLMGQAFAPGGVWVNMASLGDAA	APPGINVSADGRYVDAGGEQVWIDVLRAS	160
Qy	142	GVSPVSTWYLYHTVGGTISNGGIGGVFR	NGPLVSNVLELDVITGKGMLTCSRQINPE	201
Db	161	GVAPRWNWLYLYTVGGTISNAGISQAF	HRHQPIINVLMDVITGHEWVTCCKQLNAD	220
Qy	202	LFYGVGLGQOFGIITRAKIVLDHAPKRW	KFMLYSDFTFTKQOERLISMANDTG----	258
Db	221	LFDVGLGLGQFGVITTRARIVAPAPAR	ARWRFVVTDFAAFSADQOERLTAPRPGG	280
Qy	259	---VDILEGQIF-----LSNGVVTST	PEPDSQKQVADLVKQHG--IIVLEVAKYY	309
Db	281	FGPMYSYVEGFFVFNQSLATDLANTGFT	TDADVARIVVALAGERNATTVYSIEATLN	340
Qy	310	--LPITISKVIDTLTKLSYLPFGFISM	HDVAYDFLNRHVVEENKLSLGLWELPHW	367
Db	341	AAAAVDQELASVLGTLSYVEGFAFQD	VAYAAFLDRVHGEEVALNKLGLWRVPHW	400
Qy	368	YVPSKRIIDFHNGVVKDILKQKSAGL	ALLIYTNKKNKDNRSAMTPEDEDEVIYI	427

Db 401 FVPRSRADFRGVFKGI-LQGTDIVGLIYVPLNKSMDGMSAATP--SEDFVYAVSL 457

QY 428 L-QSATPKDLPEVSNKEIIRFKCDSKGIKQYLMHYTSKEDWIEHFG-SKNWDFSKRK 485

Db 458 LFSSVAPNDLARLQONRRILRFDCLAGIQKTYLARHTDRSDWVRHFGAAKNRFVEMK 517

QY 486 DLFDPKLLSPGQDIF 501

Db 518 NKYDPKLLSPGQDIF 533

RESULT 2

US-09-663-326-1

; Sequence 1, Application US/09663326

; Patent No. 6617497

; GENERAL INFORMATION:

; APPLICANT: Morris Ph.D., Roy O.

; TITLE OF INVENTION: A CYTOKININ OXIDASE

; FILE REFERENCE: UMO1490

; CURRENT APPLICATION NUMBER: US/09/663,326

; CURRENT FILING DATE: 2000-09-15

; PRIOR APPLICATION NUMBER: 60/054,268

; PRIOR FILING DATE: 1997-07-30

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: Patent In Ver. 2.0

; SEQ ID NO 1

; LENGTH: 534

; TYPE: PRT

; ORGANISM: Zea mays

US-09-663-326-1

Query Match 44.0%; Score 1141; DB 4; Length 534;

Best Local Similarity 47.0%; Pred. No. 2.3e-105;

Matches 233; Conservative 83; Mismatches 152; Indels 28; Gaps 11;

QY 30 SUNLSTDPISIAASHDFGNITVTPGGVICPSTADISRLLOYANGKS--TFQVAA 87

Db 42 ALDGLRTDSNATAAASDTFGNITSALPAVLYPSSSTGDLVALLS-AAANSTPGFPYITAF 100

QY 88 RQGHSLNGQASVSGGVIWMTCTID-----VWVKDKKYADVAAGTLWVDVLKTKTAEK 141

Db 101 RGEHSLMGQAPAGGVVWNASLGDAAAPPNGINSADGRYVDAGGEQWIDVLRASLAR 160

QY 142 GVSVPWTDYLIHTVGTLSNGGIGQVFRNGPLVSNVLELDVITCKGEMLTCSQLNPE 201

Db 161 GVAPRSWNDYLYTVGGTSLNAGISQAPFRHQISNVLEMDVITGHGEMVTCRQLNAD 220

QY 202 LEVGVLLGGLQFGILITRAIIVLDHAPKRAKWFRLYSDFTTFTKDOERLISMANDIG-- 258

Db 221 LFDVLLGGLQFGVITRAIIVLEPAPARARWRFVITDPAFSAQOERLTAPRPGGGAS 280

QY 259 ---VDLEGQIF----LSNGWVDTSPFPDSQSKVADLVKQHG--IIYVLEVAKYDDPN 309

Db 281 FGMSYVEGVSFVNQSLATDLANTGFTDADVARIVVALAGERNATTVYSIEATLNYDNAT 340

QY 310 --LPIISKVIDTLTKTSLYLPGFISMHDVAYDFLNRVHVEENKLSLGLWELPPLNL 367

Db 341 AAAAAVDQELASVLGTLVSVEGFQFORDVAYAAFLDRVHGEVVALNKGLMKRVPPLNLM 400

QY 368 YVFKSRILDFHNGVWVDIILKOKSAGSLALYPTNRKNWDRMSAMIPEIDEDVIYIIGL 427

Db 401 FVPRSRADFRGVFKGI-LQGTDIVGLIYVPLNKSMDGMSAATP--SEDFVYAVSL 457

QY 428 L-QSATPKDLPEVSNKEIIRFKCDSKGIKQYLMHYTSKEDWIEHFG-SKNWDFSKRK 485

Db 458 LFSSVAPNDLARLQONRRILRFDCLAGIQKTYLARHTDRSDWVRHFGAAKNRFVEMK 517

QY 486 DLFDPKLLSPGQDIF 501

Db 518 NKYDPKLLSPGQDIF 533

RESULT 3

US-08-624-447-4

; Sequence 4, Application US/08624447A

; Patent No. 6524812

; GENERAL INFORMATION:

; APPLICANT: Sherman, David H.

; APPLICANT: August, Paul R.

; APPLICANT: Flickinger, Michael C.

; TITLE OF INVENTION: Genes encoding resistance to DNA

; TITLE OF INVENTION: bioreductive alkylating or cleaving agents and methods for

; TITLE OF INVENTION: identifying agents that inhibit resistance to DNA

; TITLE OF INVENTION: bioreductive alkylating and cleaving agents

; FILE REFERENCE: 600.458US1

; CURRENT APPLICATION NUMBER: US/08/624,447A

; CURRENT FILING DATE: 1996-08-19

; EARLIER APPLICATION NUMBER: PCT/US94/11279

; EARLIER FILING DATE: 1994-10-06

; EARLIER APPLICATION NUMBER: US 08/133,963

; EARLIER FILING DATE: 1993-10-07

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 4

; LENGTH: 458

; TYPE: PRT

; ORGANISM: Arthrobacter oxidans

US-08-624-447-4

Query Match 8.3%; Score 214.5; DB 4; Length 458;

Best Local Similarity 24.5%; Pred. No. 1.3e-12;

Matches 69; Conservative 58; Mismatches 122; Indels 33; Gaps 10;

QY 35 LSTDPISIAASHDFGNITVTPGGVICP-----STADISRLLOYAA-NKSTFQVA 86

Db 9 LSIQGEVIYVQDPSGFDIAININDGRHLQRPSTIARCLSGADVAKSVRYACDNG---LEIS 65

QY 87 ARGQHSLSNGQASVSGGVIWMTCTIDVVVSKDKKYADVAAGTLWVDVLKTKTAEGVSPV 146

Db 66 VRSGHNPNGYAINDDGIVLDLRLMNSIHIDTAGSRARIGGVISGDLVKEAAKFGLAIV 125

QY 147 SWTDYLIHTVGT--GTLNNGIGQVFRNGPLVSNVLELDVITCKGEMLTCSQLNPELFY 204

Db 126 TG---MHPKVGFCGLALNGGVGLTTPKYGLASNLILGATLVATGTVICDSDDERPELFW 182

QY 205 GVLLGGLQFGIITRAIIVLDHAPKRAKWFRLYSDFTTFTKDOERLISMANDIGVDYLEG 264

Db 183 AVRGAGNFQVTEVEVQLYELP-----FKMLAGITWAPSVSELAGLITSL-LDAL-- 233

QY 265 QIFLSNGVVD---TSFPPSPDQSKVADLVKQHGIIYVLEVAK 303

Db 234 ----NEMADHIYPSVFGVDENRAPSVTVCVHGLGLDIAE 270

RESULT 4

US-09-217-490-2

; Sequence 2, Application US/09217490

; Patent No. 6165761

; GENERAL INFORMATION:

; APPLICANT: Schneider, Palle

; APPLICANT: Christensen, Soren

; APPLICANT: Dybdal, Lone

; APPLICANT: Fuglsang, Claus Crone

; APPLICANT: Xu, Feng

; APPLICANT: Golightly, Elizabeth

; TITLE OF INVENTION: Carbohydrate Oxidase And use Thereof In

; FILE REFERENCE: 5421.200-US

; CURRENT APPLICATION NUMBER: US/09/217,490

; CURRENT FILING DATE: 1998-12-21

; EARLIER APPLICATION NUMBER: PA 1997 01505

; EARLIER FILING DATE: 1997-12-22

; EARLIER APPLICATION NUMBER: PA 1998 00763

; EARLIER FILING DATE: 1998-06-04

; EARLIER APPLICATION NUMBER: 60/068,717

; EARLIER FILING DATE: 1997-12-23

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; EARLIER APPLICATION NUMBER: 60/088/725
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Microdochium nivale
US-09-217-490-2

Query Match          7.5%; Score 193.5; DB 3; Length 495;
Best Local Similarity 20.4%; Pred. No. 1.9e-10;
Matches 110; Conservative 82; Mismatches 225; Indels 121; Gaps 20;

QY 7 MITLITVMTK-----SSNGIKIDLPKSLNLTSTDPSSIISAASHDFGNITVTPGG 59
Db 11 LITASDALVTRGAIEACLSAAGVPIIDPGTAYRDVEP-----FNIRLPYIPTA 61
QY 60 VICPSSADISRLQYANGKSTFOVARGGCHLN--GQASVSGGVIVNMTCITDVVVS 117
Db 62 IAOQTTHAIOAVQCAK--KLNKVSASGSGHVSASFSGGENGHLVMQLDRMIDVISY 119
QY 118 KDKX-YADVAAG-----TLWVVLKKTAEKGVSPVSWTDYHLHITVGGTSLNNGIGQV 169
Db 120 NDKGTIAHVEPGARLGLHATVLDNDKYGRAISHGTCP-----GVGISGHFAHGFGFSS 172
QY 170 FRNGPLVSNVLELDVITGKGEMLTCSRQNLNPELFGVLGGLQFGIITRARIVLDHAPKR 229
Db 173 HMHGLAVDSVGVTVVLADGRIVEASATENADLFWGKAGSNGFIIVAVKMLATFPAPKV 232
QY 230 AKWP--RMVLSDFTTFTKQERLISMANDIG---VDYLEGQIFLNSGVVDTSPFPSPDQS 284
Db 233 LTRFGVTLNWKNTSALKGIEAIVEDYARWAPREVNFRAIGDYAGNPGIEGLYYGTPEQW 292
QY 285 KVADLVKQHGIIYVLEKAYVDDNPLIISKVIDTL-----TKTLSYLPGLFSMHDV 336
Db 293 RAA-----FQPLDLPAGYVNVPTLSLNWIESVLSNFP 327
QY 337 AYFDFELNRVHEENKRLSLGLMELPFWNLVYP-----KSRI-----LDFHNGVYK 383
Db 328 DHVDFITPQVENFVAKSLTLKSIKGDVAKNFVDYFVDSNKNVDKRFWFYQLDVHGGKNS 387
QY 384 DILLKQKSAGSGLLYPNRKNK-----DNMSAMIPEDIDEDVIILGLOSATPKD 435
Db 388 QV---TKVTNAETAYPHRDKLWLIQFYDRYDNNQT--YPE--TSFKFLDGWVNSVT-KA 438
QY 436 LPEVE---SVNEKIIKFCNKGSIKKIQLYMHYTSKEDWIEHFGSKWDDFSSKRLDFP 490
Db 439 LPKSDGMVINYADPRMDRDYATKV-----YYGENLARLQKLKAKFDP 481

RESULT 5
US-08-311-731A-47
; Sequence 47, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSES: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/311,731A
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIUM LAPRAE
US-08-311-731A-47

Query Match          7.1%; Score 183.5; DB 4; Length 459;
Best Local Similarity 30.4%; Pred. No. 1.7e-09;
Matches 55; Conservative 29; Mismatches 88; Indels 9; Gaps 3;

QY 111 ITDVV-VSKDKYADVAACTLMVDVLKKTAEKGVSPVSWTDYHLHITVGGTSLNNGIGQV 169
Db 58 LTCIGIDTEARTADVAGMCTYEDLVAATLPVGLLPVLPQLKTTITLGGAVTGLGIESAS 117
QY 170 FRNGPLVSNVLELDVITGKGEMLTCSRQNLNPELFGVLGGLQFGIITRARIVLDHAPKR 229
Db 118 FRNGLPHESVLEMDILTGAELLTVSANQHGLYRAFNPSTGLGYSTRFRISLEPVTFF 177
QY 230 AKWFRMLYSDFTTFTKQERLISMANDIG---VDYLEGQIFLSN-----GVVDTSFPPPS 281
Db 178 VALHRFRHLLIEMVTAMENIIDTGGHDGVPDYLDGVVFSANESYLCIGKTTTPGPVS 237
QY 282 D 282
Db 238 D 238

RESULT 6
US-09-266-965-128
; Sequence 128, Application US/09266965
; Patent No. 6495348
; GENERAL INFORMATION:
; APPLICANT: Sherman, D
; APPLICANT: Mao, Y
; APPLICANT: Varogiu, M
; APPLICANT: He, M
; APPLICANT: Sheldon, P
; TITLE OF INVENTION: Mitomycin biosynthetic gene cluster
; FILE REFERENCE: 600.456US1
; CURRENT APPLICATION NUMBER: US/09/266,965
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US 08/524,447
; EARLIER FILING DATE: 1996-08-19
; EARLIER APPLICATION NUMBER: PCT/US94/11279
; EARLIER FILING DATE: 1994-10-06
; EARLIER APPLICATION NUMBER: US 08/133,963
; EARLIER FILING DATE: 1993-10-07
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 128
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Streptomyces lavendulae
US-09-266-965-128

Query Match          6.9%; Score 178; DB 4; Length 472;
```





APPLICANT: Porro, Danilo  
APPLICANT: Sauer, Michael  
TITLE OF INVENTION: Ascorbic Acid Production from Yeast  
FILE REFERENCE: 2028.594000  
CURRENT APPLICATION NUMBER: US/09/630,983A  
CURRENT FILING DATE: 2000-08-02  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 600  
TYPE: PRT  
ORGANISM: Brassica oleracea  
US-09-630-983A-3

Query Match 6.8%; Score 175.5; DB 4; Length 600;  
Best Local Similarity 19.8%; Pred. No. 1.7e-08;  
Matches 98; Conservative 90; Mismatches 217; Indels 91; Gaps 18;  
QY 63 PSSTADISRLLOVAANGKSTFQVAARQGHSLNGQASVSGGVVNMTCITDVV-VSKDKK 121  
DB 119 PETLADLEALVKEAHEKN-RIRPVGSLSPNG-IGLSRSGMVNLMALMDKVLVDKKEK 175  
QY 122 YADVAAGTLWVDVVKTAEGKVSFVSWTDVHLHITVGGTSLNGGIGGVFNGPLVSNVLE 181  
DB 176 RVRVQAGIRVQQLVDAQOEVGLTLQNFASIREQQIGIIVGAHTGA-RLPFIDBQVIG 234  
QY 182 LDVITGKGMELTCSRQNPFLFYGLGGLGQFGIITRAIVLDHAPKRAKWFRLYSDFT 241  
DB 235 MKLVTPAKGTIELSKNDPFLHARGLGLGVV-AEVTQCVREQLLEHTYVSTLE 292  
QY 242 TFTKQDERLISMANDIG--VDLEGQIFLNGVVDTSFFPPSQSK-----VADL 289  
DB 293 EIKNNHKKLLSTNHVKYLYFTDTVVVVTNCPVSKWSGAPKPKYTTTEALKHVRDL 352  
QY 290 VKQHGIIY-VLEVAKYDDNPLPIISKIDTLTKTLVLPGFISMHD-VAYFDFLNRVHV 347  
DB 353 YRESIVKRVQSSKPTDSEPDINEL-----SFTLRKLLALDPLNDVHV 400  
QY 348 EENKLSRSLGW-----ELPWPVNLVVPKSRILDFENG 381  
DB 401 GKVNQAEAEFWKSGVRVGSDEILDFCGGQGVWSETCFPAGTLAKPSMKOLEYIE-Q 459  
QY 382 VKDILLKQKSGALLYPTN-RNKWNR-----MSAMPEIDEDVYIIGLLQSATPKOL 436  
DB 460 LKELIQKE-----AIPAPSPIEQRTGRSKSPSPAFSTAEEDIFSWVGLIIMLPTADP 513  
QY 437 PEVESVNEKIIRFCXDSGIKIKQYLMHYTSKEDWT-----BHFSGKW--D 479  
DB 514 RQRKDITDEFFHYRHLTQAKLWD---QYSAVEHWAKIEIPKDKBELEALQERLRKRPVD 570  
QY 480 DFKRKLDFDPKLLS 495  
DB 571 AYNKARRELDPNRILS 586

RESULT 10  
US-09-328-352-6023  
Sequence 6023, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 6023  
LENGTH: 468  
TYPE: PRT  
ORGANISM: Acinetobacter baumannii  
US-09-328-352-6023

Query Match 6.7%; Score 174; DB 4; Length 468;  
Best Local Similarity 19.7%; Pred. No. 1.6e-08;  
Matches 104; Conservative 77; Mismatches 136; Indels 152; Gaps 20;  
QY 35 LSTDPISIISAASHDFGNITTVTGGVLCPSSTADISRLLOVAANGKSTFQVAARQGHSL 94  
DB 23 IKTDADSLNENWGKDHTEHFNPNPSPVIVPSTTEQVEVVKLA-----NQFNIAITPSG--- 75  
QY 95 NQASVSGGVVNMTCITDVVVSQDK-----KIADVAAGTLWVDVVKTAEGV 143  
DB 76 -GRTGLSAGAVATN--GEIVISMDKNNQILEFFPADRMVVRQAGVVTEQLQNYAEQGM 131  
QY 144 -SPVSWTDYHLHITVGGTSLNGGIGGVFNGPLVSNVLELDVITGKGMELTCSRQL----- 198  
DB 132 YYPVDFASAGSSQIGGNITGNAGGIVIKYGMTRNWLJGLTVVTKGDIILNKGMIKNA 191  
QY 199 -NPELFYVGLGGLGQFGIITRAIVLDHAPKRAKWFRLYSDFTTFTKQDERLISMANDI 257  
DB 192 TGYALQHLFIGEGTGLVTEAEIKLERQPN--LQVLVGVDPDFDAVMPVLHAFQKDI 248  
QY 258 GVDYLEGQIFLNGVVDTSFFPPSQSKVAD-----LVQHGIIYVLEVAKYDDNPL 310  
DB 249 DLTAPE-----FFGELAMQKVLDRGHVQRPFETQCPFYVLE-----FEAPYE 291  
QY 311 PIISKVIDTLTKTSL--YLPGFISMHDVAYFDFLNRVHVEENKLSLGLWELPHPLNL 367  
DB 292 PIIDKAMEIFEHCHMGQWVLDGMSQS-----LDQVE-----SLWR----- 327  
QY 368 YVPKSRILDFHNGVVVKDILLKQKSGALLYPTNRRNKWDMRMSAMPEIDEDVYIIGL 427  
DB 328 -----LREDISESIAPFIP-----YKNDISVLIITHVPAPFIREIDAI 363  
QY 428 LQSATP-----KD--LPEVESVNEKIIRFC----- 451  
DB 364 VOENVPDFEICWFGHIGDGNLHNLKPENLTQDEFFAKQVNVKVVDTVKYDGSISA 423  
QY 452 --DSGIIKIKQYLMHYTSKEDWTIEHFGSKWDDFSKRDLPDKKLLSPQG 498  
DB 424 EHGVMGTTKPYLEYSRABE-IEY-----MKALKKVDFDPKGINNPGK 464  
RESULT 11  
US-09-630-983A-9  
Sequence 9, Application US/09630983A  
Patent No. 6630330  
GENERAL INFORMATION:  
APPLICANT: Porro, Danilo  
TITLE OF INVENTION: Ascorbic Acid Production from Yeast  
FILE REFERENCE: 2028.594000  
CURRENT APPLICATION NUMBER: US/09/630,983A  
CURRENT FILING DATE: 2000-08-02  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 9  
LENGTH: 440  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-09-630-983A-9  
Query Match 6.5%; Score 169; DB 4; Length 440;  
Best Local Similarity 19.8%; Pred. No. 4.5e-08;  
Matches 96; Conservative 73; Mismatches 174; Indels 148; Gaps 17;  
QY 63 PSSTADISRLLOVAANGKSTFQVAARQGHSLNGQASVSGGVVNMTCITDVV-VSKDKK 121  
DB 27 PTSVEEVREVLALAREQKKVAV--GGHS-PSDIACDTGFMHGMKNRVLQVDKKEK 83  
QY 122 YADVAAGTLWVDVVKTAEGKVSFVSWTDVHLHITVGGTSLNG-----GIGQVFRNGPLVS 177  
DB 84 QITVEAGILLADLPQLDEHGLAMSLNGLAVSDVTVAVIGSGTHNTGI-----KHGILAT 138  
QY 178 NVLELDVITGKGMELTCSRQNPFLFYGLGGLGQFGIITRAI----- 221

Db 139 QVVALTMTADGEVLECSERNADVFQARVHLGCLGIIITVTLQCVFQFQLOQTSFSP 198  
Qy 222 ---VLDHAP---KRAKWRMLYSDF---TFTKQDERLISMANDIGVDYLEGQIFLSN 270  
Db 199 LKEVLNDLSHLKSEYERFLWPFHTKSVIYQDHTKAPSSASNFWFVAIG----- 252  
Qy 271 GWVDTSPFPDQSKVADLVKQHGIIYVLEKAKYVDDPNLPIISKVIDTTLTKLSYLP-- 328  
Db 253 -----FYLEF-----LWSTSTYLPCL 269  
Qy 329 -GFIS-----MHDVAYDFELNVRVHVEENKRLSLGLWELP-HPWMLNYV 369  
Db 270 VGWINRFFFWMLFNCKESSNLSHKIFTYECRFKQHVQD-----WAIPEKTEKALL 321  
Qy 370 PKSRLLDFHNGVVKDKLLKQKASGLALLYPTRNRKNDNRMSAMPEIDEDVIVIIIGLLQ 429  
Db 322 ELKAMLEHAKFVVAHYVFEVRETRDDIL-----LSPCFQRDSCTWMIIMY 367  
Qy 430 SATPKDLPESVNEKIIIRFCXDSGIIKQVIMHYTSKEDWIEHFGSKWDDFSKRKOLF- 488  
Db 368 RPYGKDVPRL-----DYWLAYETIMKFGGRPHWAKAHNCTQKDFEEMYPTEH 415  
Qy 489 ---DPKLLSP 496  
Db 416 KFCDIRKLDLP 426

RESULT 12  
US-09-647-390-18  
; Sequence 18, Application US/09647390  
; Patent No. 6465636  
; GENERAL INFORMATION:  
; APPLICANT: Stuijver, Maarten  
; APPLICANT: Custers, Jerome  
; APPLICANT: Simons, Lambertus  
; TITLE OF INVENTION: Pathogen-Inducible Promoter  
; FILE REFERENCE: MOG 5707/UST  
; CURRENT APPLICATION NUMBER: US/09/647,390  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR FILING DATE: 1998-03-25  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 540  
; TYPE: PRT  
; ORGANISM: Lactuca sativa  
US-09-647-390-18

Query Match 6.5%; Score 168.5; DB 4; Length 540;  
Best Local Similarity 23.5%; Pred. No. 7.1e-08;  
Matches 81; Conservative 50; Mismatches 124; Indels 89; Gaps 14;  
Qy 28 PKSINLTSLDPSIIASAHDGFIITVTGGVICPSSTADISRLLOAANGKSTFQVAA 87  
Db 81 PKPILITLHPHQIAA-----VVC-----AKTHLLMKTRSG----- 114  
Qy 88 RGQCHSLNGQASVGG-----VIVNMTICITDVVSKKKYADVAAGTLVDVVLKKTAEK-- 141  
Db 115 ---GHDYEGLSYVTNSNQPFVVDVDFNLRSINSIEDTAWQAGATLGEVYVIRAEKN 171  
Qy 142 -----GVSPVSWTDYLIHTVGGTSLNNGGIGGVGFNGPLVSNVLELDVITKGEMLTCS 195  
Db 172 SHAPPAGVCTP-----VGVGGHFGSGGYGNLMGKGLSDVNDIVDAQLIDVNGKLLN-R 223  
Qy 196 RQNLNPELFGVGLGGLG-QFGIITRARIIVLDHAPKRAKWRMLYSDDTTFTKQDERLISMA 254  
Db 224 KSMGEDLFWAITGGGVSFGVWAYKIKLVVRVTTVTVFNVQRTSEQNLSITIAHRQVIA 283  
Qy 255 NDIGVDYLEGQIFLS---NGVVDTS-----PFP-----PSDQSKY 286

Db 284 -----DKLNDLFLRMTFNVINNTNGEKTIRGLFTLYLGNSTALVALLNKDFPGLGVEI 338  
Qy 287 ADLVKQHGIIYVLEKAKYVDDPNLPIISKVIDTTLTKLSYLPFG 330  
Db 339 SOCIEMSWIESVL-----FY--TNFPIGPTTALLSRTQRLNPF 376

RESULT 13  
US-09-423-468A-15  
; Sequence 15, Application US/09423468A  
; Patent No. 6469149  
; GENERAL INFORMATION:  
; APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol  
; APPLICANT: Guy Jerome Corneel Bauw  
; APPLICANT: Mark William Davey  
; APPLICANT: Jens Ostergaard  
; APPLICANT: Marc Charles Ernest Van Montagu  
; TITLE OF INVENTION: PRODUCTION OF ASCORBIC ACID IN PLANTS  
; FILE REFERENCE: DECLES 001APC  
; CURRENT APPLICATION NUMBER: US/09/423,468A  
; PRIOR FILING DATE: 2000-02-15  
; PRIOR FILING DATE: 1997-05-07  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-423-468A-15

Query Match 6.4%; Score 166.5; DB 4; Length 592;  
Best Local Similarity 19.9%; Pred. No. 1.3e-07;  
Matches 94; Conservative 84; Mismatches 198; Indels 97; Gaps 19;  
Qy 63 PSTADISRLLOAANGKSTFQVAAAGQGHSLNGQASVSGGVIVNMTICITDVV-VSKDKK 121  
Db 129 PENLADLEALVKESHEKK--LRIRPVGSLSPNG-TGLSRGMVNLALMDKVLVEDEKK 185  
Qy 122 YADVAAGTLVDVVLKKTAEKGVSPVSWTDYLIHTVGGTSL-----NGGIGGVGFNGPLV 176  
Db 186 RVTVQAGIRVQQLVDAIKDYGLTLQNFASIREQIIGIIQVFFVYVQVGAHTGARTLPID 245  
Qy 177 SNVLELDVITKGEMLTCSRLNPELFGVGLGGLGQFGIITRARIIVLDHAPKRAKWRML 236  
Db 246 EQVISMKLVTPAKGTIELSREKDPFLFLARCGLGLGVV--AEVTLQCVARHELVEHTY 303  
Qy 237 YSDEFTTFTKQDERLISNAND-----IGVDYLEGQIFLSNGVVDTSFPPSPDQSK----- 285  
Db 304 VSNLQEIKNKHKKLLS-ANKHVLYIPIYTDVTVVVTVCNVPVSKWSPGPKDKPYTTDEAV 362  
Qy 286 --VADLVKQHGIIY--VLEKAKYVDDPNLPIISKVIDTTLTKLSYLPFGFISMED-VAYFD 340  
Db 363 QHVRDLVRESIVKYRRVQDSGKKSPDSSEPDIOEL-----SFTELDKLLALD 410  
Qy 341 FLNRVHVEENKRLSLGLWELP-----HPWLN-----LVVPKSR 374  
Db 411 PLNDVHVGVKNQABAEFVKKSEGVYRVGWSDEILFCGQGGQWYSESFCPAGTLANPSMKD 470  
Qy 375 LDFHNGVVKDKLLKQKASGLALLYPTRNRKNDNRMSAMIP---EIDEDVIY--IIGLLQ 429  
Db 471 LEYIEELKK--LIEKEALPAPAPI-----EQRTARKSPISAPSTSEDDIIFSWVGIIM 524  
Qy 430 SATPKDLPESVNEKIIIRFCXDSGIIKQVIMHYTSKEDWIEHFGSKWDDFS 482  
Db 525 YLPADPRQRKIDTDEFFHY-----RHLTQKQ-----LWDQFS 557

RESULT 14  
US-09-489-039A-10266  
; Sequence 10266, Application US/09489039A  
; Patent No. 6610836

GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489.039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 10266  
; LENGTH: 1036  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-10266

Query Match 6.4%; Score 166; DB 4; Length 1036;  
Best Local Similarity 18.8%; Pred. No. 3.8e-07;  
Matches 114; Conservative 102; Mismatches 200; Indels 190; Gaps 27;

Qy 4 LRLMITLITVLMYKSSNGIKIDLPKSL--NLTLSTDPISIAASHDFGNITTTVPGVICPSSTA 61  
Db 30 VQLVNLQVL-----EQGGFTGDTATSYADRLTWTATNSIVQ-----LLPDVAVI 74

Qy 62 CPSGTADISRLLOVAANGK-STFOVAARGQGHSLNGQASGGVIVNMTCITD--VVVSK 118  
Db 75 FPRSTADVALLARVAABEPFKSLIFTPRGGGTGTNGQA-LNGGIIVDMRYMNRRIEINP 133

Qy 119 DKKYADVAAGTLWVDLKKTAEGKVSFVSW-----TDYLHITVGGTILSN--GGIGGOVFRNGPLV 176  
Db 134 BEGWVRVBAE-----VIKQDLNQLPKPYGFPAPELSTSNRATLGGMINTDASQGSLSVY 188

Qy 173 GPLVSNVLELDVITGKGEML-----TCSRQ----- 197  
Db 189 GKTSDHVGLRAVLGGDILDTQAVPALAETLGNTPSTVGRINYVYQRCQAQRDLIID 248

Qy 198 ----LNP-----ELFYVGLGGIQQGIIITRARIIVLDHAPKRAKWM 235  
Db 249 KPPKLNRELTYGLRHVFNDEMSEPDRLTILTSGSEGLAFITEARLDITRLPKVRLVNV 308

Qy 236 LYSDFTTTKQERLISMANDIGVDYLEGQIFLSNGVVDTSFPPSDQSKVADLVKQ--- 292  
Db 309 KYDSFDSALRNAPFVWE-AKALSVEITVD-----SKVLNAREDIVVHVS 347

Qy 293 -HGI-----IYVLEVAKYDDPNLPISKVID--TLTKLSYLPQGFISMHDVA-YFD 340  
Db 348 WHSVSELITDVPDKMGLNIVEFAGD-DAALIDQQVTLQRLDCLMNGEGGVIGYQVCDNLA 394

Qy 333 MDVAYDFLNRVHVEENKLSLGLW-----ELPHPLW-NLYVPKSRILDFHNGVVKDI 451  
Db 407 CHDL---EGVERIYAMRKX--AVGLLGNAGKHAKEIPFVEDTCVPEHLADY-----ITE 439

Qy 386 LLKQKSASGLALLYPTNRNKNDRMSAMPEIDEVDVIYIIGLQSATPKDLPEVSNEKIIRFCK 451  
Db 459 AL--LDSHGLSY-----GMFGHVDAGVLRVHPALDWCDCPQOEQLMKTISDEIVALT 491

Qy 446 IIRFKDSGIKTKOYLMHYTSKEDWIEH-----FG-SKWDDFSKRLDFDPK 492  
Db 503 VVALTAKYGGLL-----WGEHGKGFRAEYSPAFFGETLYAELRKIKAVFDPDN 550

Qy 493 LLSPGQ 498  
Db 551 RLNPGK 556

RESULT 15  
US-09-543-681A-4447  
; Sequence 4447, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543.681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 4447  
; LENGTH: 1019  
; TYPE: PRT  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-4447

Query Match 6.2%; Score 160; DB 4; Length 1019;  
Best Local Similarity 19.2%; Pred. No. 1.5e-06;  
Matches 114; Conservative 99; Mismatches 208; Indels 172; Gaps 27;

Qy 10 LITVLMYKSSNGIKIDLPKSL--NLTLSTDPISIAASHDFGNITTTVPGVICPSSTA 67  
Db 15 LTTEFLNLRQNGFTGDISSTYADRLTWTATNSIVQ-----LLPDVAVI 63

Qy 68 DTSRLLOVAANGK-STFOVAARGQGHSLNGQASGGVIVNMTCITD--VVVSKDKKYAD 124  
Db 64 DVTIVARLVDERPRHLSLITPRGGGTGTNGQA-LTEGIVVDLSRYMKRIIEINPEQRWYK 122

Qy 125 VAAGTLWVDLKKTAEGKVSFVSW-----TDYLHITVGGTILSN--GGIGGOVFRNGPLV 176  
Db 123 VEAG-----VIKDELNLFLPKPYGFPAPELSTSNRATLGGMINTDASQGSLSVY 175

Qy 177 SNVLELDVITGKGEML-----TCSRQ----- 203  
Db 176 DHVLGVRVLLGELLETRAMDLSALAEITAKEDSAVGRIYQVLSRCAQRLILEKFPK 235

Qy 204 -----YG-----VLGGLQFGIITRARIIVLDHAPKRAKWM 239  
Db 236 LNRFLTYGLRHVFSDDMKHFDLTRLITSGSEGLAFITEATLDTIPKORSLVNVKYDS 295

Qy 240 FTTFTTKQERLISMANDIGVDYLEGQIFLSNGVVDTSFPPSDQSKVADLVKQ---HGI 295  
Db 296 FDSALRNAPFLV-AKALSVEITVD-----SKVLNAREDIVVHVS 334

Qy 296 -----IYVLEVAKYDDPNLPISKVID--TLTKLSYLPQGFISMHDVA-YFD 340  
Db 335 NALITDVPDKMGLNIVEFAGD-DKTLIASQVEDLQRLDCLMNGEGGVIGYQVCDNLA 394

Qy 341 FLNRVHVEENKLSLGL-----WELPHPLW-NLYVPKSRILDFHNGVVKDI 393  
Db 395 DINRIYAMRKX--AVGLLGNAGKHAKEIPFVEDTCVPEHLADY-----ITE 439

Qy 394 GLALL--YPTNRNKNDRMSAMPEIDEVDVIYIIGLQSATPKDLPEVSNEKIIRFCK 451  
Db 440 FRALLDSYQLN-----YGMFGHVDAGVLRVHPALDWCDCPQOEQLMKTISDEIVALT 491

Qy 452 DSGIKI-----KOYLMHYTSKEDWIEHFG-SKWDDFSKRLDFDPK 498  
Db 492 KYGGLWGEHGKGFRAEYSP-----EFFGETLYHELRLQIKTVFDPNRLNPGK 539

Search completed: April 5, 2004, 17:46:46  
Job time : 24 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 5, 2004, 17:45:47 ; Search time 46 Seconds  
(without alignments)  
2860.031 Million cell updates/sec

Title: US-10-014-101-4

Perfect score: 2596  
Sequence: 1 MANRLMITLTVLMTKSS.....SKRDLFDPKLLSPQDIF 501

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1071436 seqs, 262597696 residues

Total number of hits satisfying chosen parameters: 1071436

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pap.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pap.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pap.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pap.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pap.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pap.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pap.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pap.\*
- 9: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pap.\*
- 10: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pap.\*
- 11: /cgn2\_6/ptodata/2/pubpaa/US09D\_PUBCOMB.pap.\*
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- 13: /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pap.\*
- 14: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pap.\*
- 15: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pap.\*
- 16: /cgn2\_6/ptodata/2/pubpaa/US10E\_NEW\_PUB.pap.\*
- 17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pap.\*
- 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2596	100.0	501	12	US-10-311-453-4
2	2596	100.0	501	14	US-10-014-101-4
3	1822	70.2	524	12	US-10-311-453-8
4	1822	70.2	524	14	US-10-014-101-8
5	1292	49.8	523	12	US-10-311-453-6
6	1292	49.8	523	14	US-10-014-101-6
7	1184	45.6	536	12	US-10-311-453-10
8	1184	45.6	536	14	US-10-014-101-10
9	1184	45.6	539	12	US-10-311-453-35
10	1184	45.6	539	14	US-10-014-101-35
11	1126.5	43.4	611	9	US-09-829-549A-48
12	1056.5	40.7	575	12	US-10-311-453-2
13	1056.5	40.7	575	14	US-10-014-101-2
14	993	38.3	504	12	US-10-311-453-12
15	993	38.3	504	14	US-10-014-101-12

16	950.5	36.6	407	12	US-10-424-599-152644
17	939	36.2	513	12	US-10-424-599-220961
18	805.5	31.0	392	12	US-10-425-114-39823
19	745	28.7	324	12	US-10-424-599-144567
20	745	28.7	324	12	US-10-425-114-42126
21	661.5	25.5	292	12	US-10-425-114-40061
22	661.5	25.5	299	12	US-10-424-599-162425
23	620.5	23.9	334	12	US-10-424-599-155687
24	612	23.6	290	12	US-10-425-114-39759
25	587	22.6	290	12	US-10-424-599-144566
26	457	17.6	487	14	US-10-166-087-14
27	440.5	17.0	230	12	US-10-424-599-255266
28	421	16.2	173	12	US-10-425-114-52875
29	401.5	15.5	214	12	US-10-424-599-200943
30	379	14.6	276	12	US-10-425-114-46334
31	353	13.6	143	12	US-10-424-599-205473
32	336	12.9	229	12	US-10-425-114-39997
33	326.5	12.6	203	12	US-10-424-599-148081
34	324	12.5	187	12	US-10-424-599-220960
35	314.5	12.1	202	12	US-10-424-599-212362
36	293	11.3	99	12	US-10-424-599-204492
37	293	11.3	99	12	US-10-425-114-56907
38	235	9.1	118	12	US-10-424-599-256584
39	226.5	8.7	515	9	US-09-738-628-4135
40	214	8.2	88	12	US-10-424-599-148123
41	214	8.2	296	12	US-10-425-114-42202
42	206	7.9	122	12	US-10-424-599-220958
43	193.5	7.5	495	14	US-10-314-190-2
44	185	7.1	439	14	US-10-156-761-9946
45	179.5	6.9	461	15	US-10-369-493-11223

## ALIGNMENTS

### RESULT 1

US-10-311-453-4  
; Sequence 4, Application US/10311453  
; Publication No. US20040031073A1  
; GENERAL INFORMATION:  
; APPLICANT: Schilling, Thomas  
; APPLICANT: Warner, Tom s  
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and  
; TITLE OF INVENTION: Physiology  
; FILE REFERENCE: 1226-4  
; CURRENT FILING DATE: 2002-12-16  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR FILING DATE: 2000-12-27  
; PRIOR FILING DATE: 2000-12-27  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 501  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-311-453-4

Query Match 100.0%; Score 2596; DB 12; Length 501;  
Best Local Similarity 100.0%; Pred. No. 9.6e-233;  
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MANRLMITLTVLMTKSSNGIKIDLPKSNLTLSTDPSTISASHDFGNITVTGGV 60  
Db 1 MANRLMITLTVLMTKSSNGIKIDLPKSNLTLSTDPSTISASHDFGNITVTGGV 60  
Qy 61 ICPSTADISRLQYANGKSTFQVARGQGHSLNGQASVGGVYVNMTCITDVVSKDK 120  
Db 61 ICPSTADISRLQYANGKSTFQVARGQGHSLNGQASVGGVYVNMTCITDVVSKDK 120

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QY 121 KYADVAAGTLDVWVTKTAEGKVSPTSVDYHITVGGTSLNGGIGGVFRNGPLVSNVL 180
DB 121 KYADVAAGTLDVWVTKTAEGKVSPTSVDYHITVGGTSLNGGIGGVFRNGPLVSNVL 180
QY 181 ELDVITGKEMLTCSRQNLPELFGVGLGQFGIITRARIIVLDHAPKAKFRMLYSDF 240
DB 181 ELDVITGKEMLTCSRQNLPELFGVGLGQFGIITRARIIVLDHAPKAKFRMLYSDF 240
QY 241 TTTTKDQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSDQSKVADLVKQHGIIYVLE 300
DB 241 TTTTKDQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSDQSKVADLVKQHGIIYVLE 300
QY 301 VAKYDDPNLPIISKVIDTLTKTSLVPGFISMDHVAVFDFLNRVHVEENKLSLGLWEL 360
DB 301 VAKYDDPNLPIISKVIDTLTKTSLVPGFISMDHVAVFDFLNRVHVEENKLSLGLWEL 360
QY 361 PHPWNLVYPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRNKNWDMRMSAMIPEIDED 420
DB 361 PHPWNLVYPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRNKNWDMRMSAMIPEIDED 420
QY 421 VYIIGLQSATPKDPEVESVNEKIIRCKDSGIIKIQYLMHYTSKEDWIEHFGSKWDD 480
DB 421 VYIIGLQSATPKDPEVESVNEKIIRCKDSGIIKIQYLMHYTSKEDWIEHFGSKWDD 480
QY 481 FSKRKOLFDPKLLSPGQDIF 501
DB 481 FSKRKOLFDPKLLSPGQDIF 501

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RESULT 2

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US-10-014-101-4
; Sequence 4, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom S
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; FILE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-014-101-4

```

```

Query Match 100.0%; Score 2596; DB 14; Length 501;
Best Local Similarity 100.0%; Pred. No. 9.6e-233;
Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MANLRMLTILVITLMTKSSNGIKIDLPKSLNLTSLDPSIIISAASHDFGNITVTPGV 60
DB 1 MANLRMLTILVITLMTKSSNGIKIDLPKSLNLTSLDPSIIISAASHDFGNITVTPGV 60
QY 61 ICPSSTADISRLLQYANGKSTTQVAARGQGHSLNGQASVSGGVIIVNMTCTIDVVVSKDK 120
DB 61 ICPSSTADISRLLQYANGKSTTQVAARGQGHSLNGQASVSGGVIIVNMTCTIDVVVSKDK 120
QY 121 KYADVAAGTLDVWVTKTAEGKVSPTSVDYHITVGGTSLNGGIGGVFRNGPLVSNVL 180
DB 121 KYADVAAGTLDVWVTKTAEGKVSPTSVDYHITVGGTSLNGGIGGVFRNGPLVSNVL 180

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QY 181 ELDVITGKEMLTCSRQNLPELFGVGLGQFGIITRARIIVLDHAPKAKFRMLYSDF 240
DB 181 ELDVITGKEMLTCSRQNLPELFGVGLGQFGIITRARIIVLDHAPKAKFRMLYSDF 240
QY 241 TTTTKDQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSDQSKVADLVKQHGIIYVLE 300
DB 241 TTTTKDQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSDQSKVADLVKQHGIIYVLE 300
QY 301 VAKYDDPNLPIISKVIDTLTKTSLVPGFISMDHVAVFDFLNRVHVEENKLSLGLWEL 360
DB 301 VAKYDDPNLPIISKVIDTLTKTSLVPGFISMDHVAVFDFLNRVHVEENKLSLGLWEL 360
QY 361 PHPWNLVYPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRNKNWDMRMSAMIPEIDED 420
DB 361 PHPWNLVYPKSRILDFHNGVVKDILLKQKSASGLALLYPTNRNKNWDMRMSAMIPEIDED 420
QY 421 VYIIGLQSATPKDPEVESVNEKIIRCKDSGIIKIQYLMHYTSKEDWIEHFGSKWDD 480
DB 421 VYIIGLQSATPKDPEVESVNEKIIRCKDSGIIKIQYLMHYTSKEDWIEHFGSKWDD 480
QY 481 FSKRKOLFDPKLLSPGQDIF 501
DB 481 FSKRKOLFDPKLLSPGQDIF 501

RESULT 3
US-10-311-453-8
; Sequence 8, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom S
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; FILE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 524
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-311-453-8

Query Match 70.2%; Score 1822; DB 12; Length 524;
Best Local Similarity 66.7%; Pred. No. 1.3e-160;
Matches 345; Conservative 69; Mismatches 79; Indels 24; Gaps 5;

QY 7 MITLITVLM-----ITKSSNGIKIDLPKSLNLTSLDPSIIISAASHDFGNITVTPGV 61
DB 9 LITLITLISLTPTLIKSDGIDVFLPISLNLTLVLTDPFSISAASHDFGNITDENPGAVL 68
QY 62 CPSTADISRLLQYANG-----KSTFQVAARGQGHSLNGQASVSGGVIIVNMTCT 111
DB 69 CPSTTTEVARLLRFPANGFYSYNGKSTSPASTFQVAARGQGHSLNGQASVSGGVIIVNMTCT 128
QY 112 -----TDVVVSKDKYADVAAGTLDVWVTKTAEGKVSPTSVDYHITVGGTSLNGGI 165
DB 129 AMAAKPAAVVISADGTYADVAAGTLDVWVTKAAVDRGVSPTWTDYLYLSVGGTSLNAGI 188
QY 166 GQVFRNGPLVSNVLELDVITGKEMLTCSRQNLPELFGVGLGQFGIITRARIIVLDH 225
DB 189 GQVFRNGPQISNYHELDVITGKEMMTCSKLPNELFGVGLGQFGIITRARIIVLDH 248
QY 226 APKAKFRMLYSDFTTFTKQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSDQSK 285
DB 226 APKAKFRMLYSDFTTFTKQERLISMANDIGVDYLEGQIFLSNGVVDTSFFPPSDQSK 285

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QY 405 KWNDRMSAMIPEDIDEDVIYIGLQSAATPKDLPVSVNEKIIRFKCDGSGIKIKQYLMHY 464  
 DB 423 KWNDRMSAAIPE--EDVYAVGFLRSAGFDNWEAFDQENMEILKFCEDANMGVIQYLPYH 480  
 QY 465 TSKEDWIEHFGSKWDDFKRDLDPKLLSPGQDIF 501  
 DB 481 SSQEGWVRHFGPRNIFVERKYKDYDKMILSPGQNI 517

RESULT 6  
 US-10-014-101-6  
 ; Sequence 6, Application US/10014101  
 ; Publication No. US20030074698A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schmulling, Thomas  
 ; APPLICANT: Werner, Tom s  
 ; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and  
 ; TITLE OF INVENTION: physiology  
 ; FILE REFERENCE: 1195-2  
 ; CURRENT APPLICATION NUMBER: US/10/014,101  
 ; PRIOR FILING DATE: 2001-12-10  
 ; PRIOR APPLICATION NUMBER: PCT/EP01/06833  
 ; PRIOR FILING DATE: 2001-06-16  
 ; PRIOR APPLICATION NUMBER: EP 00870132.8  
 ; PRIOR FILING DATE: 2000-06-16  
 ; PRIOR APPLICATION NUMBER: US 60/258,415  
 ; PRIOR FILING DATE: 2000-12-27  
 ; PRIOR APPLICATION NUMBER: EP 01870053.4  
 ; PRIOR FILING DATE: 2001-03-16  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 523  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis thaliana  
 US-10-014-101-6

Query Match 49.8%; Score 1292; DB 14; Length 523;  
 Best Local Similarity 48.5%; Pred. No. 3.2e-111;  
 Matches 251; Conservative 106; Mismatches 138; Indels 22; Gaps 6;

QY 3 NLRMLITLIT--VLMITKSSNGIKIDLPKSNL-----TLSTDPSIISAASHDFGN 51  
 DB 5 NLRQVRLIAITVITLSTPTTNTSPQWNILSHNEFAGKLTSSSSVESAATDFGH 64  
 QY 52 IITVPGGVCPSSTADISRLQYAAAGKSTQVAARGGHSINGQASVSGGVVNMTCI 111  
 DB 65 VTKIFPSAVLIPSSVEDITDLKLSFDSQSPLAARGHGHGHSAGAKGVVNMRS 124  
 QY 112 TD----VWVSKDKYADVAAGTLWVDVLLKKTAEKGVSPVSWTDYHLITVGGTSLNGGIG 167  
 DB 125 VNRDRGKYVSRCTCLYVDVDAWLWIEVLNKTLEGLTPVSWTDYLVLTVGGTSLNGGIG 184  
 QY 168 QVFRNGPLVSNVLELDVITGKEMLTCSRQNLNPELFGVGLGQFGIITRARIIVLDHAP 227  
 DB 185 QTPRYGPQITNVLEMDVITGKGIACTCKDMNSDLFFAVLGGJGQGIITRARIKLEVP 244  
 QY 228 KRAKWFRLMSDFTTFTKQERLISMANDIGVDYLEGQIFLSNGVVD---TSFFPPSDOS 284  
 DB 245 KRAKWLFLYIDSEFTROERVISKTD--GVDFLESGIWDVGRPDNWRSTVYPSDEL 302  
 QY 285 KVADLVKQHGIIYVLEVAKYDDPNLPITSKVIDTTLKLSYLPFGFISHMDVAYDFLNR 344  
 DB 303 RIASWVRHRVYICLVVVKYIDETSTQVTNNEEELSDSLNVRGFMVKDYMDFLNR 362  
 QY 345 VHYEENKLSLGLWELPPLNLYVPKSRILDFHNGVVKDILLKQKASGLALLYPTNRN 404  
 DB 363 VRTGELNLSKGGQWVDPHPLNLFVPTQISKSDGDFGKCIILRNITSGPVLVPMNEN 422  
 QY 405 KWNDRMSAMIPEDIDEDVIYIGLQSAATPKDLPVSVNEKIIRFKCDGSGIKIKQYLMHY 464  
 DB 423 KWNDRMSAAIPE--EDVYAVGFLRSAGFDNWEAFDQENMEILKFCEDANMGVIQYLPYH 480

QY 465 TSKEDWIEHFGSKWDDFKRDLDPKLLSPGQDIF 501  
 DB 481 SSQEGWVRHFGPRNIFVERKYKDYDKMILSPGQNI 517

RESULT 7  
 US-10-311-453-10  
 ; Sequence 10, Application US/10311453  
 ; Publication No. US20040031073A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schmulling, Thomas  
 ; APPLICANT: Werner, Tom s  
 ; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and  
 ; TITLE OF INVENTION: physiology  
 ; FILE REFERENCE: 1226-4  
 ; CURRENT APPLICATION NUMBER: US/10/311,453  
 ; CURRENT FILING DATE: 2002-12-16  
 ; PRIOR APPLICATION NUMBER: EP 00870132.8  
 ; PRIOR FILING DATE: 2000-06-16  
 ; PRIOR APPLICATION NUMBER: US 60/258,415  
 ; PRIOR FILING DATE: 2000-12-27  
 ; PRIOR APPLICATION NUMBER: EP 01870053.4  
 ; PRIOR FILING DATE: 2001-03-16  
 ; NUMBER OF SEQ ID NOS: 36  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 10  
 ; LENGTH: 536  
 ; TYPE: PRT  
 ; ORGANISM: Arabidopsis thaliana  
 US-10-311-453-10

Query Match 45.6%; Score 1184; DB 12; Length 536;  
 Best Local Similarity 48.8%; Pred. No. 3.9e-101;  
 Matches 233; Conservative 84; Mismatches 142; Indels 18; Gaps 7;

QY 39 PSIISAASHDFGNI--TIVTPGGVICPSSSTADISRLQYAAAGKSTQVAARGGHSINGQ 97  
 DB 44 PSDLASVSSDFGMLKSPPEPLAYLHPSAEADVRLVRYAGSATAPFVSARGHGHINGQ 103  
 QY 98 ASVS--GGVIVNM---TCITDVVSKDKYADVAAGTLWVDVLLKKTAEKGVSPVSWTDYL 152  
 DB 104 AAAGRGVVVEMNHGVTGTPTKPLVRPDMYVDMVGGELWVDVLLKKTLEHGLAPKSWTDYL 163  
 QY 153 HITVGGTSLNGGCGQVFRNGPLVSNVLELDVITGKEMLTCSRQNLNPELFGVGLGQ 212  
 DB 164 YLTVGGTSLNAGISGQAFHHPGQISNVLELDVITGKEMRCSEENRFLFHGVLGGLQ 223  
 QY 213 FGIITRARIIVLDHAPKAKWFLMSDFTTFTKQERLISMANDIGVDYLEGQIFLSNGV 272  
 DB 224 FGIITRARIISLEPAPQVRVIRVLYSSFKYFTDEQVLIISHGQLKDFYVGVIVDEGL 283  
 QY 273 VD---TSFFPPSDOSKVDLVKQHGIIYVLEVAKYDDPNLPITSKVIDTTLKLSYLP 329  
 DB 284 VNNWRSSFFSPRNPKVISSVSSNGSVLYCLEITKNYHSDSDSEIVDQVEILMKKLNFIPT 343  
 QY 330 FISHMDVAYDFLNRVVEENKLSRLGLWELPPLNLYVPKSRILDFHNGVVKDILLKQ 389  
 DB 344 SVFTTDLQYVDFLDRVHKAELKSKNLWEPHPLNLFVPKSRISDFDKGVFKGIL--G 401  
 QY 390 KASGLALLYPTNRKNDRMSAMIPEDIDEDVIYIGLQSA-----TPKDLPEVESVNE 444  
 DB 402 NKTSGPTLIYPMNKDKWDRSSAVTP--DBEVFVLLALLRSALTGDGETQKLEYLKQNR 459  
 QY 445 KIRFKCDGSGIKIKQYLMHYTSKEDWIEHFGSKWDDFKRDLDPKLLSPGQDIF 501  
 DB 460 RILEFCEQAKINVKQYLPHPHATQSEWVAHFGDKWDRFRLSKAEFPDPRHILATGQRI 516

RESULT 8  
 US-10-014-101-10  
 ; Sequence 10, Application US/10014101  
 ; Publication No. US20030074698A1  
 ; GENERAL INFORMATION:



```
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-014-101-10

Query Match 45.6%; Score 1184; DB 14; Length 536;
Best Local Similarity 48.8%; Pred. No. 3.9e-101;
Matches 233; Conservative 84; Mismatches 142; Indels 18; Gaps 7;

QY 39 PSIIASAASHDFGNI-TTVPQGVICPSTADISILLOYAANGKSTFOVAARGQGHSLNGQ 97
Db 44 PSDLASVSSDFGMLKSPPEPLAVLHPSSAEADVLRVTAYGSAATFVPSARGHSHINGQ 103
QY 98 ASVS-GGVIVNM---TCITDVVSKKYYADVAAGTLWVDVLTAKTAEKGVSPVSWTDYL 152
Db 104 AAGRGVGVVEMNHGVTGTPKPLVRPDEMYVDVWGGLWVDVLTAKTAEKGVSPVSWTDYL 163
QY 153 HITVGGTILNSGIGGVFRNGPLVSNVLELDVITKGEMLTCSRLQNPFLFYGVLLGLGQ 212
Db 164 YLTVGGTILNSAGISGAOFHHGQISNVLELDVITKGEMLTCSRLQNPFLFYGVLLGLGQ 223
QY 213 FGIITRARIIVLDPHAKRWFMLYSDFTTFTKDOERLISMANDIGVDYLEGOIFLNGV 272
Db 224 FGIITRARIISLEPAPQVRWIRVLYSSFKVTEQDEYLIISMHGQLKDFYVGVFVDEGL 283
QY 273 VD---TSFPSPDSQKADLVKQHGIIYVLEAKYDDPNPIISKVIDTLTKLSVLP 329
Db 284 VNNRSSFSPSPRNPKVSISSVNGSVLYCLEITKNYHSDSEIVDQEVIELMKLNFIPT 343
QY 330 FISMHDVAYFDLNRVHVEENKLSGLWELPHEPMLNLVYPKSRILDPHNGVVKDILLKQ 389
Db 344 SVFTTDLQYVDFLDRVHKAELKLSKNLWEPHPLNLVFPKSRISDFDKGVFKGIL--G 401
QY 390 KSASGLALLYPTNRKNWDRMSAMIPEIDEDVIYIIGLLQSA-----TPKDLPEVESVNE 444
Db 402 NKTSGPILYPMNKDKWDRSSAVTP--DEEVYVALLRSALTGDEETQKLEYLKQDNR 459
QY 445 KIIFCKDSGKIKQYLMHYTSKEDWIEHFGSKWDDFSKRDLFPKLLSPGQDIF 501
Db 460 RILEFCEQAKINVQYLPHPHATQBEWVAHFGDKWDRFSRLKAEFDPRHILATGORIF 516

RESULT 9
US-10-311-453-35
; Sequence 35, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
```

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; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-311-453-35

Query Match 45.6%; Score 1184; DB 12; Length 539;
Best Local Similarity 48.8%; Pred. No. 3.9e-101;
Matches 233; Conservative 84; Mismatches 142; Indels 18; Gaps 7;

QY 39 PSIIASAASHDFGNI-TTVPQGVICPSTADISILLOYAANGKSTFOVAARGQGHSLNGQ 97
Db 47 PSDLASVSSDFGMLKSPPEPLAVLHPSSAEADVLRVTAYGSAATFVPSARGHSHINGQ 106
QY 98 ASVS-GGVIVNM---TCITDVVSKKYYADVAAGTLWVDVLTAKTAEKGVSPVSWTDYL 152
Db 107 AAGRGVGVVEMNHGVTGTPKPLVRPDEMYVDVWGGLWVDVLTAKTAEKGVSPVSWTDYL 166
QY 153 HITVGGTILNSGIGGVFRNGPLVSNVLELDVITKGEMLTCSRLQNPFLFYGVLLGLGQ 212
Db 167 YLTVGGTILNSAGISGAOFHHGQISNVLELDVITKGEMLTCSRLQNPFLFYGVLLGLGQ 226
QY 213 FGIITRARIIVLDPHAKRWFMLYSDFTTFTKDOERLISMANDIGVDYLEGOIFLNGV 272
Db 227 FGIITRARIISLEPAPQVRWIRVLYSSFKVTEQDEYLIISMHGQLKDFYVGVFVDEGL 286
QY 273 VD---TSFPSPDSQKADLVKQHGIIYVLEAKYDDPNPIISKVIDTLTKLSVLP 329
Db 287 VNNRSSFSPSPRNPKVSISSVNGSVLYCLEITKNYHSDSEIVDQEVIELMKLNFIPT 346
QY 330 FISMHDVAYFDLNRVHVEENKLSGLWELPHEPMLNLVYPKSRILDPHNGVVKDILLKQ 389
Db 347 SVFTTDLQYVDFLDRVHKAELKLSKNLWEPHPLNLVFPKSRISDFDKGVFKGIL--G 404
QY 390 KSASGLALLYPTNRKNWDRMSAMIPEIDEDVIYIIGLLQSA-----TPKDLPEVESVNE 444
Db 405 NKTSGPILYPMNKDKWDRSSAVTP--DEEVYVALLRSALTGDEETQKLEYLKQDNR 462
QY 445 KIIFCKDSGKIKQYLMHYTSKEDWIEHFGSKWDDFSKRDLFPKLLSPGQDIF 501
Db 463 RILEFCEQAKINVQYLPHPHATQBEWVAHFGDKWDRFSRLKAEFDPRHILATGORIF 519

RESULT 10
US-10-014-101-35
; Sequence 35, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; CURRENT FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
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US-09-829-549A-48
Query Match 43.4%; Score 1126.5; DB 9; Length 611;
Best Local Similarity 46.8%; Pred. No. 1.1e-95;
Matches 232; Conservative 83; Mismatches 152; Indels 29; Gaps 12;

QY 30 SNNLTSTDPISIAASHDFGNITVTTPGGVTCPSSTADISRLQLQYAANGKS--TFQVAA 87
DB 109 ALDGLKRLTSDNATAAASDFGNITTSALPAVLYP-STGDLVALLS-AANSTPGWPTIAF 166

QY 88 RQGHSLNGQASVSGVIVNMTCTID-----VVVKDKKYADVAAGTLDVLDLKTAEK 141
DB 167 RRGHSLNGQAFAPGGVYVNNWASLGDAAPPRINVSADGRIVDAGGQVWIDVRLASLAR 226

QY 142 GVSVPSTWTDYLTHTVGGTSLNGGIGGVFRNGPLVSNVLELDVITGKGMLTCSRQLNPE 201
DB 227 GVAPRSWNDYLTHTVGGTSLNAGISGQAFRHGPQISNVLEMDVITGHEMVTCSKQLNAD 286

QY 202 LFYGVGLGQGFQGIITRARIIVLDHAPKAKWFMVLYSDFTTFTKQDRLISMANDIG-- 258
DB 287 LFDVJGGGUGQGVITRARIIVAPAPARWVRVYTTDFAAFSADQERLTAPRGGGGAS 346

QY 259 ---VDYLEGQIF-----LSNGVVDTSPFPSPQSKVADLVKQHG--IYVLVAKYDDPN 309
DB 347 FGPMSYVEGSPVFNQSLATDLANTGFTDADVARIVALAGERNATTVYSIEATLNYDNAT 406

QY 310 --LPIISKVIDTLTKTSLVLPGLFISMHDVAYDFELNRVHVEENKLSLGLWELPHPMLNL 367
DB 407 AAAAVDQELASVLTGTSYVEGFAPQDVAAAFLDVRVGEVVALNKLGLRVHPHPLNM 466

QY 368 YVPKSRILDFHNGVVKDILLKOKSAGLALYPTNNRKNWDMNSAMIPEDIDVYIIGL 427
DB 467 FVPSRIADFGRVFKGI--LQGTDIVGLVPLVPLNKSMDWDDGMSAATP--SEDVFPYAVSL 523

QY 428 L-QSATPKDLPEVESVNEKIRFCXDSGKIKQYLMHYTTSKEDMTEHFG-SKWDDFSXK 485
DB 524 LFSVAPNDLRLQEQNRRLRFLCDLAGIQYKTYLARHTDSRDVHRHFGAAKWRFYEMK 583

QY 486 DLFPDKLLSPGQDIF 501
DB 584 NKYDPRKLLSPGQDIF 599

RESULT 12
US-10-311-453-2
; Sequence 2, Application US/10311453
; Publication No. US20040031073A1
; GENERAL INFORMATION:
; APPLICANT: Schilling, Thomas
; APPLICANT: Werner, Tom s
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; TITLE OF INVENTION: physiology
; FILE REFERENCE: 1226-4
; CURRENT APPLICATION NUMBER: US/10/311,453
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 575
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-311-453-2

Query Match 40.7%; Score 1056.5; DB 12; Length 575;
Best Local Similarity 39.8%; Pred. No. 3.3e-89;
Matches 213; Conservative 102; Mismatches 167; Indels 53; Gaps 12;

US-09-829-549A-48
Query Match 45.6%; Score 1184; DB 14; Length 539;
Best Local Similarity 48.8%; Pred. No. 3.9e-101;
Matches 233; Conservative 84; Mismatches 142; Indels 18; Gaps 7;

QY 39 PSIIASAASHDFGNI--TTVTTPGGVTCPSSTADISRLQLQYAANGKSTFQVAAAGQGHSLNGQ 97
DB 47 PSDLASVSDFGMLKSPPEPLAVLHPESAEDVARLVRTAYGATAPFVSARGHGHSLNGQ 106

QY 98 ASVS--GGVIVNM---TCITDVVVKDKKYADVAAGTLDVLDLKTAEKGVSPVSWTDYL 152
DB 107 AAAGRNVVVEMNHGVTGPKPLVRPDEMYVDVWGGELWVDVLLKXLEHGLAPKSWTDYL 166

QY 153 HTVGTSLNGGIGGVFRNGPLVSNVLELDVITGKGMLTCSRQLNPELFGVGLGQ 212
DB 167 YLTVGTSLNAGISGQAFHGHGPQISNVLELDVITGKGMVRCSESENTRLRHLGHVGLGQ 226

QY 213 FGIITRARIIVLDHAPKAKWFMVLYSDFTTFTKQDRLISMANDIGVLYEGQIFLSNGV 272
DB 227 FGIITRARIIVLDHAPKAKWFMVLYSDFTTFTKQDRLISMANDIGVLYEGQIFLSNGV 286

QY 273 VD---TSFPSPQSKVADLVKQHGIIYVLEKAYVDDPENLPIISKVIDTLTKSLVLP 329
DB 287 VNNRSSFSPRPVFKISSVSSNGSVLYCLEITKNYHSDSEIVDQEVVEILMKLNFIPT 346

QY 330 FISMHDVAYDFELNRVHVEENKLSLGLWELPHPMLNLYVPPKSRILDFHNGVVKDILLKQ 389
DB 347 SVFTTDLQVDFLDVRVHKAELKLSKNLWEVHPHMLNLFVPSKRSISDFDKGVFKGIL--G 404

QY 390 KASGALALYPTNNRKNWDMNSAMIPEDIDVYIIGLQSA-----TPKDLPEVESVNE 444
DB 405 NKTSGPILYPMNKDKWDESSAVTP--DEEVYLVALLRSALTGGETQKLEYLKQNR 462

QY 445 KIRFCXDSGKIKQYLMHYTTSKEDMTEHFGSKWDDFSKXKDLFPDKLLSPGQDIF 501
DB 463 RILEFCEQAKINVKYLPHPATQEEWVAHFGDKWDRFSRLKAEFPDRHILATGQRF 519

RESULT 11
US-09-829-549A-48
; Sequence 48, Application US/09829549A
; Patent No. US20020052484A1
; GENERAL INFORMATION:
; APPLICANT: The Curators of the University of Missouri
; TITLE OF INVENTION: PHAGE DISPLAY SELECTION OF ANTI FUNGAL PEPTIDES
; FILE REFERENCE: UMO 1521.1
; CURRENT APPLICATION NUMBER: US/09/829,549A
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 60/195,785
; PRIOR FILING DATE: 2000-04-10
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48
; LENGTH: 611
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(85)
; OTHER INFORMATION: Mat-alpha secretory sequence
; NAME/KEY: DOMAIN
; LOCATION: (86)..(600)
; OTHER INFORMATION: Cytokinin oxidase 1
; NAME/KEY: DOMAIN
; LOCATION: (601)..(602)
; OTHER INFORMATION: Linker
; NAME/KEY: DOMAIN
; LOCATION: (603)..(611)
; OTHER INFORMATION: Random peptide PC 87

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QY 9 TLITVLM-----TKSSNGIKIDLPKSNLTLSTDPSTISAA----- 45  
Db 16 TPLGIFMILVLSICPGRTNLCNSHVSSTPKELP---SSNPSDIRSSLVSLDLEGVIFDD 72  
QY 46 ----SHDFGNITVTGGVICPSTADISRLQYAAN--GKSTFQVAARGHSLNGQAS 99  
Db 73 VHNVAKDFGNRYQPLPAILHPRSVFDISSNMKHIIVHLGSTSNLTVAAARGHSLNGQAL 132  
QY 100 VSGGVIIVNMTCI--TDVVVSKOKK--YADVAAGTLWVDVLKKTAEKGVSPVSWTDYLIHTV 156  
Db 133 AHQGVWIKMESLRSPDIRIYKQKQPVYVSGGEIWINILRETLYKGLSPKSWTDYLIHTV 192  
QY 157 GGTLSNGIGGOVFRNGPLYSNVLELDVITGKEMLTCSRQLNPELFGVGLGGLGQFGII 216  
Db 193 GGTLSNAGISGOAFKHPGQINNVIQLEIVTGKGEVVTCSKRNSELFFSVLGLGQFGII 252  
QY 217 TRARIVLDHAPKRAKWRFLYSDFTTTKDQERLISMANDIGVDYLEGOIFLSNGVVD-- 274  
Db 253 TRARISLEPAPHMVKWIRVLVSDFSASRDOEYLSKEKTF--DYVEGFVIINR--TDLL 308  
QY 275 ---TSFPPPSQSKVADLVKQHGIIYVLEVAKYDDNPLPIISKVIDTLTKTSLVLPGEI 331  
Db 309 NNWRSSFPNDSTQASRFKSDGKTLVLEVVKYFNPEEASMDQETGKLLSELNIPSTL 368  
QY 332 SMHDVAVDFLNRVHVENKLSLGLWELPHPLNLYVPKSRILDFHNGVVKDILLKQKS 391  
Db 369 PSSEVPYIEFLDRVHIAERKLRAKGLWEVPHPLNLLIPKSSIQAFATEVFNILTSNN-- 427  
QY 392 ASGLALTYPTNRKNDNRMSAMIPEIDEDVIYIIGLQSATP-----KDLPEVESVNEKI 446  
Db 428 -NGPILIVPVNOSKWKHTSLITP--NEDIFLVAFLPSAVPNSGKNLDLEYLLKQNRV 484  
QY 447 IRFCXDSGKIKOYLWHYTSKEDWIEHFGSKWDDFSKRDLPDPKLLSPGQDIF 501  
Db 485 MNFCAANLNKQYLPHYETQKWKSHFGKRWETFAQRKQAYDPLAILAPGORIF 539

RESULT 13

US-10-014-101-2  
; Sequence 2, Application US/10014101  
; Publication No. US20030074698A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmulling, Thomas  
; APPLICANT: Werner, Tom s  
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and  
; FILE REFERENCE: 1195-2  
; CURRENT APPLICATION NUMBER: US/10/014,101  
; PRIOR FILING DATE: 2001-12-10  
; PRIOR APPLICATION NUMBER: PCT/EP01/06833  
; PRIOR FILING DATE: 2001-06-16  
; PRIOR APPLICATION NUMBER: EP 00870132.8  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: US 60/258,415  
; PRIOR FILING DATE: 2000-12-27  
; PRIOR APPLICATION NUMBER: EP 01870053.4  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 575  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-014-101-2

Query Match 40.7%; Score 1056.5; DB 14; Length 575;  
Best Local Similarity 39.8%; Pred. No. 3.3e-89;  
Matches 213; Conservative 102; Mismatches 167; Indels 53; Gaps 12;  
QY 9 TLITVLM-----TKSSNGIKIDLPKSNLTLSTDPSTISAA----- 45  
Db 16 TELGIFMILVLSICPGRTNLCNSHVSSTPKELP---SSNPSDIRSSLVSLDLEGVIFDD 72

QY 46 ---SHDFGNITVTGGVICPSTADISRLQYAAN--GKSTFQVAARGHSLNGQAS 99  
Db 73 VHNVAKDFGNRYQPLPAILHPRSVFDISSNMKHIIVHLGSTSNLTVAAARGHSLNGQAL 132  
QY 100 VSGGVIIVNMTCI--TDVVVSKOKK--YADVAAGTLWVDVLKKTAEKGVSPVSWTDYLIHTV 156  
Db 133 AHQGVWIKMESLRSPDIRIYKQKQPVYVSGGEIWINILRETLYKGLSPKSWTDYLIHTV 192  
QY 157 GGTLSNGIGGOVFRNGPLYSNVLELDVITGKEMLTCSRQLNPELFGVGLGGLGQFGII 216  
Db 193 GGTLSNAGISGOAFKHPGQINNVIQLEIVTGKGEVVTCSKRNSELFFSVLGLGQFGII 252  
QY 217 TRARIVLDHAPKRAKWRFLYSDFTTTKDQERLISMANDIGVDYLEGOIFLSNGVVD-- 274  
Db 253 TRARISLEPAPHMVKWIRVLVSDFSASRDOEYLSKEKTF--DYVEGFVIINR--TDLL 308  
QY 275 ---TSFPPPSQSKVADLVKQHGIIYVLEVAKYDDNPLPIISKVIDTLTKTSLVLPGEI 331  
Db 309 NNWRSSFPNDSTQASRFKSDGKTLVLEVVKYFNPEEASMDQETGKLLSELNIPSTL 368  
QY 332 SMHDVAVDFLNRVHVENKLSLGLWELPHPLNLYVPKSRILDFHNGVVKDILLKQKS 391  
Db 369 PSSEVPYIEFLDRVHIAERKLRAKGLWEVPHPLNLLIPKSSIQAFATEVFNILTSNN-- 427  
QY 392 ASGLALTYPTNRKNDNRMSAMIPEIDEDVIYIIGLQSATP-----KDLPEVESVNEKI 446  
Db 428 -NGPILIVPVNOSKWKHTSLITP--NEDIFLVAFLPSAVPNSGKNLDLEYLLKQNRV 484  
QY 447 IRFCXDSGKIKOYLWHYTSKEDWIEHFGSKWDDFSKRDLPDPKLLSPGQDIF 501  
Db 485 MNFCAANLNKQYLPHYETQKWKSHFGKRWETFAQRKQAYDPLAILAPGORIF 539

RESULT 14

US-10-311-453-12  
; Sequence 12, Application US/10311453  
; Publication No. US20040031073A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmulling, Thomas  
; APPLICANT: Werner, Tom s  
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and  
; FILE REFERENCE: 1226-4  
; CURRENT APPLICATION NUMBER: US/10/311,453  
; CURRENT FILING DATE: 2002-12-16  
; PRIOR APPLICATION NUMBER: EP 00870132.8  
; PRIOR FILING DATE: 2000-06-16  
; PRIOR APPLICATION NUMBER: US 60/258,415  
; PRIOR FILING DATE: 2000-12-27  
; PRIOR APPLICATION NUMBER: EP 01870053.4  
; PRIOR FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 504  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-311-453-12

Query Match 38.3%; Score 993; DB 12; Length 504;  
Best Local Similarity 41.5%; Pred. No. 2.2e-83;  
Matches 217; Conservative 100; Mismatches 152; Indels 54; Gaps 14;  
QY 6 LMITLITVLMIT-----KSSNGIKIDLPKSNLTLSTDPSTISAAHDFGNITV 55  
Db 2 LIVRSFTLLSLSIAFKLACCFSS-----ISSLKALPLVGHLEFEHVHASKDFGNRYQL 57  
QY 56 TPGGVICPSTADISRLQ--YAANGKSTFQVAARGHSLNGQASVSGVIVNMTCIDT 113  
Db 58 IPLAVLHPKSVSDIATIRHWMGTHSOLTVAARGHSLNGQAOQTRHGIVITHMESLHP 117  
QY 114 -----VVVSKDKKXVADVAAGTLWVDVLKKTAEKGVSPVSWTDYLIHTVGGTLNGGIGGQ 168

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Db 118 QKQVSDPAPVVDVSGGELMINILHETLKYGLAPKSWTDYHLTVGGLTSLNAGISGQ 177
QY 169 VFRNGPLVSNVLELDVITGKGMELTCSRQLNPELFGVGLGQFGIITRARIVLDPHAPK 228
Db 178 AFRHGPQISNVHQLIEIVTGKEILNCTKRONSDLFNGVLGQFGIITRARIAPAP- 236
QY 229 RAKWFRMLYSDFTTFTKQERLISMANDIGVDYLEGQIFLS-NGVVDT---SFFPPSDQS 284
Db 237 -----TMDQEQQLIS-AQGHKFDYIEGFVIINRTGLLNSWRLSF--TAEAP 278
QY 285 KVADLVKQHG-IIVYLEVAKYDDNPLIISKVDTLTKTSLYLPFGFTSMHDVAYFDFLN 343
Db 279 LEASQKFDGRTLYCLELAKYLKQDNKDVINQEVKETLSLSYVTSITLFTTEVAYEAFD 338
QY 344 RVHVEENKLRSLGLWELPMPWLNLYVPKSRILDFHNGVVKDILKQKASGLALLYPTNR 403
Db 339 RVHSEVKLRSGQWEPHPWLNLLVPSKINEFARGVFGNLL--TDTSGPVIYVPVK 396
QY 404 NKWNRMSAMTPEIDEDVIYIIGLQSATP---KD-LPEVESVNEKIIIFCKDSGKIK 458
Db 397 SKWDNQTSVATPE--BEVYFVILVAILTSASPGSAGKGVVEILRRNRRIEFSEAGIGLK 454
QY 459 QYLMHYTSKEDWIEHFGSKWDDFSKRKDLFDPKLLSPGQDIF 501
Db 455 QYLPHYTTREWRSHFGDKWGEFVRKSRYPDLAILAPGHRIF 497
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RESULT 15
US-10-014-101-12
; Sequence 12, Application US/10014101
; Publication No. US20030074698A1
; GENERAL INFORMATION:
; APPLICANT: Schmulling, Thomas
; APPLICANT: Werner, Tom S
; TITLE OF INVENTION: Method for modifying plant morphology, biochemistry and
; FILE OF INVENTION: physiology
; FILE REFERENCE: 1195-2
; CURRENT APPLICATION NUMBER: US/10/014,101
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/06833
; PRIOR FILING DATE: 2001-06-16
; PRIOR APPLICATION NUMBER: EP 00870132.8
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/258,415
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: EP 01870053.4
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-014-101-12
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Query Match 38.3%; Score 993; DB 14; Length 504;
Best Local Similarity 41.5%; Pred. No. 2.2e-83;
Matches 217; Conservative 100; Mismatches 152; Indels 54; Gaps 14;

QY 6 LMITLITVLMIT-----KSSNGIKIDLPKSLNLTJLSTDPSTIISAASHDFGNITTV 55
Db 2 LIVRSFTILLSCIAKLAACFFSS----ISSLKALPLVGHLEFEHVHASKDFGNRYQL 57
QY 56 TPGGVICPSSTADISRLQ--YAANGKSTFQVAARGGSHLNGQASVSGGVVNNMTCITD 113
Db 58 IPLAVLHPKSVSDIATIRHWMGTHSQLTVAARGGSHSQQAQTRHGIVIHMSLHP 117
QY 114 -----VVVSKDKKADYVAAGTLDVLTAEKGVSPVSWTDYHLTVGGLTSLNAGISGQ 168
Db 118 QKQVSDPAPVVDVSGGELMINILHETLKYGLAPKSWTDYHLTVGGLTSLNAGISGQ 177
QY 169 VFRNGPLVSNVLELDVITGKGMELTCSRQLNPELFGVGLGQFGIITRARIVLDPHAPK 228
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Search completed: April 5, 2004, 17:51:28  
Job time : 48 secs